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(21) International Application Number: PCT/US00/08621 (22) International Filing Date: 31 March 2000 (31.03.00) (30) Priority Data: <table border="0"> <tr> <td>60/127,607</td> <td>31 March 1999 (31.03.99)</td> <td>US</td> </tr> <tr> <td>60/127,636</td> <td>2 April 1999 (02.04.99)</td> <td>US</td> </tr> <tr> <td>60/127,728</td> <td>5 April 1999 (05.04.99)</td> <td>US</td> </tr> <tr> <td>09/540,763</td> <td>30 March 2000 (30.03.00)</td> <td>US</td> </tr> </table> (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications <table border="0"> <tr> <td>US</td> <td>60/127,607 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>31 March 1999 (31.03.99)</td> </tr> <tr> <td>US</td> <td>60/127,636 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>2 April 1999 (02.04.99)</td> </tr> <tr> <td>US</td> <td>60/127,728 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>5 April 1999 (05.04.99)</td> </tr> <tr> <td>US</td> <td>09/540,763 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>30 March 2000 (30.03.00)</td> </tr> </table> (71) Applicant (for all designated States except US): CURAGEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).		60/127,607	31 March 1999 (31.03.99)	US	60/127,636	2 April 1999 (02.04.99)	US	60/127,728	5 April 1999 (05.04.99)	US	09/540,763	30 March 2000 (30.03.00)	US	US	60/127,607 (CIP)	Filed on	31 March 1999 (31.03.99)	US	60/127,636 (CIP)	Filed on	2 April 1999 (02.04.99)	US	60/127,728 (CIP)	Filed on	5 April 1999 (05.04.99)	US	09/540,763 (CIP)	Filed on	30 March 2000 (30.03.00)	(72) Inventors; and (75) Inventors/Applicants (for US only): SHIMKETS, Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US). LEACH, Martin [GB/US]; 884 School Street, Webster, MA 01570 (US). (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published Without international search report and to be republished upon receipt of that report.	
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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"																															
(57) Abstract <p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>																															

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NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2*n*-1, wherein *n* is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2*n*, wherein *n* is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

In a another aspect, the invention provides a method of determining the presence of or
30 predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The
5 polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded
10 polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide.
15 Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled
20 "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal
25 identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF n according to the invention (wherein n is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2 n -1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2 n . For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a
30 polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected.

Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu/>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

5 **Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 10
15 Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoetin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

25 **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5 **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_rna_bind	DNA/RNA binding protein/factor
	dna_rna_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase	phosphorylase
	PIR	PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase	polymerase
	potassium_channel	potassium channel protein
	prostaglandin	prostaglandin
	protease	protease
	proteaseinhib	protease inhibitor
	reductase	reductase
10	ribosomalprot	ribosomal associated protein
	RTR	EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
	SIM	similar
15	SPTR	EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
	struct	structural associated protein
20	sulfotransferase	sulfotransferase
	SWP	SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN	SWISS-PROT Update (release 11-NOV-98)
	synthase	synthase
25	tgf	transforming growth factor
	tgfreceptor	transforming growth factor receptor
	thioesterase	thioesterase
	thiolase	thiolase
	tm7	seven transmembrane domain G-protein coupled receptor
30	tnf	necrosis factor receptor
	traffic	tumor necrosis factor
	tnfreceptor	tumor trafficking associated protein
	TRN	EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor	transcription factor
	transferase	transferase
	transport	transport protein
	tubulin	tubulin
40	ubiquitin	ubiquitin
	unclassified	Protein not categorized into one of the aforementioned protein families
	water channel	water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are
5 useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to
10 identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

ORFX Nucleic Acids

15 The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

20 In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the
25 disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

analogs and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic
20 acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any
5 of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

10 A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an
15 automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or
20 complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be
25 chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence
30 shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

5 As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.

10 Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the
15 nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,
20 and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but
25 differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or
30 analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (e.g., 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and
5 Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A
10 non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as
15 employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative mutations

20 In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions
25 leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present
30 invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2 n (wherein $n = 1$ to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2 n -1 for the corresponding n , such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-1124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX-like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein.

Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2n (wherein n = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2n (wherein n = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2n (wherein n = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2n (wherein n = 1 to 3161).

Determining homology between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch 1970 J Mol Biol 48: 443-453*. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5 For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10 In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells
15 (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion
20 proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX
25 cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of
30 ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477).

Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can
5 be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the proteins of the invention.

10 An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in
15 any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one
20 embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6 contiguous amino acids of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example,
25 the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as
30 immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein $n = 1$ to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND
5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*,
10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by
15 techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized
20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent
25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J. Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, e.g., the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," *Reviews--Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

5 Transgenic animals

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences
10 have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal
15 includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous
20 recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding
25 nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to
30 the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

5 The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, 10 antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human 15 serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

20 A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent 25 such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with 30 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5 This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

Screening Assays

10 The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

15 In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam
20 (1997) *Anticancer Drug Des* 12:145).

25 Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

30 Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409), plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirlla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested
5 with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an
10 individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA
15 sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency
20 of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to
25 differentiate individuals. The noncoding sequences of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent).

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

Use of Partial ORFX Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, *e.g.*, hair or skin, or body fluids, *e.g.*, blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs: __ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

10 Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

20 The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX
5 nucleic acids of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) may be used to detect DNA
containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene,
or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue,
as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological
10 sample involves obtaining a biological sample from a test subject and contacting the biological
sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*,
mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected
in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled
15 nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid
probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID
NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion thereof, such as an oligonucleotide of at least 15,
30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under
stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable
probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein,
preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably,
monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The
term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of
the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent
that is directly labeled. Examples of indirect labeling include detection of a primary antibody
using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin
such that it can be detected with fluorescently labeled streptavidin. The term "biological sample"
is intended to include tissues, cells and biological fluids isolated from a subject, as well as
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention
can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for
5 identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained
10 from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder
15 associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample
20 is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a
25 proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion
30 of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g., U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.

5 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

10 In other embodiments, genetic mutations in ORFX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through
15 long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one
20 complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS*
25 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeye *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

30 Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, e.g., Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, e.g., Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5 The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10 Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

15 Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be
20 considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate
25 dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30 Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a
5 common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic
10 polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor
15 metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic
20 response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation
25 content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus
30 enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent
5 determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical
10 trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an
15 agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by
20 Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the
25 agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a
30 subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

Determination of the Biological Effect of a Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models,
5 in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

10 Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or
15 suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number
20 in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the
25 epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein.

Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5 A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),
10 transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein
15 (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for
20 example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be
25 treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons, Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immunol* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy
5 in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without
10 limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue
15 transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in
20 conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the
25 corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte
30 antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples
30 of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be
5 capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a
10 subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression
15 of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells.
20 In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on
25 the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a
30 B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Invest* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

5 A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

20 Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

25 A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

30

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and
ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and
their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell
interactions and their ligands (including without limitation, cellular adhesion molecules (such as
selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,
10 antigen recognition and development of cellular and humoral immune responses). Receptors and
ligands are also useful for screening of potential peptide or small molecule inhibitors of the
relevant receptor/ligand interaction. A protein of the present invention (including, without
limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of
receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the
following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:
CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and
Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp.*
Med. 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenberg *et al.*,
J Immunol Methods 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the
inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example,
cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory
process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
of other factors which more directly inhibit or promote an inflammatory response. Proteins
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or
5 entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

10 EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular
15 embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to
20 those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gij4691395[embjCAB41562.1] - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gij2828506[spjP71559]SUCC. MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)	Contains protein domain (PF00349) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264636, 264587
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264805, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264780, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22278002, 264563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gij4415926[gbjAAD20137] - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264595, 264598, 264758, 264603, 264604, 264780, 264782, 264683, 264768, 264787, 264689, 35695917, 264690, 264692, 264693, 33857109, 264628, 264629, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264488
8	56924278 (15, 16)	Novel Protein sim. GBank gij585562[spjQ06458]NIRB. KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT		reductase	264907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79556459 (19, 20)			UNCLASSIFIED	264906
11	20414027 (21, 22)			UNCLASSIFIED	264605
12	94141210 (23, 24)	Novel Protein sim. GBank gij3878145[embjCAA99871] - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gij2832781[embjCAA12845] - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696286, 35696052, 264510, 35695917, 264691, 264628, 35696423, 264555, 264558, 264559, 83373044
15	20456307 (29, 30)	Novel Protein sim. GBank gij1710791[spjQ10234]RT05. SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20292744 (33, 34)	Novel Protein sim. GBank gjl1174884[sp]P44391[URE1_HAEIN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)]	Contains protein domain (PF00449) - Urease	264600	
18	80246804 (35, 36)	Novel Protein sim. GBank gij2281102 (AC002333) - SF16 Isolog [Arabidopsis thaliana]		28331827, 264555, 264557, 264638, 264558	
19	80076624 (37, 38)	Novel Protein sim. GBank gij2506112[sp]P43672[UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP]	UNCLASSIFIED transport	22278998, 264907, 264910, 264600, 264693	
20	20724558 (39, 40)	Novel Protein sim. GBank gij1730203[sp]P50442[GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)]	UNCLASSIFIED	22278995, 264908, 265008, 265010, 265011, 264602, 264605, 264766, 264688, 21906764, 264681, 18108376, 264636, 18108387, 264486	
21	80417554 (41, 42)	Novel Protein sim. GBank gij1877329[emb]CAB07071 - (Z82771) fadE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	264685 264488, 264907, 264909, 264600, 264602, 264603, 264605, 264682, 264766, 32833986, 264636, 264486	
22	11705858 (43, 44)			264600	
23	80418178 (45, 46)			264593	
24	20291697 (47, 48)			22278998, 56182435, 265018, 264566	
25	80253774 (49, 50)			18108370, 35698423, 264635, 264555	
26	80255394 (51, 52)				
27	80235795 (53, 54)	Novel Protein sim. GBank gij4808369[emb]CAB42783.1] - (AL049841) putative 30S ribosomal protein S14 (Streptomyces coelicolor)	UNCLASSIFIED ribosomal prot		
28	78403561 (55, 56)			264638	
29	82448765 (57, 58)	Novel Protein sim. GBank gij3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]	UNCLASSIFIED kinase	264601, 284762, 264766, 264769, 264638	
30	78199333 (59, 60)				
31	19848158 (61, 62)			264908, 265018, 264687, 21906764, 21906766	
32	82448495 (63, 64)	Novel Protein sim. GBank gij3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	264534	
33	78582628 (65, 66)	Novel Protein sim. GBank gij2129003[pir]G64507 - Hypothetical protein MJ1665 - Methanococcus jannaschii	UNCLASSIFIED	264905, 264605, 264762, 264766, 264687, 264689	
34	87467657 (67, 68)			264687	
35	95005170 (69, 70)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	60432289, 264600, 264602, 264760, 18108357, 264768, 265020, 264691	
36	19842042 (71, 72)	Novel Protein sim. GBank gij3287739[sp]P73538[BIOB_SYNY3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)]	UNCLASSIFIED	264600, 264687, 264556, 264639	
37	20368215 (73, 74)	Novel Protein sim. GBank gij2313134[gb]AAD07128.1] - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26695]	synthase dehydrogenase	264566 264603	

38	20466334 (75, 76)	Novel Protein sim. GBank gij3805970[emb CAA06231] - (AJ004833) periplasmic nitrate reductase, large subunit [Rhodospseudomonas sp.]			reductase	264605	
39	94300715 (77, 78)	Novel Protein sim. GBank gij1929448 (L63543) - endodermin [Xenopus laevis]		Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264906, 264907, 68712502, 264908, 264909, 264511, 265008, 264910, 55812038, 264758, 265011, 264762, 264682, 264763, 264764, 264766, 265022, 264693, 264628, 264631, 264634, 264635, 264555, 264638, 18109381, 264558, 18109385, 264482, 264592	
40	20636625 (78, 80)				UNCLASSIFIED	264591, 35895917	
41	80023287 (81, 82)	Novel Protein sim. GBank gij85405[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264602	
42	20724566 (83, 84)				synthase	264605	
43	20467069 (85, 86)	Novel Protein sim. GBank gij3820584 (AF086781) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]					
44	13085287 (87, 88)	Novel Protein sim. GBank gij2494784[sp Q50729 GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]		Contains protein domain (PF00956) - GMP synthase C terminal domain	synthase	264769, 264636	
45	39384711 (89, 90)	Novel Protein sim. GBank gij1881736 (U89888) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]			UNCLASSIFIED	264769, 264510, 264508	
46	95003398 (91, 92)				ngf	264566	
47	11688624 (93, 94)				UNCLASSIFIED	264689	
48	78407218 (95, 96)					18108385, 264635, 264828	
49	21659844 (97, 98)				UNCLASSIFIED	264603	
50	80503996 (99, 100)					264508, 264603, 264769, 264689, 264636, 264558, 264488	
51	80255569 (101, 102)	Novel Protein sim. GBank gij3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]			UNCLASSIFIED	264593, 18108387	
52	78208528 (103, 104)	Novel Protein sim. GBank gij3914992[sp Q26284 ISM41_HEMPU - 41 KD SPIGULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)]			struct	264634	
53	36986970 (105, 106)	Novel Protein sim. GBank gij3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]			UNCLASSIFIED	264762	
54	78570887 (107, 108)						
55	80202703 (109, 110)	Novel Protein sim. GBank gij1633572 (U52084) - Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]			UNCLASSIFIED	264630, 264909, 264766	
56	8758408 (111, 112)	Novel Protein sim. GBank gij4321580[gb A015785] - (AF050114) alginate lyase [Pseudomonas sp. W7]				29331824, 264102, 285018, 18108376	
57	11223388 (113, 114)			Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264604	
						284557	

58	91227508 (115, 116)	Novel Protein sim. GBank gi 5816074 gb AAD45616.1 AF08194 - (AF081943) protease- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	56182575, 264259, 60432049, 35686052, 66712502, 264909, 265008, 265010, 265011, 264681, 29148784, 35695917, 60170615, 264691, 264692, 264693, 18108374, 35696423, 56182323, 60432113 264600, 264688, 264638
59	80077371 (117, 118)	Novel Protein sim. GBank gi 1172920 sp P45830 RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTTRANSFERASE	Contains protein domain (PF00953) - transferase Glycosyl transferase	
60	12956341 (119, 120)	Novel Protein sim. GBank gi 1172920 sp P45830 RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTTRANSFERASE		
61	80426808 (121, 122)	Novel Protein sim. GBank gi 11710216 (U78260) - unknown [Homo sapiens]		264689 264766
62	13504868 (123, 124)			
63	16474553 (125, 126)			264630
64	20724578 (127, 128)	Novel Protein sim. GBank gi 420945 p j A47041 - transposase homolog (insertion element ISAE1) - Alcaligenes eutrophus	UNCLASSIFIED UNCLASSIFIED	265019 264602
65	78326308 (129, 130)	Novel Protein sim. GBank gi 3122312 sp O06134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - kinase Pyruvate kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gi 3828723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]	transport	22278986, 264558
67	78952543 (133, 134)	Novel Protein sim. GBank gi 231985 sp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE [40 KD ANTIGEN]	dehydrogenase	265021
68	79817382 (135, 136)			264909
69	79841784 (137, 138)			264908
70	79871329 (139, 140)		UNCLASSIFIED	264908, 264908
71	65897456 (141, 142)		UNCLASSIFIED	264602, 265021
72	87734977 (143, 144)	Novel Protein sim. GBank gi 4415926 gb AAD20157 - (AC006282) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264480, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87188474, 264682, 264766, 264688, 264689, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 264629, 264631, 264639, 22278000
73	80025241 (145, 146)		UNCLASSIFIED	60424178, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 18108387
74	20377410 (147, 148)		UNCLASSIFIED	264605
75	11818032 (149, 150)	Novel Protein sim. GBank gi 2653098 emb CAA15914 - (AL021787) vacuolar protein sorting [Schizosaccharomyces pombe]	UNCLASSIFIED	264689
76	95105303 (151, 152)	Novel Protein sim. GBank gi 446881 emb CA838212 - (AL035601) putative protein [Arabidopsis thaliana]		
77	10144718 (153, 154)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	83373044, 264906, 264557
78	87582568 (155, 156)		UNCLASSIFIED	264563
			UNCLASSIFIED	264604

79	94140180 (157, 158)	Novel Protein sim. GBank gij5689453[bj][BAA83010.1] - (AB028881) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		3568286, 2227898, 29331822, 29331824, 29331825, 29331827, 284905, 284906, 284907, 66712502, 284908, 284909, 285008, 285009, 284910, 60170831, 55812038, 33109954, 265017, 265018, 264288, 264768, 56181592, 21906785, 21906789, 28148784, 265020, 284690, 284691, 284692, 284693, 60431528, 35698423, 284631, 284632, 284634, 284636, 284639, 83373044, 264564, 284566, 284567
80	82314840 (159, 160)			UNCLASSIFIED	284769, 284601, 265006, 284910, 284604, 284605, 284634, 284636, 284805, 284782, 284637, 284592, 284628, 284907, 284691, 284908, 284587, 284909, 284786
81	20467247 (161, 162)	Novel Protein sim. GBank gij1723442[sp]Q10258[YD2A_SCHPO - HYPOTHETICAL 89.0 KO PROTEIN C58F8.10 IN CHROMOSOME I		reductase	284605
82	16331388 (163, 164)	Novel Protein sim. GBank gij2898869 (AF045770) - methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]		dehydrogenase	284567
83	94741180 (165, 166)	Novel Protein sim. GBank gij3402673 (AC004697) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 284508, 284509, 284905, 284908, 284909, 284511, 284591, 284593, 284594, 284595, 284596, 284768, 284603, 284760, 284681, 18108351, 284762, 284682, 284784, 284684, 284766, 284686, 284632, 284637, 284537, 284638, 284639, 18108385, 284566
84	80355375 (167, 168)	Novel Protein sim. GBank gij1173364[sp]P45380[SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTIporter)]		transport	284508, 284908, 284907, 284908, 284909, 284910, 284760, 284763, 284764, 284768, 284768, 284769, 35695855, 284636, 284637
85	80499600 (169, 170)	Novel Protein sim. GBank gij2120998[p]rj[S70682 - glycosyltransferase homolog - Bordetella pertussis (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]		transferase	284605, 284762, 284687, 284769, 18108374, 284636, 284486
86	38559043 (171, 172)	Novel Protein sim. GBank gij3256023[emb]CAA17228.1] - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]			284910
87	13858808 (173, 174)			UNCLASSIFIED	284093

88	95344718 (175, 176)	Novel Protein sim. GBank gl 559703 dbj BAA07552 - (D38549) ha1025 is new [Homo sapiens]		52644507, 52846365, 18108398, 65274572, 56182575, 56994075, 35698286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432228, 29331827, 29331828, 35696052, 33856970, 264105, 264508, 264905, 264906, 264907, 264908, 29331830, 66712502, 52844045, 58182435, 265007, 265009, 264910, 60170831, 264592, 60431735, 60433356, 33657402, 264757, 60433438, 55812038, 264758, 21906754, 52646317, 33109954, 52844296, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265018, 264448, 264369, 264288, 264766, 52844228, 21906768, 21908787, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 60170615, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33857349, 35695763, 264628, 263972, 18108374, 55810764, 35696423, 55811576, 65274791, 35695655, 60431850, 264636, 52844332, 56182323, 60170394, 83373044, 18108385, 18108387, 18108388, 58526486, 87168518, 60432113, 22279000, 22279002, 264482, 264564, 264489, 264600
89	60077389 (177, 178)	Novel Protein sim. GBank gl 1710383 sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		
90	82115999 (179, 180)			
91	78906950 (181, 182)	Novel Protein sim. GBank gl 2498891 sp P78403 YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGK INTERGENIC REGION	UNCLASSIFIED protease	264760 265006
92	78554871 (183, 184)	Novel Protein sim. GBank gl 3367754 emb CAA20078 - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]	UNCLASSIFIED	264691
93	80496778 (185, 186)	Novel Protein sim. GBank gl 2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		
94	79846649 (187, 188)	Novel Protein sim. GBank gl 1171919 sp P45920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUAA	ATPase_associated Contains protein domain (PF00571) - transport CBS domain	264907, 264908, 264910, 265009, 264605, 264769 264906
95	11080238 (189, 190)			264594

96	94322126 (181, 182)	Novel Protein sim. GBank gii4588560[dbj]BAA76802.1] - (AB023175) KIA0858 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 284259, 29331822, 29331826, 35696052, 29146499, 284509, 284806, 284907, 284908, 284909, 285007, 285008, 284910, 285009, 284593, 285010, 285017, 284604, 285019, 18108351, 284288, 284766, 284768, 284769, 21906765, 21906767, 21906769, 285020, 284692, 33657182, 35695763, 284628, 284629, 18108379, 284831, 284636, 18108381, 284559, 18108382, 83373044, 22278002, 284508
97	78605200 (193, 194)	Novel Protein sim. GBank gii4583559[embj]CAB40388.1] - (AJ005255) OxyR [Erwinia chrysanthemi]		UNCLASSIFIED	
98	78427000 (195, 196)	Novel Protein sim. GBank gii1001693[dbj]BAA10430] - (DB4002) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	284809
99	20466524 (197, 198)	Novel Protein sim. GBank gii1168479[sp]P43925[IEFG_HAEN - ELONGATION FACTOR G (EF-G)]		UNCLASSIFIED	284605
100	78640113 (199, 200)	Novel Protein sim. GBank gii460887[prj]S37485 - gene		UNCLASSIFIED	284693
101	80203288 (201, 202)	Novel Protein sim. GBank gii2894166[embj]CAA11773.1] - (AJ223988) PCZA361.18 [Amycolatopsis orientalis]		UNCLASSIFIED	285020, 284102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank gii1731040[sp]P54509[QHH_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION]		synthase	284605
103	20466368 (205, 206)	Novel Protein sim. GBank gii854085[embj]CAA56337] - (X63413) U98 [Human herpesvirus 6]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	284605
104	80247572 (207, 208)	Novel Protein sim. GBank gii1685117 (U70770) - furrowed [Drosophila melanogaster]		UNCLASSIFIED	284591, 284595, 264602
105	78605208 (208, 210)	Novel Protein sim. GBank gii1705503[sp]P54729[BS4_MOUSE - BS4 PROTEIN]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complement	284508
106	28382058 (211, 212)	Novel Protein sim. GBank gii4887229[gb]AAD32244.1[AF150755] microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	284511, 285008
107	80057791 (213, 214)	Novel Protein sim. GBank gii299120] similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]		ATPase-associated	28331824, 284591, 21906754, 285019
108	80237638 (215, 216)	Novel Protein sim. GBank gii2330781[embj]CAB11265] - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]	Contains protein domain (PF00005) - ABC transporter	transport	18108374, 35685917, 22278996, 264113, 284600, 284602, 284603, 285017, 284910, 284906, 284636, 284766
109	95194148 (217, 218)			UNCLASSIFIED	284758, 284603, 284630, 284636, 284637
110	78582823 (219, 220)				284687
111	39565458 (221, 222)				284584
112	7856038 (223, 224)			UNCLASSIFIED	284908
113	17859439 (225, 226)			UNCLASSIFIED	285007
114	80502101 (227, 228)			UNCLASSIFIED	284769

115	80251003 (229, 230)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52645156, 52845080, 33656870, 264592, 21908754, 27486264, 18108379, 35696423, 264635, 52644332, 18108382
116	81288888 (231, 232)				264905, 264908, 264907, 264908, 264909, 264910, 264756, 265010, 264763, 264682, 264764, 264766, 264685, 264686, 264788, 264789, 33657023, 264683, 33657109, 264628, 18108374, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 56528488, 264565, 264566
117	79836895 (233, 234)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	264639, 264693
118	80222170 (235, 236)				263974
119	91013071 (237, 238)	Novel Protein sim. GBank gij732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 28331824, 60432289, 265007, 60433438, 264603, 264605, 18108351, 264769, 264689, 265020, 264534, 27486261, 264558, 83373044, 18108385, 264564
120	8756401 (239, 240)	Novel Protein sim. GBank gij2131219 [pir][S50157 - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)]		kinase	264603
121	80026153 (241, 242)				264595
122	20457620 (243, 244)	Novel Protein sim. GBank gij2052147 [emb][CAB08137] - (Z94752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - transferase Ribosomal RNA adenine dimethylases		264605
123	8758278 (245, 246)				264604
124	79104017 (247, 248)	Novel Protein sim. GBank gij2833385 [sp]Q43134 [UGST_SORBI - GRANULE-BOUND GLYCOPROTEIN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265006, 265007, 265008, 265010, 265011, 18108355, 18108378, 18108380, 18108384
125	87797986 (249, 250)	Novel Protein sim. GBank gij475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00080) - misc_channel		264508, 264906, 265009, 264596, 22278002
126	56701283 (251, 252)	Novel Protein sim. GBank gij5102785 [emb][CAB45200.1] - (AL079308) putative transcriptional regulator [Streptomyces coelicolor]	Ligand-gated ion channel		264511
127	20467287 (253, 254)				264605
128	80248473 (255, 256)	Novel Protein sim. GBank gij130120 [sp]P23820 [PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED phosphatase	264907, 264909, 264910, 264600, 264601, 264603, 264605, 18108351, 264693, 264557
129	95280543 (257, 258)	Novel Protein sim. GBank gij2506493 [sp]P38036 [YGCB_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35696423, 35695855, 264600, 264602, 264603, 264604, 264605, 264508, 264908, 264564, 264628, 264682, 264565, 264683
130	80085583 (259, 260)	Novel Protein sim. GBank gij854065 [emb][CAA58337] - (X83413) U88 [Human herpesvirus 6]			264634
131	94995022 (261, 262)	Novel Protein sim. GBank gij1076038 [sp] [S54860 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 264769, 29331826, 264688, 22278996, 265021, 264600, 264511, 264601, 264602, 264605, 264905, 264638

132	10887692 (263, 284)	Novel Protein sim. GBank gll1877340[emb]CAB07058] - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264636 264905, 264689
133	94630883 (265, 266)	Novel Protein sim. GBank gll1877340[emb]CAB07058] - (Z92771) accA3 [Mycobacterium tuberculosis]			
134	79834680 (267, 268)	Novel Protein sim. GBank gll1877340[emb]CAB07058] - (Z92771) accA3 [Mycobacterium tuberculosis]		dehydrogenase	264905, 264605, 265021
135	19885057 (269, 270)	Novel Protein sim. GBank gll1460074[emb]CAB01049] - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			264634
136	79846083 (271, 272)	Novel Protein sim. GBank gll212589[emb]CAA7351] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]		synthase	264508
137	79819770 (273, 274)				
138	79835971 (275, 276)	Novel Protein sim. GBank gll5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264683, 264685, 264686, 264691, 264692, 264693 18108374, 18108385, 33657109, 33657182, 265010, 22278998, 265006, 265007, 265008, 265009, 264693
139	86880078 (277, 278)	Novel Protein sim. GBank gll5689912[emb]CAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01617) - Chorismate mutase	dehydrogenase	22278996, 265007, 264910, 60433356, 265010, 264602, 264605, 264766, 264688, 264769, 264693, 32833986, 18108374, 18108387
140	79825759 (279, 280)			UNCLASSIFIED	264908
141	20700094 (281, 282)			nuclease	264600 264602, 265017
142	80028104 (283, 284)	Novel Protein sim. GBank gll3581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]			
143	11072274 (285, 286)			UNCLASSIFIED	264600
144	95008102 (287, 288)	Novel Protein sim. GBank gll3334127[sp]P97303BAC2_MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)			263976, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264556, 264908, 264629, 264639
145	80027058 (289, 290)	Novel Protein sim. GBank gll3757569[emb]CAA21315] - (AL031863) 1-evidence=predicted by content: 1; method=genefinder;084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]		UNCLASSIFIED	22278996, 264602
146	13085662 (291, 292)	Novel Protein sim. GBank gll140807[sp]P24538[Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN]	Contains protein domain (PF01675) - Transposase		264687
147	94320366 (293, 294)	Novel Protein sim. GBank gll2827608[emb]CAA16663] - (AL021646) uvrD2 [Mycobacterium tuberculosis]		helicase	264905, 264906, 264909, 264510, 265009, 60433356, 264600, 264601, 264604, 264605, 264687, 264769, 18108385, 65274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank gll2916947[emb]CAA17585] - (AL021989) hypothetical protein Rv0986 [Mycobacterium tuberculosis]		transport	265009, 265010, 264600, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (297, 298)	Novel Protein sim. GBank gij1723073[sp]Q11040[Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01 (AJ224340) GBank gij3724125[emb]CAA110051 - sanfrancisco]	Contains protein domain (PF000005) - ABC transporter	transport	265010, 264600, 264601, 264603, 264604, 27486265, 264636
150	20294748 (299, 300)	Novel Protein sim. GBank gij3724125[emb]CAA110051 - sanfrancisco]			264600
151	20726390 (301, 302)	Novel Protein sim. GBank gij1729312[sp]P07651[DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	264602
152	95002877 (303, 304)	Novel Protein sim. GBank gij2497952[sp]P55667[Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM		peptidase	264602
153	80256665 (305, 306)	Novel Protein sim. GBank gij3123021[sp]Q90508[VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	264593
154	82305966 (307, 308)	Novel Protein sim. GBank gij419697[pir]JUN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	mapolymerase	264910, 264762, 264691, 264634 264605
155	20429889 (309, 310)	Novel Protein sim. GBank gij628710[pir]JS41739 - hypothetical protein - Escherichia coli		UNCLASSIFIED	264565
156	39564742 (311, 312)	Novel Protein sim. GBank gij3695013 (AF052586) - Citra (Pseudomonas aeruginosa)	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/HrcC family	hydrolase	264691
157	10358887 (313, 314)	Novel Protein sim. GBank gij1073072[pir]C55543 - cnaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	264805
158	79761838 (315, 316)	Novel Protein sim. GBank gij1073072[pir]C55543 - cnaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	265008 264605
159	78890376 (317, 318)	Novel Protein sim. GBank gij1123023[sp]P46789[RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat		
160	11075119 (319, 320)	Novel Protein sim. GBank gij6304869[emb]CAB46028.1] - (AL031685) dJ863K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00327) - Ribosomal protein L30p/L7e	ribosomal prot	22278996, 264600, 264603, 35695917, 32833988, 35696423, 264636
161	80055007 (321, 322)	Novel Protein sim. GBank gij6304869[emb]CAB46028.1] - (AL031685) dJ863K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukin	264112, 264532, 22279002
162	80016371 (323, 324)	Novel Protein sim. GBank gij2681691[emb]CAA15795] - (AL009204) putative protease [Streptomyces coelicolor]		UNCLASSIFIED	264639
163	11692308 (325, 326)	Novel Protein sim. GBank gij4416478[gb]AAD20378] - (AF125999) transposase [Mycobacterium avium]		UNCLASSIFIED	264905, 264907, 264600 264691
164	80077902 (327, 328)	Novel Protein sim. GBank gij4416478[gb]AAD20378] - (AF125999) transposase [Mycobacterium avium]		UNCLASSIFIED	264605, 264486
165	10856067 (329, 330)	Novel Protein sim. GBank gij76177[pir]Q9ECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli		UNCLASSIFIED	265010
166	88095003 (331, 332)	Novel Protein sim. GBank gij76177[pir]Q9ECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli			264600
167	16395460 (333, 334)	Novel Protein sim. GBank gij76177[pir]Q9ECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli			264556, 264557, 264558, 264559
168	80079362 (335, 336)	Novel Protein sim. GBank gij76177[pir]Q9ECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli			
169	80239581 (337, 338)	Novel Protein sim. GBank gij76177[pir]Q9ECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli			

170	79812364 (339, 340)	Novel Protein sim. GBank gij140888[sp]P278471YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECO-PLDB INTERGENIC REGION (F138)	Contains protein domain (PF01810) - LysE type translocator		264906 264595, 264604
171	85293073 (341, 342)				
172	37797007 (343, 344)	Novel Protein sim. GBank gij4210905[g]b[AAD12048.1] - (AF045609) AgIG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264769
173	57529860 (345, 346)	Novel Protein sim. GBank gij132854[sp]P02387[RL2_ECOLI - 50S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00181) - Ribosomal Proteins L2	ribosomal prot	264769
174	95293078 (347, 348)	Novel Protein sim. GBank gij1881350[d]b[BAA19377] - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIBIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]		transport	264510, 264593, 264602, 264603, 264605, 264762, 264693
175	79756270 (349, 350)	Novel Protein sim. GBank gij2072722[emb]CAB08326[- (Z95121) manA [Mycobacterium tuberculosis]		isomerase	264565
176	80066896 (351, 352)	Novel Protein sim. GBank gij1055198 (U40187) - similar to PIR-A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen		UNCLASSIFIED	264907, 264910, 264681, 264558
177	86684852 (353, 354)	[Caenorhabditis elegans] Novel Protein sim. GBank gij2326738[emb]CAB10952[- (Z98286) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	264768, 60424179, 264687, 264688, 264769, 29331826, 60432289, 18108376, 264689, 18108387, 32833986, 22278996, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264762, 264636, 264906, 264564, 264637, 264638, 264486, 60433356, 264766
178	79559528 (355, 356)	Novel Protein sim. GBank gij1906596 (U81788) - kinasin-73 [Drosophila melanogaster]		struct	264693, 33657109, 264635
179	20263112 (357, 358)			UNCLASSIFIED	264563
180	80488958 (359, 360)	Novel Protein sim. GBank gij1169367[sp]P45256[DNAB_HAEIN - REPLICATIVE DNA HELICASE		helicase	264769
181	79585369 (361, 362)	Novel Protein sim. GBank gij3170615 (AF038485) - DOC4 [Mus musculus]		UNCLASSIFIED	21808787, 264635, 264639, 18108384
182	80577809 (363, 364)				
183	11614017 (365, 366)	Novel Protein sim. GBank gij1076627[pir]JS54172 - Inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco		UNCLASSIFIED	264259, 35666052, 56182435, 264511, 265018, 33657109, 264555, 264586
184	10174167 (367, 368)	Novel Protein sim. GBank gij4371280[g]b[AAD18138] - (AC006260) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264680 264510

185	21660822 (369, 370)	Novel Protein sim. GBank gl 3006178 emb CAA18398.1 - (AL022304) putative mima transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gl 2828802 sp P94408 CYCLE_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION		transport	264595
187	80186611 (373, 374)	Novel Protein sim. GBank gl 3150260 emb CAA19178 - (AL023834) cyclin [Schizosaccharomyces pombe]		UNCLASSIFIED	264389
188	20464842 (375, 376)	Novel Protein sim. GBank gl 2145853 pir S72938 - hMX protein - Mycobacterium leprae		kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gl 1881244 db BAA18271 - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	UNCLASSIFIED	35686052, 264602, 264605, 264782, 264689, 35695917, 18108370, 18108372, 264638, 264595
190	80086821 (379, 380)	Novel Protein sim. GBank gl 120226 sp P28725 FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE)	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	synthase	264593
191	80095012 (381, 382)	Novel Protein sim. GBank gl 4980892 gb AAD35474.1 AE00171 - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]		isomerase	264508, 264604, 264605, 264759, 264555
192	16333378 (383, 384)	Novel Protein sim. GBank gl 1705461 sp P53656 BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)			264567
193	79910127 (385, 386)	Novel Protein sim. GBank gl 3122305 sp Q27778 K6PF_SCHMA - 6-PHOSPHOHEXOKINASE (PHOSPHOHEXOKINASE)			264908, 264693
194	20464949 (387, 388)	Novel Protein sim. GBank gl 1781203 emb CAB06110 - (Z83859) gnd [Mycobacterium tuberculosis]		transport	264605
195	13518309 (389, 390)	Novel Protein sim. GBank gl 2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]			264636
196	95005509 (391, 392)	Novel Protein sim. GBank gl 2894376 emb CAA74911.1 - (Y14573) ring finger protein [Hardyana vulgaris]			265008
197	80248655 (393, 394)	Novel Protein sim. GBank gl 2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]		UNCLASSIFIED	264595, 264596
198	78163635 (395, 396)	Novel Protein sim. GBank gl 2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]		UNCLASSIFIED	29331826, 265007, 264512, 33657402, 264596, 265017, 18108351, 264682, 264683, 264767, 264628, 55810784, 264634, 264635, 55182323, 60432113, 22278000
199	78890715 (397, 398)	Novel Protein sim. GBank gl 2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]		UNCLASSIFIED	
200	79413849 (399, 400)	Novel Protein sim. GBank gl 2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]		UNCLASSIFIED	
201	86945924 (401, 402)	Novel Protein sim. GBank gl 2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]		UNCLASSIFIED	

202	76588046 (403, 404)	Novel Protein sim. GBank gi231772 sp P30598 CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01844) - Chitin synthase	synthase	264600
203	78843927 (405, 406)	Novel Protein sim. GBank gi1504042 dbj BAA13220 - (D86984) similar to yeast adenylate cyclase (S68776) [Homo sapiens]			22278995, 28331822, 28331825, 28331827, 264908, 21908754, 264683, 21908768, 21908769, 35898423, 284556
204	78855188 (407, 408)	Novel Protein sim. GBank gi2633808 emb CAB13310 - (Z89111) similar to hypothetical proteins [Bacillus subtilis]		UNCLASSIFIED transport	264809 264909
205	10080583 (409, 410)	Novel Protein sim. GBank gi2134381 pir S60678 - polybromo 1 protein - chicken		UNCLASSIFIED	264604 284556
206	8758473 (411, 412)	Novel Protein sim. GBank		UNCLASSIFIED	264605
207	20754522 (413, 414)	Novel Protein sim. GBank gi2501040 sp O05814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)		UNCLASSIFIED	264605, 264689
208	20289281 (415, 416)	Novel Protein sim. GBank			264905, 284907, 284909, 264766, 264687, 264691, 284629, 18108374, 264638
209	80071089 (417, 418)	Novel Protein sim. GBank			263978
210	80168800 (419, 420)	Novel Protein sim. GBank gi5031809 ref NP_005538.1 p SLR - immunoglobulin superfamily containing leucine-rich repeat		UNCLASSIFIED	264508, 264905, 264908, 264907, 284908, 264600, 264762, 264534, 264632, 264634, 264635, 264639, 264488
211	80034539 (421, 422)	Novel Protein sim. GBank gi3122358 sp O33123 LEU2_MYCLE - 3- ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - Aconitase family (aconitase hydratase)	isomerase	22278998, 284508, 284900, 264602, 264603, 264605, 33657023, 284565, 264488
212	82442474 (423, 424)	Novel Protein sim. GBank gi116238 sp P19421 CH60_COX8U - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	264600, 264693
213	80249562 (425, 426)	Novel Protein sim. GBank			
214	80079381 (427, 428)	Novel Protein sim. GBank gi2506924 sp P49754 VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)		UNCLASSIFIED dna_rna_bind	264629 284448
215	14973283 (429, 430)	Novel Protein sim. GBank gi1173288 sp P38106 RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	Contains protein domain (PF00086) - Zinc finger, C2H2 type		264508
216	80177716 (431, 432)	Novel Protein sim. GBank gi1173288 sp P38106 RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN		mapolymerase	264594
217	78603634 (433, 434)	Novel Protein sim. GBank gi1173288 sp P38106 RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN		synthase	264604
218	80258475 (435, 436)	Novel Protein sim. GBank gi1173288 sp P38106 RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN		nucleaseinhib	264689
219	20438787 (437, 438)	Novel Protein sim. GBank gi1781097 emb CAB06231 - (Z83884) giLB [Mycobacterium tuberculosis]		UNCLASSIFIED	264555
220	13489572 (439, 440)	Novel Protein sim. GBank gi2084703 (AF052427) - unknown [Trypanosoma cruzi]			
221	11287498 (441, 442)	Novel Protein sim. GBank gi4587313 dbj BAA76708.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]			

222	79862802 (443, 444)	Novel Protein sim. GBank gij1877268[embjCAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 264769, 35696423
223	83053869 (445, 446)			UNCLASSIFIED	264908, 264907, 264603
224	79557820 (447, 448)			UNCLASSIFIED	264684, 264693
225	78559541 (449, 450)			UNCLASSIFIED	264692
226	78172397 (451, 452)	Novel Protein sim. GBank gij2274851[dbjBAA21515] - (D64159) 3-7 gene product [Homo sapiens]		UNCLASSIFIED	22278998, 264112, 33657023, 263981
227	81777196 (453, 454)	Novel Protein sim. GBank gij868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	35695917, 264636, 264907
228	79872285 (455, 456)			UNCLASSIFIED	264768, 264907, 264908, 264692, 264593, 264639
229	79838266 (457, 458)				264908, 264910
230	11013209 (459, 460)			UNCLASSIFIED	264631
231	20622207 (461, 462)	Novel Protein sim. GBank gij1835114[embjCAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]			264906, 264600, 264603, 264692
232	80055035 (463, 464)			UNCLASSIFIED	264600, 264603, 264605, 264687, 264769
233	80063054 (465, 466)	Novel Protein sim. GBank gij2642340 (AF032970) - Imidazole propionate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
234	7523898 (467, 468)	Novel Protein sim. GBank gij3510505 (AF030881) - polypeptide [Fugu rubripes]		UNCLASSIFIED	264369
235	80203871 (469, 470)			UNCLASSIFIED	264106
236	78940001 (471, 472)	Novel Protein sim. GBank gij2104609[embjCAB08805] - (Z85398) PckA [Mycobacterium leprae]		UNCLASSIFIED	264805
237	11755273 (473, 474)				264681
238	78461401 (475, 476)			UNCLASSIFIED	264639
239	82435190 (477, 478)	Novel Protein sim. GBank gij2495617[spjQ57252]YDIJ_HAEIN - HYPOTHETICAL PROTEIN HI1163	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.	UNCLASSIFIED	264908, 265010, 264603, 264762, 264682, 264638, 264638, 264486
240	21635575 (479, 480)	Novel Protein sim. GBank gij3183458[spjP75796]YLIA - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA	transport		264259, 264769
241	80377307 (481, 482)	Novel Protein sim. GBank gij3875920[embjCAB04111] - (Z81503) predicted using GeneFinder, similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264908, 264808, 264784, 264639
242	82148454 (483, 484)			UNCLASSIFIED	264489, 264907, 264908, 264511, 264760, 264784, 264692, 264635, 264637
243	79633207 (485, 486)			UNCLASSIFIED	264908
244	80248682 (487, 488)	Novel Protein sim. GBank gij2624302[embjCAA15575] - (AL008967) ald [Mycobacterium tuberculosis]		UNCLASSIFIED	264600, 264602, 264605, 264769, 264689
245	79863543 (489, 490)	Novel Protein sim. GBank gij2920625 (AF044499) - vgrE protein [Escherichia coli]	dehydrogenase	UNCLASSIFIED	264907, 264758
246	78162920 (491, 492)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NiU-like domain		264637, 18108381, 18108387, 264565

247	79873185 (483, 494)	Novel Protein sim. GBank gll1039006[emb]CA806848] - (Z85982) argB [Mycobacterium tuberculosis]		Kinase	264809, 264691, 35696423, 18108387
248	80488983 (495, 496)	Novel Protein sim. GBank gll1168574[sp]P42484[ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35698286, 264807, 264511, 264602, 264788, 264688, 265021, 35698855, 18108385
249	79764845 (487, 498)			UNCLASSIFIED	264807, 264910, 265011, 264782, 264638
250	78619980 (498, 500)				21808768, 264692
251	84359489 (501, 502)			UNCLASSIFIED	52645156, 20331822, 20331824, 52644045, 265018, 21808765, 21808768, 265020, 27488281, 27488265, 35695763, 18108376, 264558, 264559, 264585
252	79737758 (503, 504)	Novel Protein sim. GBank gll3327166[db]BAA31651] - (AB014576) KIAA0876 protein [Homo sapiens]			264685, 264687, 264632
253	20443124 (505, 506)	Novel Protein sim. GBank gll3038880[emb]CAA18513] - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank gll3915489[sp]O34881YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	264508, 264806, 264602, 264687, 265021, 284486
255	11388315 (508, 510)	Novel Protein sim. GBank gll1665720[db]BAA04134] - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank gll465787[sp]P34422]YL31_CAEEL - HYPOTHETICAL 86.0 KD PROTEIN F4489.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	264602, 264692
257	20288282 (513, 514)	Novel Protein sim. GBank gll1172039[sp]P42315ISCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459464 (515, 516)	Novel Protein sim. GBank gll3127836[emb]CAA18902] - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	79810152 (517, 518)			collagen	264681, 264686, 264692
260	20378437 (518, 520)			UNCLASSIFIED	264692, 264558
261	20285883 (521, 522)	Novel Protein sim. GBank gll123781[sp]P24221[HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	265017, 264389
263	88085045 (525, 526)	Novel Protein sim. GBank gll3924708[emb]CAA84846] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blast score 71); cDNA EST EMBL:702089 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264909, 264512, 204910, 264758, 264596, 264604, 265019, 264605, 264760, 18108351, 264783, 264784, 264288, 264768, 264788, 264769, 264691, 264692, 264693, 264628, 264634, 264635, 264555, 264638, 264639
264	87370826 (527, 528)	Novel Protein sim. GBank gll3043734[db]BAA25531] - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264908, 21808754, 265018, 265019, 265020

265	95355646 (529, 530)	Novel Protein sim. GBank gij4589624(dbj)[BAA76834.1] - (AB023207) KIAA0980 protein [Homo sapiens]		kinase	264488, 35696286, 28331824, 56182181, 35696052, 264508, 264905, 264908, 264907, 66712502, 264908, 264909, 264511, 264512, 264910, 264592, 264595, 264758, 264596, 55811386, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264782, 264681, 264764, 264288, 264766, 264768, 264769, 21908765, 21908767, 21908769, 265020, 264891, 33657023, 33657109, 33657182, 264628, 35686423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 83373044, 56528486, 87168518, 284564, 284566, 264488
266	78588075 (531, 532)				264800
267	11362222 (533, 534)			UNCLASSIFIED	264828
268	78809568 (535, 536)			UNCLASSIFIED	264887, 264769, 264689
269	80025810 (537, 538)			UNCLASSIFIED	264602
270	84361144 (539, 540)	Novel Protein sim. GBank gij4507387[refNP_003182.1]pTARS - threonyl-tRNA synthetase		UNCLASSIFIED	264693
271	78552301 (541, 542)	Novel Protein sim. GBank gij4980738[gib AAD3331.1]AE00170 - (AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		UNCLASSIFIED	264909, 264693
272	9874778 (543, 544)	Novel Protein sim. GBank gij1168224[sp P44569]5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		synthase	264908
273	12840694 (545, 546)			UNCLASSIFIED	264688
274	39524246 (547, 548)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Cryptosporidium parvum]			264564
275	82787041 (549, 550)	Novel Protein sim. GBank gij134920[sp P21897]SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)		UNCLASSIFIED	264907, 264908, 264909, 264766, 264768, 264691, 264632, 264638
276	86671073 (551, 552)	Novel Protein sim. GBank gij128021[sp P20864]OBG_BACSU - SPO0B-ASSOCIATED GTP-BINDING PROTEIN			265008, 60432229
277	80079735 (553, 554)			ribosomal prot	264600, 18108387
278	12866947 (555, 556)	Novel Protein sim. GBank gij78839[pir][S03812 - uwB protein - Micrococcus luteus		UNCLASSIFIED	264689
279	95292719 (557, 558)			nuclease	264508, 264604, 21906764, 264638, 264557, 264404
280	5603817 (559, 560)	Novel Protein sim. GBank gij3123160[sp Q18964]YLN2 CAEL - HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II			264259
281	80249589 (561, 562)				18108392, 264634, 264555, 264556, 264557, 264558
282	18598682 (563, 564)			UNCLASSIFIED	265019
283	20614211 (565, 566)			UNCLASSIFIED	264555

284	81212160 (567, 568)	Novel Protein sim. GBank glj2428094 (U58632) - acetyl xylan esterase; AxeA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 29331828, 264508, 264905, 264800, 264602, 264605, 264682, 264764, 56181562, 21908764, 18108376, 264638, 264558, 18108387
285	8757940 (569, 570)			UNCLASSIFIED	264803
286	80503235 (571, 572)	Novel Protein sim. GBank glj2072674 [embjCAB08305] - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	ATPase-associated	35696052, 264769, 264638
287	12745521 (573, 574)	Novel Protein sim. GBank glj765323 [bbsj157676] - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori= silkworms, Peptide Partial, 633 aa] [Bombyx mori]		UNCLASSIFIED	264689
288	20756502 (575, 576)	Novel Protein sim. GBank glj1870009 [embjCAB06860] - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]		collagen	264557
289	80043804 (577, 578)	Novel Protein sim. GBank glj625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]	Contains protein domain (PF00440) - Bacterial regulatory proteins, telR family	ribosomal prot	264593, 264600
290	80430175 (579, 580)	Novel Protein sim. GBank glj2508864 [spjP40120] YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264768
291	20747431 (581, 582)	Novel Protein sim. GBank glj625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim. GBank glj1718065 [spjP53528] UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG		UNCLASSIFIED	264605
293	80062518 (585, 586)	Novel Protein sim. GBank glj117422 [spjP10040] CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	helicase		264909, 264605, 264687, 264688, 264692
294	79830303 (587, 588)	Novel Protein sim. GBank glj1181619 [dbjBAA11565] - (D82384) a variant of TSC-22 [Gallus gallus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696052, 264906, 265011, 264628, 55811576
295	79444180 (589, 590)	Novel Protein sim. GBank glj3649789 [dbjBAA33403] - (AB012226) SecA [Vibrio alginolyticus]			52844507, 29331822, 264592, 265020, 264639
296	79607076 (591, 592)	Novel Protein sim. GBank glj5689967 [embjCAB52004.1] - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]	synthase		264508
297	79631297 (593, 594)			UNCLASSIFIED	264905, 264687, 264638
298	80418888 (595, 596)			UNCLASSIFIED	264905, 264691, 264639, 264766

299	95293288 (597, 598)	Novel Protein sim. GBank gij220637[dbj BAA01471] - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	264488, 263984, 56994075, 22278987, 22278998, 20281099, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 52644045, 264909, 264511, 265008, 264910, 264585, 264598, 264756, 33657084, 87168559, 265018, 265019, 264764, 264288, 264766, 264687, 58161582, 264769, 21908765, 21908768, 21908769, 33657023, 264692, 33657109, 27488281, 18108370, 264628, 264629, 55811576, 35695855, 264631, 264634, 264635, 264638, 264639, 63373044, 18108387, 87168518, 22279000, 22279002, 264565, 264566, 264567
300	20711340 (599, 600)	Novel Protein sim. GBank gij145922 (M20881) - Iron		264602
301	13511332 (601, 602)	diclrate transport protein precursor [Escherichia coli]		264687
302	9875260 (603, 604)	Novel Protein sim. GBank gij1174661[sp P44594]TGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		264908
303	79574895 (605, 606)	Novel Protein sim. GBank gij67985[sp HJUNVAV - helicase		264689
304	20711344 (607, 608)	(EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus	helicase	264602
305	80412520 (609, 610)	Novel Protein sim. GBank gij728867[sp P40602]APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264763
306	8515876 (611, 612)	Novel Protein sim. GBank gij1657554[gb AAB18082.1] - (U73857) hypohelical protein [Escherichia coli]	UNCLASSIFIED	263978
307	80222801 (613, 614)		UNCLASSIFIED	265010, 21906768, 265020, 18108374, 263977
308	80084305 (615, 616)	Novel Protein sim. GBank gij1710612[sp Q10793]RNIH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNAse HII)	Contains protein domain (PF01351) - Ribonuclease HII	264910, 264600, 264605, 264687, 264689, 264638, 18108387
309	80504138 (617, 618)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		264769
310	80053616 (619, 620)			264603
311	11090859 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	264602
312	80054347 (623, 624)			
313	80046168 (625, 626)		UNCLASSIFIED	264566, 264603, 264567

314	87645112 (627, 628)	Novel Protein sim. GBank gij3661583 (AF092175) - ikaros [Danio rerio]	Contains protein domain (PF00320) - dna_rna_bind GATA zinc finger	264259, 60432289, 29331828, 264805, 264806, 264908, 264909, 265008, 264910, 60432229, 33657402, 60433438, 33109854, 265011, 265017, 264603, 265018, 264288, 264768, 264682, 35695763, 264628, 264629, 264639, 50170394, 22279002, 264568 264508, 264600, 264762, 264687, 264768, 52644228, 264768, 264689, 264635, 264636, 264638, 264488 264693 264605
315	82356091 (628, 630)	Novel Protein sim. GBank gij1652620(jb)[BAA17540] - (D90907) pyridine nucleotide transhydrogenase beta subunit [Synecocystis sp.]		
316	79911071 (631, 632)	Novel Protein sim. GBank gij118244[sp]P24176[DAPE, ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP)]	UNCLASSIFIED	
317	20468944 (633, 634)	Novel Protein sim. GBank gij4680228[gb]AAD27583.1[AF118274] DNB-5 [Homo sapiens]	UNCLASSIFIED	
318	94141838 (635, 636)	Novel Protein sim. GBank gij1149693[amb][CAA60220] - (X86499) rbsC [Clostridium perfringens]	transport	264908, 264909, 264910, 264593, 264594, 264760, 264288, 264768, 264769, 21908769, 264691, 264693, 264628, 65274791, 264635, 264636, 264638, 83373044, 22278002, 264566 285018
319	17288360 (637, 638)	Novel Protein sim. GBank gij1149693[amb][CAA60220] - (X86499) rbsC [Clostridium perfringens]	transport	
320	13527675 (639, 640)	Novel Protein sim. GBank gij2811033[sp]D05314[GLGC, MYCTU - GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)]	synthase	264687
321	94134387 (641, 642)	Novel Protein sim. GBank gij1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]	cyto450	264508, 264906, 264907, 264908, 265009, 264596, 264764, 264628, 264634, 264635, 264638, 264639, 83373044, 264567 55811150, 264691, 60431528, 55810764
322	68489053 (643, 644)	Novel Protein sim. GBank gij1160355 (U33058) - UNC-89 [Caenorhabditis elegans]	UNCLASSIFIED	
323	94653725 (645, 646)		UNCLASSIFIED	264488, 265009, 264593, 264628, 264635 264687
324	78174383 (647, 648)		UNCLASSIFIED	264683
325	78852091 (649, 650)		UNCLASSIFIED	264288, 18108385
326	28774974 (651, 652)		UNCLASSIFIED	264488, 264805, 264509, 264910
327	79776267 (653, 654)	Novel Protein sim. GBank gij451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		
328	80253202 (655, 656)		UNCLASSIFIED	264592
329	10173821 (657, 658)		UNCLASSIFIED	264510
330	86597767 (659, 660)	Novel Protein sim. GBank gij4191358 (AF087825) - claudin-7 [Mus musculus]	UNCLASSIFIED	264259, 264908
331	79754888 (661, 662)	Novel Protein sim. GBank gij80741[pir][S20912 - regulatory protein whIB - Streptomyces coelicolor]	transcriptfactor	264910, 264687, 264688, 264636, 264567
332	80071440 (663, 664)	Novel Protein sim. GBank gij114049[sp]P19480[AHPF, SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)]	reductase	35696423, 264636, 264638, 264565
333	13009555 (665, 666)			264687

334	80230771 (667, 668)	Novel Protein sim. GBank glj322228[pir][S32227 - glutamate dehydrogenase (NADP+)] (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	284905, 284600, 264604, 264486
335	80057026 (669, 670)	Novel Protein sim. GBank glj218393[emb][CAB09602] - (Z96800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264603, 264683, 18108374, 264636, 18108387
336	80414319 (671, 672)			UNCLASSIFIED	265009, 264766, 264688
337	11080828 (673, 674)				264602
338	85413134 (675, 676)	Novel Protein sim. GBank glj5454074[ref][NP_006303.1]pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nuc_recpt	264569, 18108397, 22278998, 29331822, 20281099, 29331824, 58182181, 68714117, 29331825, 35696052, 28331828, 264508, 264509, 284905, 264806, 264807, 264908, 264909, 265006, 265008, 264910, 265009, 264768, 55812038, 65274444, 265011, 87168559, 265017, 265018, 265019, 264760, 55811150, 264681, 264762, 18108351, 264768, 52644229, 264689, 55811957, 35695917, 264692, 264693, 264628, 18108370, 18108374, 55811576, 35696423, 35695855, 264635, 264555, 264636, 264556, 264637, 264557, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87188518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank glj4001713[dbj][BAA35087.1] - (AB015879) DnaK [Porphyrromonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank glj2842689[sp][Q92353]UBPC_SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C8G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	264905, 265019, 264768, 18108374
341	11075188 (681, 682)	Novel Protein sim. GBank glj2688580 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00290) - Tryptophan synthase alpha chain	isomerase	264605
342	80054188 (683, 684)	Novel Protein sim. GBank glj1684738[emb][CAA70601] - (Y09452) Yed J hypothetical protein [Pseudomonas syringae]			264603, 264604
343	20468782 (685, 686)				
344	80428870 (687, 688)	Novel Protein sim. GBank glj2117275[emb][CAB09104] - (Z95818) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
345	80258853 (689, 690)	Novel Protein sim. GBank glj3023317[sp][Q48935]APHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE		histone	264593
346	78831058 (691, 692)	Novel Protein sim. GBank glj4239787[emb][CAA75437] - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264805

347	78156195 (693, 694)	Novel Protein sim. GBank gl 731675 sp P38795 YHN4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION	UNCLASSIFIED	265008, 265008, 265010, 265018, 263987, 263981
348	80020208 (695, 698)	Novel Protein sim. GBank gl 1073610 p gl S47672 - ugpB protein - Escherichia coli	transport	264602, 18108351, 18108387
349	17282112 (697, 698)	Novel Protein sim. GBank gl 3281599 emb CAB009171 - (277137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]	nuclease	285007 265008, 264768, 264689, 18108370
351	80501805 (701, 702)	Novel Protein sim. GBank gl 2859367 emb CAA179211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]	glycoprotein	264769, 264905, 264908
352	11611585 (703, 704)	Novel Protein sim. GBank gl 4416302 gb AAD203071 - (AF105718) copia-type pol protein [Zea mays]	protease	264595
353	80061653 (705, 708)	Novel Protein sim. GBank gl 1174887 sp P42873 URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	UNCLASSIFIED	264604
354	56828130 (707, 708)	Novel Protein sim. GBank	UNCLASSIFIED	264628
355	80046344 (709, 710)	Novel Protein sim. GBank	UNCLASSIFIED	264809, 264585, 264683, 22279002
356	80043835 (711, 712)	Novel Protein sim. GBank gl 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	transcript factor	264809, 264581, 264592
357	80070568 (713, 714)	Novel Protein sim. GBank gl 497637 (J03839) - cytochrome oxidase d subunit I [Escherichia coli]	oxidase	264605
358	37032756 (715, 716)	Novel Protein sim. GBank gl 2280990 (AF006000) - Brg 1 [Bordetella pertussis]	UNCLASSIFIED	264768
359	80501488 (717, 718)	Novel Protein sim. GBank	UNCLASSIFIED	264604, 264769
360	80026748 (719, 720)	Novel Protein sim. GBank gl 3510839 (AF049344) - UDP- GalNAc:polypeptide N-acetylglucosaminyltransferase T5 [Rattus norvegicus]	UNCLASSIFIED	264594
361	80584075 (721, 722)	Novel Protein sim. GBank gl 113784 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	transferase	22278996, 284259, 28331822, 28331824, 264605, 55811857, 265022
362	13089485 (723, 724)	Novel Protein sim. GBank	amylase	264688
363	79750145 (725, 726)	Novel Protein sim. GBank		264568
364	82443593 (727, 728)	Novel Protein sim. GBank gl 2828818 sp P85171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	dehydrogenase	264769, 264602, 264604, 264508, 264762, 264638, 264486

365	88040288 (729, 730)	Novel Protein sim. GBank gij4828268jgbjAAD33924.1] - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264488, 21806766, 21806767, 55811576, 21906768, 29148629, 22278985, 22278986, 265020, 265022, 264634, 264681, 264593, 33857023, 33857402, 264693, 264639, 264594, 29331824, 264758, 18108385, 28331827, 87168559, 265018, 22278000, 265019, 264482, 264761, 264681, 18108351, 265017, 264757
366	81821838 (731, 732)	Novel Protein sim. GBank gij4503843jrefjNP_003908.1pG2AD - UNKNOWN	Contains protein domain (PF01602) - glycoprotein	60424178, 65274572, 56182575, 22278994, 56894075, 22278996, 264259, 29331822, 29331824, 56182181, 60424268, 68714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264905, 264828, 56182435, 265008, 264512, 265008, 264591, 55812038, 55811386, 265010, 87168559, 265017, 285018, 264604, 265019, 55811150, 264448, 264369, 264288, 264686, 264768, 56181562, 21908768, 21806768, 55811957, 35695917, 265022, 80170615, 33657023, 65274620, 18108365, 263967, 33657109, 33857349, 35695783, 264628, 18108376, 55811576, 65274791, 35695855, 56182323, 83373044, 60432113, 264563, 264564, 264567, 264509
367	85357471 (733, 734)			
368	78607285 (735, 736)	Novel Protein sim. GBank gij3913028jsepjP94967jALR_MYCSM - ALANINE RACEMASE	UNCLASSIFIED	264508, 264604, 264605, 264636
369	95292817 (737, 738)			
370	88080966 (739, 740)	Novel Protein sim. GBank gij3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]	Contains protein domain (PF01715) - transferase	264905, 264592, 264605, 264766, 264691
371	85282599 (741, 742)	Novel Protein sim. GBank gij2995299jembjCAA18328] - (AL022268) putative IRNA delta(2)-isopenitienylpyrophosphate transferase [Streptomyces coelicolor]		
372	80021107 (743, 744)	Novel Protein sim. GBank gij2506393jsepjP31576jFIXX_ECOLI - FERREDOXIN LIKE PROTEIN		264564
373	78663768 (745, 746)	Novel Protein sim. GBank gij3341640jembjCAA13184] - (AJ231122) z811 [Vibrio cholerae]	UNCLASSIFIED	264909
374	78847568 (747, 748)			
375	91230181 (749, 750)	Novel Protein sim. GBank gij5456934jgbjAAD43716.1] - (AF152322) protocadherin gamma A2 [Homo sapiens]	UNCLASSIFIED	264905, 264806
376	80505214 (751, 752)	Novel Protein sim. GBank gij1805408jdbjBAA008970] - (D50453) homologues to nitrate hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	cadherin	65274572, 264259, 29331826, 56182435, 60433358, 60433436, 264757, 55812038, 264758, 55811957, 264690, 33657023, 264769
377	10339083 (753, 754)		UNCLASSIFIED	264906

378	80056153 (755, 756)	Novel Protein sim. GBank gl 1076013 pir A49930 - carB protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Contains protein domain (PF00289) - synthase	UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)	Novel Protein sim. GBank gl 216555 dbj BAA02174 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - dehydrogenase	264789	264604
380	80060837 (759, 760)	Novel Protein sim. GBank gl 3327136 dbj BAA31636 - (AB014561) KIAA0661 protein [Homo sapiens]	UNCLASSIFIED	264684	264592
381	11769027 (761, 762)			264595, 265017, 265021, 264638, 87188518, 22278002	
382	80054377 (763, 764)			264259, 28331822, 60432289, 28331827, 264288, 264768, 283887, 85274781, 35695855, 263881, 83373044, 264567	
383	83258025 (765, 766)			264692	
384	95314255 (767, 768)			264808	
385	10237679 (769, 770)	Novel Protein sim. GBank gl 1073456 pir S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00465) - iron-containing alcohol dehydrogenases	UNCLASSIFIED	264760
386	78633434 (771, 772)	Novel Protein sim. GBank gl 1460074 emb CA801049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily		
387	17860837 (773, 774)	Novel Protein sim. GBank gl 4240169 dbj BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	35696286, 264805, 88712502, 60432229, 264593, 60433356, 264688, 264688, 21906765, 264691, 22278000, 264482	
388	87741378 (775, 776)			18108394, 22278986, 264630, 264556, 22278002	
389	79316971 (777, 778)			264600	
390	80078949 (779, 780)	Novel Protein sim. GBank gl 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		264482	
391	7657302 (781, 782)	Novel Protein sim. GBank gl 3378523 emb CAA08867 - (AJ009832) cyclomaldextrinase glucanotransferase [Thermotoga neapolitana]	UNCLASSIFIED	264908	
392	79786058 (783, 784)			264602, 21906764	
393	33206031 (785, 786)				
394	10104463 (787, 788)			264693	
395	80228010 (789, 790)	Novel Protein sim. GBank gl 2677780 (U70327) - unknown [Pareitropus polyacis]	UNCLASSIFIED	264508, 264563	
396	20436224 (791, 792)	Novel Protein sim. GBank gl 4507808 ref NP_000368.1 (pWAS) - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	Contains protein domain (PF00047) - struct	264556	
397	80417014 (793, 794)	Novel Protein sim. GBank gl 1518458 (U45986) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - transport	265007, 265009, 264508, 264556, 264629, 264768	
398	91230517 (795, 796)			18108398, 22278995, 22278996, 56984075, 22278999, 264259, 26331824, 28331826, 264905, 264808, 265007, 285008, 265009, 21906754, 33657084, 285017, 264448, 264288, 264768, 21906765, 21906766, 21906767, 265020, 265021, 33657023, 33657108, 264628, 35696423, 35695855, 264952, 18108380, 264567, 18108391	

399	80055278 (797, 799)	Novel Protein sim. GBank gi 3358091 dbj BAA31895 - (AB015974) glycerol Kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - Kinase FGGY family of carbohydrate kinases	284592, 284595
400	84117490 (799, 800)	Novel Protein sim. GBank gi 728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII	Contains protein domain (PF00580) - cadherin Leucine Rich Repeat	18108394, 56182575, 22278995, 22278997, 22278998, 264259, 29331824, 285006, 285007, 285009, 80432229, 33657402, 21808764, 285010, 265017, 265018, 265019, 18108351, 18108357, 21808765, 285021, 285022, 264691, 264692, 33657023, 18108370, 65274791, 264634, 264636, 60170394, 56182323, 264594
401	11397491 (801, 802)	Novel Protein sim. GBank gi 4828292 gb AAD33527.1 AF132117 FhuA [Staphylococcus aureus]	transport	
402	95420294 (803, 804)	Novel Protein sim. GBank gi 5688487 dbj BAA83027.1 - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - phosphatase Src homology domain 2	55274572, 56182575, 35696288, 22278996, 22278998, 264093, 264259, 29331822, 29331824, 29331825, 29331826, 80432289, 29331827, 29331828, 264908, 264907, 264909, 265006, 264511, 285007, 265008, 264910, 264591, 33657402, 60433356, 60433438, 264596, 21808754, 52644296, 285010, 265011, 87188559, 285017, 265018, 265019, 264681, 18108351, 264682, 264448, 264288, 264684, 264766, 264767, 264686, 21808765, 21808768, 21808767, 21808768, 21808789, 55811957, 285020, 285021, 265022, 264690, 264693, 65274620, 35695763, 264628, 18108370, 264629, 18108378, 35898423, 55811578, 264635, 264636, 264557, 264639, 18108385, 22279002, 264563, 264564, 264565, 264566, 264768, 264632, 264639, 264663, 264682, 265009, 264682
403	80438913 (805, 806)	Novel Protein sim. GBank gi 266164 emb CAA15755 - (AL009198) dnaE2 [Mycobacterium tuberculosis]	UNCLASSIFIED	
404	11809865 (807, 808)		polymerase	
405	79471280 (809, 810)		Contains protein domain (PF00159) - Pancreatic hormone peptides	18108357, 264693
406	78634172 (811, 812)		UNCLASSIFIED	
407	80478229 (813, 814)		UNCLASSIFIED	
408	80079556 (815, 816)		UNCLASSIFIED	
409	5840627 (817, 818)	Novel Protein sim. GBank gi 3047117 (AF058918) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]	helicase	284789, 264600, 264259

410	95357498 (818, 820)	Novel Protein sim. GBank gij475016[dbj BAA08184] - (D28801) Unknown [Mus musculus]		UNCLASSIFIED	264488, 52646365, 52646842, 56181886, 35896286, 52645080, 28331822, 29331824, 56182181, 29331825, 60424289, 35896052, 33569970, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 265007, 264512, 265008, 264910, 33657402, 264758, 52646317, 55811388, 265010, 265011, 265017, 264604, 265018, 55811150, 264762, 264764, 264768, 264687, 264768, 264769, 52644228, 21808768, 265020, 265021, 264534, 52644150, 264692, 33857023, 65274620, 33857109, 33857182, 27486261, 35685783, 264828, 264829, 60431528, 18108376, 263978, 35688423, 35895855, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 56182323, 264559, 60432113, 22278002, 264563, 264565, 264486
411	80501970 (821, 822)			UNCLASSIFIED	264769
412	60241662 (823, 824)				264807, 264810, 263973, 22278002
413	11078446 (825, 826)	Novel Protein sim. GBank gij3261784[emb CAB08997] - (Z95558) htpX [Mycobacterium tuberculosis]		eph	264605
414	82050554 (827, 828)	Novel Protein sim. GBank gij128036[sp P20707 ODO1_AZOVI - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)]		dehydrogenase	18108374, 264760, 264769, 264602, 264638, 264603, 264908, 264605
415	84453144 (828, 830)	Novel Protein sim. GBank gij4868350[gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87168518
416	60402775 (831, 832)	Novel Protein sim. GBank gij2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		kinase	264488, 264600, 264602, 264764, 264636
417	20153787 (833, 834)	Novel Protein sim. GBank gij1709171[sp P52311 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)]	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		264605
418	94125841 (835, 836)			UNCLASSIFIED	264688, 264683
419	85314273 (837, 838)			collagen	264908, 264810, 264764, 264639
420	37036349 (838, 840)	Novel Protein sim. GBank gij3261659[emb CAB03751] - (Z81388) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	phosphatase	264769
421	95282942 (841, 842)	Novel Protein sim. GBank gij2816942[emb CAA17580] - (AL021989) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264808, 264600, 264601, 264603, 264604, 264760, 264769
422	78471293 (843, 844)	Novel Protein sim. GBank gij231752[sp Q00767 CH61_STRAL - 60 KD CHAPERONIN 1 (PROTEIN CPN60 1) (GROEL PROTEIN 1) (HSP58)]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	22278996, 264682, 18108376, 18108387
423	78604948 (845, 846)			UNCLASSIFIED	264509

424	78986557 (847, 848)	Novel Protein sim. GBank gij4826814[ref]NP_004877.1 pKTN1 - kinesin 1 (kinesin receptor)		struct	265019	
425	80431450 (849, 850)	Novel Protein sim. GBank gij170370 bbsj178462 - KRP5-kinesin-related protein [rais, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264909, 265007, 55811386, 264768, 55810764	
426	80064522 (851, 852)				264605, 264559	
427	80057232 (853, 854)	Novel Protein sim. GBank gij231828 sp P29929 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	264603, 264636	
428	78487798 (855, 856)				264683	
429	80091252 (857, 858)	Novel Protein sim. GBank gij181286 pir S22697 - extensin - Volvox cartet (fragment)		UNCLASSIFIED	35696423, 35695763, 35695855, 265017, 284564, 264762	
430	80504192 (859, 860)	Novel Protein sim. GBank gij1808154 emb CAB06451 - (284395) hypothetical protein Rv0688 [Mycobacterium tuberculosis]	reductase		284508, 264905, 264509, 264908, 264909, 265008, 264600, 284687, 284769, 284689, 284636, 264638, 18108385, 264486	
431	20624249 (861, 862)				264566	
432	16523372 (863, 864)				265020	
433	81494303 (865, 866)	Novel Protein sim. GBank gij3123552 emb CAA18609 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	264907, 264908, 264909, 264910, 284592, 264595, 284756, 264604, 264760, 264762, 284763, 284638, 284637, 22279002	
434	84326323 (867, 868)	Novel Protein sim. GBank gij2495272 sp Q89629 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 56182181, 56181562, 28331828, 35696052, 55810764, 55811576, 65274791, 35695855, 60432113, 55811150, 264636, 284768	
435	80502738 (869, 870)	Novel Protein sim. GBank gij114105 sp P08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	284595, 264769	
436	41085953 (871, 872)					
437	11399291 (873, 874)			UNCLASSIFIED	265020, 22279002	
438	11773835 (875, 876)			UNCLASSIFIED	264593	
439	80018495 (877, 878)			UNCLASSIFIED	264666	
440	79841062 (879, 880)	Novel Protein sim. GBank gij3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana] Novel Protein sim. GBank gij229123 gb AA865351.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA), Score=268.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]			284905, 284600, 264602, 264604	
441	20396935 (881, 882)	Novel Protein sim. GBank gij5638946 gb AAD45904.1 AF16132 - (AF161328) histidine kinase CstS [Corynebacterium diphtheriae]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)		35696052, 264905, 264908, 264909, 265011, 35696423	
442	85281056 (883, 884)	Novel Protein sim. GBank gij1184780 (U46068) - von Ebner minor salivary gland protein [Mus musculus]			264605	
443	82456427 (885, 886)	Novel Protein sim. GBank gij5688993 emb CAB52056.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	29331830, 264909	
444	11395587 (887, 888)	Novel Protein sim. GBank gij1783249 dbj BAA11726 - (D83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	35696052, 264508, 264906, 284512, 264604, 264762, 264769, 284689, 284636	

445	79552709 (889, 890)	Novel Protein sim. GBank gij5531272[embjCAB50897.1]- (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	264693
446	78610937 (891, 892)	Novel Protein sim. GBank gij538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcript factor	264509
447	80438888 (893, 894)	Novel Protein sim. GBank gij1542814[embjCAB02185] - (Z80108) fmi [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	dehydrogenase	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gij118794[spjP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264508, 264600, 264603, 264605, 264682, 264768, 18108382, 264634, 18108387
449	20460634 (897, 898)	Novel Protein sim. GBank gij4589505[dbjBAA76775.1] - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C		264605, 264559
450	94631210 (899, 900)			UNCLASSIFIED	55274572, 22278988, 29331824, 29331826, 264906, 264910, 264592, 52846317, 265017, 21906767, 55811857, 55526466, 22279002
451	21433609 (901, 902)			UNCLASSIFIED	264486
452	10267276 (903, 904)	Novel Protein sim. GBank gij2650814 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	264692
453	52560096 (905, 906)	Novel Protein sim. GBank gij2493000[spjQ09450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	264907, 264600
454	38523922 (907, 908)	Novel Protein sim. GBank gij4468699[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		transferase	264603
455	13088692 (909, 910)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	UNCLASSIFIED	264687
456	79563081 (911, 912)			UNCLASSIFIED	264691
457	78831273 (913, 914)			UNCLASSIFIED	264905
458	78581227 (915, 916)			kinase	55812038, 265010, 265018, 264681
459	80567359 (917, 918)	Novel Protein sim. GBank gij4506075[re]NP_002733.1[prPKC - protein kinase C, mu]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	22278997, 264259, 29331826, 285018, 264448, 264369, 21906765, 35688423
460	79245880 (919, 920)	Novel Protein sim. GBank gij113158[spjP25516]ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)		UNCLASSIFIED	264906
461	95287618 (921, 922)	Novel Protein sim. GBank gij1168574[spjP42484]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33857023, 264559

462	79606589 (923, 924)	Novel Protein sim. GBank gi11346891 sp145597 PTF1_XANCP. (CONTAINS: PHOSPHORYL TRANSFER PROTEIN (MTP) PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ... Novel Protein sim. GBank gi1854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	Contains protein domain (PF00391) - PEP-utilizing enzymes	UNCLASSIFIED	264907
463	79766417 (925, 926)			UNCLASSIFIED	264905, 264906, 264908, 264909, 264910, 264991, 264995, 265011, 264632, 264635, 264636, 264637, 264638, 264639
464	82340151 (927, 928)			UNCLASSIFIED	264834
465	83005730 (929, 930)			UNCLASSIFIED	265017, 21906764, 265020
466	20460645 (931, 932)	Novel Protein sim. GBank gi15689776 emb CA852137.1 - (AJ242832) calpain [Homo sapiens] Novel Protein sim. GBank gi11808175 emb CAB06470 - (Z84395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00848) - Calpain family cysteine protease Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	UNCLASSIFIED	264605, 264559
467	80409035 (933, 934)	Novel Protein sim. GBank gi1548705 sp136949 RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	264764
468	52862208 (935, 936)			UNCLASSIFIED	264692
469	18520527 (937, 938)	Novel Protein sim. GBank gi2114024 emb CAB08957 - (Z85558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
470	80502756 (939, 940)	Novel Protein sim. GBank gi2809459 emb CAA17347 - (AL021929) cobQ [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264769
471	17837351 (941, 942)	Novel Protein sim. GBank gi114921 sp17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		UNCLASSIFIED	265019
472	80047458 (943, 944)			UNCLASSIFIED	264596, 264685, 264557
473	20556793 (945, 946)	Novel Protein sim. GBank gi1862343 (L10908) - Gcap1 gene product [Mus musculus]		UNCLASSIFIED	264369
474	80593365 (947, 948)			UNCLASSIFIED	22278987, 264692, 264288
475	82454665 (949, 950)			UNCLASSIFIED	264907, 264908, 264511, 265009, 264762, 264448, 264638, 264638
476	84143857 (951, 952)	Novel Protein sim. GBank gi15453556 ref NP_008328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	65274572, 60432049, 264259, 264508, 52644045, 55812038, 264758, 265011, 264288, 264686, 52844229, 65274791, 264638, 264566
477	79175833 (953, 954)			UNCLASSIFIED	264838
478	78633483 (955, 956)			UNCLASSIFIED	264690, 264693
479	80189746 (957, 958)			UNCLASSIFIED	264686, 35695855, 265008, 264631, 264910, 264632, 264638, 265018, 264389, 264909
480	78380728 (959, 960)	Novel Protein sim. GBank gi1127551 (U18939) - orf2 [Batrachocottus baikalensis]		UNCLASSIFIED	264369
481	79624578 (961, 962)			UNCLASSIFIED	264693
482	83050611 (963, 964)	Novel Protein sim. GBank gi14063042 (AF088065) - GP800; much-like glycoprotein [Cryptosporidium parvum]		UNCLASSIFIED	264909, 264666, 264768, 264683, 55811576, 56182323, 18108385

483	20283308 (965, 988)	Novel Protein sim. GBank gij2104303[emb]CAB08632] - (Z95387) hypothetical protein Rv2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1	284600	
484	11618046 (967, 988)	Novel Protein sim. GBank gij3450883 (AF083334) - fibroin [Antheraea pernyi]		UNCLASSIFIED	284594
485	80181234 (969, 970)				
486	80059042 (971, 972)	Novel Protein sim. GBank gij5042272[emb]CAB44526.1] - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		UNCLASSIFIED dehydrogenase	284368, 21908765, 22278000, 22278002 284604
487	11813339 (973, 974)				
488	81222383 (975, 978)	Novel Protein sim. GBank gij5724778[gb]AAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain	284638	284686, 68714117, 284768, 18109385, 55811576, 265008, 265008, 265009, 265019, 22279002, 284259, 18108370, 284907, 284764, 56182323, 264288, 284693
489	10867710 (977, 978)	Novel Protein sim. GBank gij3882223[db]BAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]		kinase	284639
490	95361124 (979, 980)	Novel Protein sim. GBank gij82091[pil]A25494 - hydroxyproline-rich glycoprotein - tomato (fragment)		collagen	22278996, 28331822, 29331828, 284107, 264908, 264110, 265009, 264592, 284593, 60433356, 284288, 264893, 283974, 283978, 20281071, 60432113
491	80485412 (981, 982)	Novel Protein sim. GBank gij2894206[emb]CAA17072] - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]		UNCLASSIFIED	284769
492	87421264 (983, 984)				284600
493	11692842 (985, 986)				284638
494	87726604 (987, 988)	Novel Protein sim. GBank gij5262605[emb]CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]		UNCLASSIFIED	284489, 35686286, 60432289, 29331828, 35686052, 264508, 264905, 264905, 264907, 284908, 284909, 264510, 264511, 265009, 264910, 33657402, 264762, 284764, 284768, 284769, 284688, 21908765, 21908769, 35685917, 265020, 264693, 33657109, 284628, 35688423, 35695855, 284634, 284638
495	80028599 (989, 990)	Novel Protein sim. GBank gij2781517[emb]CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	transport	284602, 284682, 284638
496	78985624 (991, 992)	Novel Protein sim. GBank gij230281[pdb]1R69] - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix		284601, 265021
497	78948661 (993, 994)	Novel Protein sim. GBank gij129736[p]P28225[PDHX_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)]		oxidase	265008

498	88095488 (995, 996)	Novel Protein sim. GBank gij1145789 (U41662) - neuroigin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	264259, 26331826, 35698052, 264508, 264509, 264905, 264806, 264907, 264908, 264909, 264510, 264511, 265008, 264910, 264991, 33657402, 264758, 265010, 265011, 264600, 264601, 264605, 264683, 264764, 264766, 264767, 264768, 264687, 264769, 21808767, 33657023, 264693, 264628, 264629, 35698423, 264630, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 18108385, 264563, 264564, 264565, 264566, 264587, 264605
499	20438222 (997, 998)	Novel Protein sim. GBank gij97480[pilr]S18739 - integral membrane protein - Rhodobacter capsulatus	UNCLASSIFIED	264605
500	11076810 (999, 1000)	Novel Protein sim. GBank gij5708250[emb]CAB52363.1] - (AL109747) putative integral membrane protein	UNCLASSIFIED	264688
501	13418034 (1001, 1002)	[Streptomyces coelicolor A3(2)]		
502	80021176 (1003, 1004)	Novel Protein sim. GBank gij4468678[emb]CAB38132.1] - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	22278986, 265011, 264602, 264605, 264635
503	20264483 (1005, 1006)		UNCLASSIFIED	264584
504	10887321 (1007, 1008)		UNCLASSIFIED	264687
505	95003068 (1009, 1010)		UNCLASSIFIED	264389
506	16454282 (1011, 1012)		Contains protein domain (PF00036) - EF hand	265010
507	20451588 (1013, 1014)	Novel Protein sim. GBank gij4033509[sp]P02598[CALM, TETPY - CALMODULIN	UNCLASSIFIED	264604
508	79841424 (1015, 1016)	Novel Protein sim. GBank gij2501069[sp]Q46127[SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN-TRNA LIGASE) (TRPRS)	UNCLASSIFIED	264808
509	11776366 (1017, 1018)	Novel Protein sim. GBank gij466088[sp]P34618[YO82, CAEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III	UNCLASSIFIED	264638
510	83373465 (1019, 1020)		UNCLASSIFIED	264687, 264639
511	16525578 (1021, 1022)		UNCLASSIFIED	265007
512	20399484 (1023, 1024)	Novel Protein sim. GBank gij2497419[sp]P5635[Y4RB, RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB	UNCLASSIFIED	264555
513	78457404 (1025, 1026)	Novel Protein sim. GBank gij1276697 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - cyclin	264683, 264688, 35698423, 264639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gij1184780 (U46068) - von Ebner minor salivary gland protein [Mus musculus]	UNCLASSIFIED	29331830, 264909
515	79462561 (1029, 1030)			22278998, 264690
516	8862020 (1031, 1032)	Novel Protein sim. GBank gij2127400[pilr]S65770 - maltotriose trehalohydrolase - Arthrobacter sp. (strain Q36)	amylase	264810

517	95292884 (1033, 1034)	Novel Protein sim. GBank gi 2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 264764, 264768, 264687, 264891, 264565
518	8491831 (1035, 1036)	Novel Protein sim. GBank gi 854085 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264487
519	91877888 (1037, 1038)	Novel Protein sim. GBank gi 5689365 dbj BAA83073.1 - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_rna_bind	52644507, 22278997, 22278998, 60432049, 264259, 52645080, 28331824, 68714117, 60424269, 28331826, 35696052, 264905, 28331830, 68712502, 264511, 265007, 264591, 60432229, 33657402, 60433438, 21908754, 33109954, 52644286, 87168474, 87188559, 265017, 265018, 264604, 265019, 264681, 264448, 264389, 264288, 264685, 21908765, 21908766, 21908767, 21908769, 265021, 60170615, 33657023, 264692, 52645129, 33657109, 27486262, 27486264, 35695763, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 56526486, 60432113
520	79889188 (1039, 1040)				264769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gi 1169126 sp P48839 CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264605
522	80435080 (1043, 1044)	Novel Protein sim. GBank gi 172869 sp P44331 RBSK_HAEIN - RIBOKINASE	Contains protein domain (PF00284) - ptkB family carbohydrate kinase	kinase	264905, 264768
523	18356013 (1045, 1046)	Novel Protein sim. GBank gi 2132243 pir S81028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gi 4033608 dbj BAA35136 - (AB012308) B2HC [Anthracidaris crassispina]		ATPase_associated	264092, 264596, 265011
525	79810046 (1049, 1050)				264907
526	36827830 (1051, 1052)	Novel Protein sim. GBank gi 4106610 emb CAA21365 - (AL031866) ORF42, len=386 aa, similarity to an aminotransferase, in P85957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap. Fasta scores: opt:488. E(): 8.5e-24, In Q64602 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504729 (1053, 1054)			UNCLASSIFIED	264769
528	85484134 (1055, 1056)			UNCLASSIFIED	56182575, 265017, 265018
529	17936810 (1057, 1058)	Novel Protein sim. GBank gi 731088 sp P24215 XUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		hydrolase	265019
530	10887336 (1059, 1060)	Novel Protein sim. GBank gi 42144 emb CAA25200 - (X00513) NusA protein (nusA) [Escherichia coli]		UNCLASSIFIED	264687
531	80226578 (1061, 1062)			UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
532	80933444 (1063, 1064)	Novel Protein sim. GBank gi 5262640 emb CAB45758.1 - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264488, 264490, 264259, 264592, 264780, 265021, 264690, 263978, 264558

533	87761531 (1085, 1086)	Novel Protein sim. GBank gl 488363 gb AAD31583.1 AF11229 - (AF11229) integral inner nuclear membrane protein MAN1 [Homo sapiens]			264907, 264908, 264768, 35859517, 264630, 264555
534	82368284 (1087, 1088)	Novel Protein sim. GBank gl 2895352 emb CAA04606.1 - (AJ001206) pep1 [Streptomyces coelicolor]	UNCLASSIFIED		
535	78841850 (1089, 1070)	Novel Protein sim. GBank gl 3878638 emb CAA88933 - (Z49128) similar to cAMP-dependent protein kinase: cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492k.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	-ATPase-associated	264905, 265011, 264601, 264602, 264605, 264782, 264768, 265020, 264693, 264638 264808
536	78907207 (1071, 1072)	Novel Protein sim. GBank gl 2495628 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5/REGION	reductase		18108376, 264805, 264908, 264907, 264909
537	94147448 (1073, 1074)	Novel Protein sim. GBank			
538	87821863 (1075, 1076)	Novel Protein sim. GBank gl 134920 sp P21897 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	collagen		265008, 264605, 65274791 29331822, 29331824, 29331825, 29331826, 29331827, 264808, 52644045, 33857402, 265017, 264762, 264883, 264288, 264685, 21806765, 35895783, 264558, 60170394, 264559, 22279002 264602, 265019
539	26398269 (1077, 1078)	Novel Protein sim. GBank gl 2498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE	histone		
540	79637077 (1078, 1080)	Novel Protein sim. GBank gl 368224 jb BAA34480.1 - (AB018303) KIAA0760 protein [Homo sapiens]	transcript factor		264693 18108394, 22278997, 22278998, 264259, 264112, 265009, 33857402, 55812038, 52846317, 265017, 21806765, 264693, 55811578, 264635, 56526486, 264566 264910, 265018, 264689, 264638, 264488
541	87762268 (1081, 1082)	Novel Protein sim. GBank gl 5042272 emb CAB44526.1 - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase		
542	95285636 (1083, 1084)	Novel Protein sim. GBank gl 2791398 emb CAA15994 - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]	UNCLASSIFIED		
543	78798290 (1085, 1088)	Novel Protein sim. GBank	UNCLASSIFIED		
544	20437191 (1087, 1088)	Novel Protein sim. GBank	UNCLASSIFIED		
545	80434504 (1089, 1090)	Novel Protein sim. GBank			
546	80248016 (1091, 1092)	gl 4887211 gb AAD32237.1 AF14744 - (AF14744) penicillin binding protein 1B [Pseudomonas aeruginosa]			264768, 264634, 264907, 264592, 264909 264600, 264602, 21806765
547	11077563 (1083, 1084)	Novel Protein sim. GBank gl 1350855 sp P19176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT) Novel Protein sim. GBank gl 2330021 AF019250 - kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]	mapolymerase		264604
548	82114936 (1095, 1096)	Novel Protein sim. GBank	UNCLASSIFIED		264488, 264805, 264910, 264760, 264693, 264639, 264583, 264564

549	95421904 (1097, 1098)	Novel Protein sim. GBank gi 4337460 gb AAD1813 - (AF056195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108398, 22278985, 22278998, 22278997, 22278998, 22278999, 264259, 29331824, 68714117, 28331825, 28331826, 3586052, 285007, 265008, 264910, 264592, 33857402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264369, 264288, 264768, 264888, 264688, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 264691, 33657023, 264692, 264693, 65274820, 52845129, 33657109, 27486261, 27486262, 27486264, 33857349, 55811576, 18108387, 60432113, 22279002
550	10886816 (1099, 1100)				264688
551	80439890 (1101, 1102)	Novel Protein sim. GBank gi 3122893 sp P94985 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	264908, 264909, 264768
552	94672870 (1103, 1104)				
553	80106002 (1105, 1106)	Novel Protein sim. GBank gi 552087 (M33753) - crumbs protein [Drosophila melanogaster]	Contains protein domain (PF000008) - EGF-like domain	UNCLASSIFIED	264689, 264639, 264563
554	78818379 (1107, 1108)	Novel Protein sim. GBank gi 501977 gb AAD37857.1 AF13326 - (AF133263) histidine protein kinase-response regulator hybrid protein CvgSY [Pseudomonas syringae pv. syringae]		kinase	55811937, 264628
555	78896347 (1109, 1110)	Novel Protein sim. GBank gi 131515 sp P02908 PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)	Contains protein domain (PF003358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	264762
556	20457127 (1111, 1112)	Novel Protein sim. GBank gi 3814014 sp P96380 IMFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)		transcriptfactor	264508, 264605, 264559
557	19523405 (1113, 1114)	Novel Protein sim. GBank gi 5042273 emb CAB44527.1 - (AL078818) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264488
558	20724429 (1115, 1116)	Novel Protein sim. GBank gi 1170933 sp P4531 METE_HAEIN - 5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)		UNCLASSIFIED	264602
559	80084353 (1117, 1118)	Novel Protein sim. GBank gi 4980567 gb AAD35173.1 AE001694 - (AE001694) iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	264634

560	80066533 (1119, 1120)	Novel Protein sim. GBank gij2492595[sp]Q53183[Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - ABC transporter	transport	18108396, 264806, 264602, 264604, 18108374
561	20293187 (1121, 1122)			UNCLASSIFIED	264600
562	11688161 (1123, 1124)			UNCLASSIFIED	264689
563	78761420 (1125, 1126)	Novel Protein sim. GBank gij4104925 (AF042276) - poly(hydroxyalcanoate) granule associated protein GA2 [Pseudomonas putida]		UNCLASSIFIED	264910, 264691
564	56716380 (1127, 1128)	Novel Protein sim. GBank gij2792310 (AF040570) - unknown [Amycolatopsis mediterranei]	dehydrogenase		264592
565	56465618 (1129, 1130)	Novel Protein sim. GBank gij3449294[dbj]BA324621 - (AB011532) MEGF8 [Rattus norvegicus]	Contains protein domain (PF00008) - EGF-like domain	synthase	265010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gij4539568[emb]CAB38487.1] - (AL035636) putative helicase [Streptomyces coelicolor]		helicase	264909, 264510, 265008, 264910, 264758, 264600, 264602, 264604, 264605, 264788, 264687, 264689, 35895917, 264683, 65274620, 264488
567	79580955 (1133, 1134)	Novel Protein sim. GBank gij100506[pir]S17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria trinervia (fragment)	Contains protein domain (PF00390) - Malic enzyme	UNCLASSIFIED	264681, 264691, 264593
568	94681793 (1135, 1136)	Novel Protein sim. GBank gij3915843[sp]Q31212[RS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00318) - Ribosomal protein S2	ribosomalprot	264565
569	39508897 (1137, 1138)				
570	78375927 (1139, 1140)	Novel Protein sim. GBank gij115122[sp]P21627[BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		UNCLASSIFIED	18108376, 18108387, 264565
571	78793981 (1141, 1142)			transport	264907, 264908
572	36986838 (1143, 1144)	Novel Protein sim. GBank gij4539223[emb]CAB39881.1] - (AL049497) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	264782
573	20715521 (1145, 1146)			UNCLASSIFIED	265007, 264601
574	13521592 (1147, 1148)				264636
575	13076416 (1149, 1150)	Novel Protein sim. GBank gij118784[sp]P10443[DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN	polymerase		264887
576	20482246 (1151, 1152)	Novel Protein sim. GBank gij5457625[emb]CAB49116.1] - (AJ248283) PAB2227 [Pyrococcus abyssi]			264805
577	66727102 (1153, 1154)	Novel Protein sim. GBank gij5042274[emb]CAB44528.1] - (AL078618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	dehydrogenase	35686052, 264636
578	11804477 (1155, 1156)				264638
579	11784723 (1157, 1158)	Novel Protein sim. GBank gij1723081[sp]Q11046[Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY60.09	transport		264682, 264556

580	80058417 (1159, 1160)					22278999, 35696032, 264555, 264556, 264558
581	79230833 (1161, 1162)				UNCLASSIFIED	264558
582	80049617 (1163, 1164)	Novel Protein sim. GBank gi 3243131 (AF045777) - ilin	Contains protein domain (PF00047) -	struct		265008, 264564
583	79321392 (1165, 1166)	[Drosophila melanogaster] Novel Protein sim. GBank gi 2501162 sp P7726 YAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION	Immunoglobulin domain	transport		265021, 264555, 264557
584	79845024 (1167, 1168)					264594
585	79561454 (1169, 1170)	Novel Protein sim. GBank gi 388222 emb BAA34470.1 - (AB018293) KIAA0750 protein [Homo sapiens]		UNCLASSIFIED		264488, 264908, 264766, 264887, 35696423
586	38277488 (1171, 1172)	Novel Protein sim. GBank gi 4467250 emb CAB37575 - (AL035589) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		UNCLASSIFIED		265018, 264884, 21908789
587	80497359 (1173, 1174)	Novel Protein sim. GBank gi 5689519 db BAA83043.1 - (AB028014) KIAA1091 protein [Homo sapiens]		hydrolyase		264908, 265007
588	79557239 (1175, 1176)			UNCLASSIFIED		264600, 264602, 264603, 264769, 264680, 264557
589	79805828 (1177, 1178)			UNCLASSIFIED		265020, 264692
590	79815929 (1179, 1180)	Novel Protein sim. GBank gi 2143293 emb CAB09390 - (Z85972) rpoB [Mycobacterium tuberculosis]		UNCLASSIFIED		22278996, 264807, 264809, 264510, 265009, 265010, 264887, 264789, 35695917, 18108376, 264634, 264638, 264638
591	10313540 (1181, 1182)			mapolymerase		264908, 264909
592	13889767 (1183, 1184)	Novel Protein sim. GBank gi 4511983 gb AAD21543.1 - (AF088898) electrotransfer ubiquinone oxidoreductase [Zymomonas mobilis]		MHC		264691
593	82348698 (1185, 1186)	Novel Protein sim. GBank gi 1272368 (U51896) - LgE		dehydrogenase		263972
594	20212392 (1187, 1188)	[Vibrio parahaemolyticus] Novel Protein sim. GBank gi 131490 sp P20966 PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II; BC COMPONENT) (EIL-FRU)		UNCLASSIFIED		264511, 264762, 264769, 264486
595	10084064 (1189, 1190)					264605
596	13085170 (1191, 1192)					264769
597	80259003 (1193, 1194)				UNCLASSIFIED	264636
598	94140216 (1195, 1196)				UNCLASSIFIED	264592
599	20385137 (1197, 1198)	Novel Protein sim. GBank gi 125328 sp P04951 KDSB_ECOLI - 3-DEOXY-MANNO- OCTULONATE CYTIDYLTRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULONIC ACID SYNTHETASE) (CKS)		UNCLASSIFIED		264758, 55810764, 264555, 264558, 264637, 83373044
600	10357663 (1199, 1200)					264603
601	79610404 (1201, 1202)	Novel Protein sim. GBank gi 2127414 p IS60064 - hypothetical protein 2 - Corynebacterium glutamicum		UNCLASSIFIED		264906

602	78250602 (1203, 1204)	Novel Protein sim. GBank gi 3522861 gb AAC34243.1 - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - kinase	265007	
603	11466087 (1205, 1208)		UNCLASSIFIED	264595	
604	81675420 (1207, 1208)		UNCLASSIFIED	264758	
605	20436657 (1206, 1210)		UNCLASSIFIED	264605	
606	80334582 (1211, 1212)	Novel Protein sim. GBank gi 175322 sp P44917 Y883_HAEIN - HYPOTHETICAL PROTEIN H10883	UNCLASSIFIED	264764	
607	96381506 (1213, 1214)	Novel Protein sim. GBank gi 5020284 gb AAD38043.1 AF15136 - (AF151363) Cdc42 GTPase-activating protein [Mus musculus]	UNCLASSIFIED	264508, 264808, 85658542, 264682, 264687, 264689, 264534, 18108376, 35898423, 264636, 264555, 264638	
608	11810888 (1215, 1216)	Novel Protein sim. GBank gi 2496701 sp P5552 Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	UNCLASSIFIED	264682	
609	80084775 (1217, 1218)		UNCLASSIFIED	264605	
610	79829413 (1219, 1220)			264692	
611	87586205 (1221, 1222)			264508, 264805, 264807, 264808, 264809, 264511, 264910, 264758, 264604, 264684, 264758, 264688, 264692, 264628, 264635, 264636, 264637, 264558	
612	95287851 (1223, 1224)	Novel Protein sim. GBank gi 1877366 emb CAB07118 - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - nuclease	264600, 264601, 264604, 264769, 264558, 264565	
613	7523475 (1225, 1226)	Novel Protein sim. GBank gi 114231 gb AAD40236.1 AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]	UNCLASSIFIED	264369	
614	79869348 (1227, 1228)	Novel Protein sim. GBank gi 1339950 gb BAA12741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	kinase	18108372, 264563	
615	39566898 (1229, 1230)	Novel Protein sim. GBank gi 1339950 gb BAA12741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	synthase	264600, 264602, 264629	
616	20465331 (1231, 1232)	Novel Protein sim. GBank gi 544367 sp P35673 GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GLACTOSE 4-EPIMERASE)	isomerase	264605	
617	91227222 (1233, 1234)	Novel Protein sim. GBank gi 2498087 sp Q60769 TNF3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	52845156, 21806765, 35698423, 21806768, 21806769, 22278994, 35898286, 22278998, 265020, 265021, 265007, 265008, 264636, 52844150, 33657023, 264692, 264693, 29331822, 29331824, 55812038, 83373044, 58182181, 60424269, 66714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35898052, 29331828, 27486262, 33657349, 56528486, 285018, 265019, 22278002, 284482, 264448, 29331830, 66712502, 284908	

618	20632843 (1235, 1236)	Novel Protein sim. GBank gl 5459388 emb CAB50746.1 - (AL088839) putative aminotransferase (Streptomyces coelicolor)		isomerase	264603	
619	91227224 (1237, 1238)				56994075, 28331826, 33656970, 265008, 33657402, 33109954, 87166559, 264448, 18108374, 83373044	
620	81183143 (1238, 1240)	Novel Protein sim. GBank gl 464335 sp Q05922 DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)		phosphatase	29146498, 264756, 264389, 29146627	
621	80239251 (1241, 1242)			UNCLASSIFIED	264558, 264558, 264639	
622	20456427 (1243, 1244)	Novel Protein sim. GBank gl 26333557 emb CAB13060 - (Z99110) ydf [Bacillus subtilis]		UNCLASSIFIED	264605	
623	10131798 (1245, 1246)	Novel Protein sim. GBank gl 1857710 gb AAB48482 - (U87224) clonatin associated protein [Rattus norvegicus]	Contains protein domain (PF00054) - Laminin G domain	laminin	264906	
624	18534127 (1247, 1248)	Novel Protein sim. GBank gl 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	264596	
625	13084619 (1248, 1250)	Novel Protein sim. GBank gl 2894252 emb CAA17114.1 - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688	
626	88062603 (1251, 1252)	Novel Protein sim. GBank gl 416592 sp P32323 ACA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 264905, 264908, 33657023, 33657109, 264558	
627	80255457 (1253, 1254)	Novel Protein sim. GBank gl 3098418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 284112, 264593, 265022, 264635	
628	80077096 (1255, 1256)	Novel Protein sim. GBank gl 1711543 sp P50526 SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264600	
629	79851602 (1257, 1258)	Novel Protein sim. GBank gl 1143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	284908, 264907	
630	39565168 (1259, 1260)	Novel Protein sim. GBank gl 3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490	
631	20598718 (1261, 1262)	Novel Protein sim. GBank gl 140687 sp P1666 YGGG_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F288)			263878	
632	27843890 (1263, 1264)			UNCLASSIFIED	264908, 264600, 264605, 264769, 264689, 264486	
633	80477772 (1265, 1266)			UNCLASSIFIED	264769	
634	17938808 (1267, 1268)				265019	
635	79574508 (1269, 1270)			UNCLASSIFIED	264689	
636	79910981 (1271, 1272)			UNCLASSIFIED	264598, 264762, 264693	

637	82455798 (1273, 1274)	Novel Protein sim. GBank gij2326739[emb CAB10953] - (Z90286) recN [Mycobacterium tuberculosis]		nuclease	264906, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264762, 264768, 264687, 264769, 264689, 35695917, 264693, 264634, 264638, 264639, 264559, 18108385
638	14997457 (1275, 1276)	Novel Protein sim. GBank gij4678662[emb CAB41074.1] - (AL049645) putative large ATP-binding protein [Streptomyces coelicolor]			264638
639	80204210 (1277, 1278)	Novel Protein sim. GBank gij4589628[dbj BAAT6638.1] - (AB023209) KIAA0992 protein [Homo sapiens]		struct	264112, 263974
640	17928579 (1279, 1280)	Novel Protein sim. GBank gij1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - Skp1 family	(m)polymerase	265009, 265010
641	79636398 (1281, 1282)			UNCLASSIFIED	264693
642	19898737 (1283, 1284)			UNCLASSIFIED	264565
643	81616220 (1285, 1286)			UNCLASSIFIED	264906, 264908, 264758, 264288, 264632, 264635, 264639, 264584
644	11751367 (1287, 1288)			UNCLASSIFIED	264684
645	95010807 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80069083 (1291, 1292)			UNCLASSIFIED	264595, 264566
647	80257085 (1293, 1294)	Novel Protein sim. GBank gij4507813[ref NP_003738.1 pTINKS - TANKYRASE	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	264906, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gij1044983[dbj 169646 - prolamine [Monodonta turbinata, gonads, Peptide, 106 aa]		UNCLASSIFIED	264600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11788316 (1299, 1300)			UNCLASSIFIED	264688
651	11776932 (1301, 1302)	Novel Protein sim. GBank gij1346916[sp P12283 PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP-ASPARTATE LIGASE)			264602, 264638
652	85516704 (1303, 1304)				
653	82124947 (1305, 1306)	Novel Protein sim. GBank gij1722977[sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	264905, 264907, 264909, 263978, 264637
654	95010569 (1307, 1308)			UNCLASSIFIED	22278996, 264510, 264511, 264512, 264593, 21906754, 264603, 264760, 18108376, 264558
655	79320692 (1309, 1310)	Novel Protein sim. GBank gij130327[sp P26647 PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)	Contains protein domain (PF01553) - Acyltransferase	UNCLASSIFIED	264906, 264595, 264632
656	80416739 (1311, 1312)				
657	20811010 (1313, 1314)			UNCLASSIFIED	264602, 264605, 264766, 264691
				UNCLASSIFIED	264557, 264558

858	87761015 (1315, 1316)	Novel Protein sim. GBank gij5689493[dbj][BAA03030.1] - (AB029001) KIAA1078 protein [Homo sapiens]		UNCLASSIFIED	22278986, 60432049, 29331822, 29331824, 29331828, 265007, 265008, 33657402, 33657084, 265017, 264448, 21906785, 21906766, 263967, 20281149, 18108370, 18108374, 264482
859	87718663 (1317, 1318)	Novel Protein sim. GBank gij2137872[pir][48724 - zinc finger protein PFZ - mouse]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcriptfactor	22278989, 60432049, 66714117, 29331827, 265007, 264766, 58181582, 18108358, 18108365, 18108370, 18108381
860	81987922 (1319, 1320)	Novel Protein sim. GBank gij134180[sp15401][SACY_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTERMINATOR]	Contains protein domain (PF00874) - Transcriptional antiterminalator bglG family	UNCLASSIFIED	264757
861	60026023 (1321, 1322)	Novel Protein sim. GBank gij454522[gb][A022450.1][AF11818 - (AF118183) SecA homolog [Actinobacillus actinomycetemcomitans]		UNCLASSIFIED	264510, 265009, 264600, 264602, 264603, 264604, 264605, 32833986, 18108376, 264636, 18108387, 22278900
862	20463731 (1323, 1324)	Novel Protein sim. GBank gij454522[gb][A022450.1][AF11818 - (AF118183) SecA homolog [Actinobacillus actinomycetemcomitans]		UNCLASSIFIED	264605
863	20626080 (1325, 1326)	Novel Protein sim. GBank gij5689250[dbj][BAA02891.1] - (AB024335) similar to orf5 [Comamonas testosteroni]		dehydrogenase	264605
864	60508512 (1327, 1328)	Novel Protein sim. GBank gij1652846[dbj][BAA17766] - (D90909) DNA photolyase [Synechocystis sp.]		UNCLASSIFIED	264769
865	60078053 (1329, 1330)	Novel Protein sim. GBank gij116841[sp121640][COBJ_PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE)]		isomerase	264600
866	78603142 (1331, 1332)	Novel Protein sim. GBank gij3261829[emb][CAB10827] - (Z98260) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	264907, 265007
867	94631802 (1333, 1334)	Novel Protein sim. GBank gij5688851[dbj][BAA02702.1] - (AB017438) Orf5 [Streptomyces coelicolor]		UNCLASSIFIED	264689, 264602, 264593
868	82051891 (1335, 1336)	Novel Protein sim. GBank gij3581853[emb][CAA20808] - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) - Ribosomal protein L20	ribosomalprot	264905, 264906, 264908, 264600, 264601, 264603, 264605, 264760, 264689, 264636, 264638, 264639
869	12867154 (1337, 1338)	Novel Protein sim. GBank gij2582531 [AF026444] - 2- isopropylmalate synthase [Streptomyces coelicolor]		UNCLASSIFIED	264637
870	80238549 (1339, 1340)	Novel Protein sim. GBank gij2582531 [AF026444] - 2- isopropylmalate synthase [Streptomyces coelicolor]		synthase	264905, 264906, 264908, 264601, 264762, 264766, 264689, 264638, 18108385, 264486
871	78601368 (1341, 1342)	Novel Protein sim. GBank gij2582531 [AF026444] - 2- isopropylmalate synthase [Streptomyces coelicolor]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264690, 264692, 264693, 264636, 18108387
872	78634371 (1343, 1344)	Novel Protein sim. GBank gij2114430 [U02703] - Olf-1/EBF-like-3 transcription factor [Mus musculus]		transcriptfactor	264910, 265017
873	82285788 (1345, 1346)	Novel Protein sim. GBank gij4580285[gb][A026430.1][AF135154] ferric alkaligin siderophore receptor [Bordetella pertussis]			264759
874	78198259 (1347, 1348)			UNCLASSIFIED	264629

675	87895870 (1349, 1350)	Novel Protein sim. GBank gi 4980755 gb AAD35347.1 AE001708) D- alanine--D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	284488, 22278989, 68714117, 264508, 284511, 265008, 60433438, 264600, 264601, 264602, 264603, 264604, 264605, 264782, 264687, 264789, 60431602, 18108374, 264636, 264638 265010
676	78898607 (1351, 1352)	Novel Protein sim. GBank gi 1723566 sp Q10478 YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07			
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi 687208 (U03976) - dynein heavy chain isotype 5C [Tripneustes gratilla]		ATPase-associated	284591, 264632
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi 1586274 pr J2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264758, 264682, 264557
679	79868855 (1357, 1358)	Novel Protein sim. GBank gi 3828723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278988, 264693
680	20726424 (1359, 1360)	Novel Protein sim. GBank			
681	84322017 (1361, 1362)	gi 5174493 ref NP_006050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264600, 264602 264102, 264907, 264908, 265008, 264693, 263972, 83373044, 264568
682	11382478 (1363, 1364)	Novel Protein sim. GBank		UNCLASSIFIED	264595
683	80083680 (1365, 1366)	gi 4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related) Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	264634 264605
684	20465387 (1367, 1368)				
685	80246735 (1369, 1370)				
686	78208608 (1371, 1372)				284809, 263967, 263881
687	80085829 (1373, 1374)				264631
688	79853412 (1375, 1376)				264693, 264635
689	88084258 (1377, 1378)	Novel Protein sim. GBank gi 2688862 (AF027768) - Lspa [Serratia marcescens] Novel Protein sim. GBank gi 3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]		peptidase	264807, 264638
690	80388750 (1379, 1380)	Novel Protein sim. GBank gi 2498941 sp Q15428 SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A68)	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264808, 264907, 265007, 265009, 60433438, 21908754, 264760, 18108358, 21808786, 21908769, 265021, 18108361, 263974, 18108379, 264557, 18108385, 22279002 264510, 264511, 264784, 264789
691	81854392 (1381, 1382)				
692	83608936 (1383, 1384)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264757 55812038, 55811957, 265018, 55811150, 18108351, 264908, 60431528, 264594
693	79586116 (1385, 1386)	Novel Protein sim. GBank gi 854065 emb CAA56337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264635
694	82455083 (1387, 1388)	Novel Protein sim. GBank gi 267327 sp Q01033 VG48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278988, 264510, 264602, 264603, 264762, 264697, 264789, 264693

695	84147849 (1389, 1390)	Novel Protein sim. GBank gij4468339[embjCAB38059.1] - (AJ010901) MUC4 [Homo sapiens]	Contains protein domain (PF00084) - von Willebrand factor type D domain	UNCLASSIFIED	56182575, 264509, 264805, 264807, 26331830, 264808, 264809, 264511, 265007, 264910, 264758, 264764, 264288, 65274781, 264905, 264595
696	79830882 (1391, 1392)	Novel Protein sim. GBank gij2649950 (AE001059) - glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	
697	11767869 (1393, 1384)	Novel Protein sim. GBank gij1731343[spQ10694]YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY48.25	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	264682
698	66695862 (1395, 1396)			UNCLASSIFIED	264688, 35985917
699	79587558 (1397, 1398)			UNCLASSIFIED	264682
700	79830908 (1399, 1400)			UNCLASSIFIED	264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gij1001236[dbjBAA10471] - (DB4003) hypothetical protein [Synectocystis sp.]		UNCLASSIFIED	264488, 264510, 264511, 264602, 264605,
702	79814789 (1403, 1404)	Novel Protein sim. GBank gij249835[spQ46338]SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT		UNCLASSIFIED	264689
703	20446820 (1405, 1406)			oxidase	264604
704	84312224 (1407, 1408)	Novel Protein sim. GBank gij3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 56181562, 33657109, 264628, 55811576
705	17832141 (1409, 1410)	Novel Protein sim. GBank gij421091[pirjIS30730] - hypothetical protein o206 - Escherichia coli		UNCLASSIFIED	265006
706	20288062 (1411, 1412)	Novel Protein sim. GBank gij3024872[spQ55790]Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074			264600
707	20638065 (1413, 1414)	Novel Protein sim. GBank gij3420608[gbjAAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]		transport	264603
708	20708292 (1415, 1416)	Novel Protein sim. GBank gij3649741[embjCAA03985] - (AJ000281) mucin [Homo sapiens]			264601, 264692
709	88001439 (1417, 1418)	Novel Protein sim. GBank gij3080423[embjCAA18744.1] - (AL022604) putative protein [Arabidopsis thaliana]		struct	18106398, 264637, 264808, 264809
710	11356683 (1419, 1420)				264369
711	17931418 (1421, 1422)	Novel Protein sim. GBank gij4758686[refjNP_002323.1]pLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Contains protein domain (PF00056) - Low-density lipoprotein receptor repeat class B	apolipoprotein	265019, 284591
712	80258164 (1423, 1424)				
713	78263126 (1425, 1426)	Novel Protein sim. GBank gij1703266[spQ11056]AM12_MYCTU - PUTATIVE AMIDASE CY50.19C		hydrolase	264806, 264807
714	27847651 (1427, 1428)	Novel Protein sim. GBank gij4502351[refjNP_001692.1]pBAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choyltransferase			264508, 264555

715	76639423 (1429, 1430)	Novel Protein sim. GBank gl 1789035 (AE000352) - ori, hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907	
716	76559072 (1431, 1432)				264692	
717	78491842 (1433, 1434)	Novel Protein sim. GBank gl 2494074 (sp P55653 GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+)) (SSDH)		dehydrogenase	264636	
718	94319658 (1435, 1436)	Novel Protein sim. GBank gl 3873579 (emb CAA94886 - (Z71178) similar to pro-collagen domains: cDNA EST EMBL:D27878 comes from this gene; cDNA EST EMBL:D27877 comes from this gene; cDNA EST EMBL:D34189 comes from this gene; cDNA EST EMBL:D84392 comes from this gene; cDNA EST EMBL...)	Contains protein domain (PF00083) - kinase von Willebrand factor type C domain		18108382, 22278984, 22278988, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21908769, 18108361, 264681, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388	
719	17679564 (1437, 1438)	Novel Protein sim. GBank gl 2104302 (emb CAB08631 - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis])		UNCLASSIFIED	265011	
720	79841684 (1439, 1440)				264908	
721	15020780 (1441, 1442)	Novel Protein sim. GBank gl 1235303 (sp P04928 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629	
722	9862603 (1443, 1444)	Novel Protein sim. GBank gl 498253 (U02372) - integrase [Vibrio cholerae]			264910	
723	19755599 (1445, 1446)	Novel Protein sim. GBank gl 2253054 (emb CAB10705 - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis])		UNCLASSIFIED	264681	
724	10126494 (1447, 1448)	Novel Protein sim. GBank gl 4083015 (AF083061) - protease PrtA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - protease Hemolysin-type calcium-binding proteins		264909	
725	76878679 (1449, 1450)					
726	13066282 (1451, 1452)			UNCLASSIFIED	264905, 264907	
727	13522872 (1453, 1454)			UNCLASSIFIED	264636	
728	20268471 (1455, 1456)	Novel Protein sim. GBank gl 2633910 (emb CAB13411 - (Z99112) similar to hypothetical proteins [Bacillus subtilis])			264634	
729	11293753 (1457, 1458)				264567	
730	18900373 (1459, 1460)	Novel Protein sim. GBank gl 2494660 (sp Q45291 GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		UNCLASSIFIED	264490	
731	80058750 (1461, 1462)	Novel Protein sim. GBank gl 1146192 (L47838) - putative [Bacillus subtilis]		isomerase	264564	
732	80258175 (1463, 1464)	Novel Protein sim. GBank gl 1168390 (sp P46861 AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		UNCLASSIFIED	264605	
733	20446839 (1465, 1466)			struct	264591, 264594, 264595	
734	20435987 (1467, 1468)	Novel Protein sim. GBank gl 3184080 (emb CAA19338 - (AL023781) hypothetical protein [Schizosaccharomyces pombe])		UNCLASSIFIED	264604	
				ubiquitin	264604	

735	11607859 (1468, 1470)	Novel Protein sim. GBank gi 401582 sp P27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELG INTERGENIC REGION			264594
736	10879734 (1471, 1472)	Novel Protein sim. GBank gi 400831 sp P31135 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264636
737	78945340 (1473, 1474)		Contains protein domain (PF00815) - Regulator of G protein signaling domain	UNCLASSIFIED	265020
738	17895353 (1475, 1476)	Novel Protein sim. GBank		oxidase	265008
739	79833870 (1477, 1478)	Novel Protein sim. GBank gi 2506867 sp P33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)			264910
740	19881557 (1479, 1480)	Novel Protein sim. GBank gi 3261828 emb CAB10925 - (Z98260) mmp [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED	264907, 264764, 264634, 264637
741	79827273 (1481, 1482)	Novel Protein sim. GBank gi 3877494 emb CAA88472.1 - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D68340 comes from this gene; cDNA EST EMBL:D65049 comes from this gene; cDNA EST EMBL:D6845...		UNCLASSIFIED	264688, 35886286, 264510, 264808, 18108362
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi 127420 sp P19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED	264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264628, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264584, 264567
743	82300051 (1485, 1486)	Novel Protein sim. GBank			18108397, 264511, 264690, 264628, 264638, 264692, 264639, 264766
744	80230421 (1487, 1488)			glycoprotein	264906
745	8841863 (1489, 1490)	Novel Protein sim. GBank gi 78921 pir S04846 - UDP-N- acetyl-muramoyl-alanyl-D-glutaryl-2, 6-diaminopimelate--D- alanyl-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli			
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi 3386354 (AF074705) - pyocellin synthetase [Pseudomonas aeruginosa]		synthase	264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi 2887411 dbj BAA24848 - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase	68714117, 264905, 264509, 264906, 264807, 264908, 264909, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264768, 264769, 21900768, 35895917, 264681, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)				264680

748	20469119 (1497, 1498)	Novel Protein sim. GBank glj1169727[sp]P44948[PPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)		UNCLASSIFIED	264604 264600	
750	20296427 (1498, 1500)	Novel Protein sim. GBank glj536008[gb]AAD2851.1[AF15968 - (AF159689) serine/threonine kinase PKN3 [Myxococcus xanthus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264605, 264559	
751	21636169 (1501, 1502)	Novel Protein sim. GBank glj1168862[sp]P44426[BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	264508, 264907, 264510, 265011, 264782, 264688, 35895855, 264638, 18108387	
753	80508718 (1505, 1506)	Novel Protein sim. GBank glj2851530[sp]P32399[YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLT TT INTERGENIC REGION (ORF8)]		UNCLASSIFIED	264908, 264600, 264602, 264604, 264760, 264769, 264634	
754	95083741 (1507, 1508)			UNCLASSIFIED	264508, 264906, 264907, 264908, 264909, 264759, 264802, 264764, 264788, 264628, 264629, 264630, 264632, 264634, 264635, 264637, 264638, 83373044, 18108385	
755	80185449 (1509, 1510)			UNCLASSIFIED	264448, 264690	
756	84631686 (1511, 1512)	Novel Protein sim. GBank glj3449276[emb]CAA20420[- (AL031317) putative dehydrogenase [Streptomyces coelicolor]		UNCLASSIFIED	264769, 264689, 264638, 264639	
757	79468533 (1513, 1514)	Novel Protein sim. GBank glj4580331[emb]CAB40107.1[- (AJ001208) putative glycogen debranching enzyme [Streptomyces coelicolor]		UNCLASSIFIED	264682, 264685	
758	78963176 (1515, 1516)	Novel Protein sim. GBank glj2911858 (AF047659) - No definition line found [Caenorhabditis elegans]	amylase	265007, 18108387, 265007, 18108387		
759	79475667 (1517, 1518)	Novel Protein sim. GBank glj3451312[emb]CAA20449[- (AL031324) membrane alase [Schizosaccharomyces pombe]		UNCLASSIFIED	264684, 264686	
760	87628888 (1519, 1520)	Novel Protein sim. GBank glj3327158[db]BAA31647[- (AB014572) KIAA0672 protein [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	29331822, 264908, 52644045, 56182435, 60170831, 21806754, 265017, 265019, 284681, 264687, 264688, 21806766, 21806768, 265020, 265021, 265022, 264635, 22279000	
761	79877966 (1521, 1522)	Novel Protein sim. GBank glj3327158[db]BAA31647[- (AB014572) KIAA0672 protein [Homo sapiens]		UNCLASSIFIED	264768	
762	80023563 (1523, 1524)	Novel Protein sim. GBank glj4981266[gb]AAD35822.1[AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdtB (Thermotoga maritima)]		UNCLASSIFIED	264907, 264593, 265020	
763	20294813 (1525, 1526)			UNCLASSIFIED	264600	
764	39515024 (1527, 1528)				264603	

765	80025347 (1528, 1530)	Novel Protein sim. GBank gi 3845083 (AE001371) - erythrocyte membrane protein PEMP3 (Plasmodium falciparum)		struct	284905, 284908, 284594, 284686, 33657023
766	82417404 (1531, 1532)	Novel Protein sim. GBank gi 541121 pir S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	284605, 284762, 18108374
767	10298742 (1533, 1534)	Novel Protein sim. GBank gi 541121 pir S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	284607
768	79416080 (1535, 1536)	Novel Protein sim. GBank gi 2882501 emb CAA06164 - (AJ004832) neuropathy target esterase [Homo sapiens]		UNCLASSIFIED	284592, 284593
769	80086594 (1537, 1538)	Novel Protein sim. GBank gi 283437 pir S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		esterase	55810764, 284559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gi 4768004 gb AAD29715.1 AF14059 - (AF140598) ring-box protein 1 [Homo sapiens]		UNCLASSIFIED	284905, 284907, 284828, 284908, 285010, 284766, 284628, 284629, 284634, 284636, 284555
771	95329508 (1541, 1542)	Novel Protein sim. GBank gi 4768004 gb AAD29715.1 AF14059 - (AF140598) ring-box protein 1 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35686286, 284259, 66714117, 284107, 66712502, 56182435, 284112, 55812038, 87168559, 284288, 21908766, 33657023, 65274620, 65274791, 18108381
772	78971362 (1543, 1544)	Novel Protein sim. GBank gi 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	284910
773	78945363 (1545, 1546)	Novel Protein sim. GBank gi 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	285020
774	78856129 (1547, 1548)	Novel Protein sim. GBank gi 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	284909
775	20820141 (1549, 1550)	Novel Protein sim. GBank gi 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	284555
776	78842893 (1551, 1552)	Novel Protein sim. GBank gi 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]	Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	UNCLASSIFIED	285019
777	79960378 (1553, 1554)	Novel Protein sim. GBank gi 4505461 ref NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)	Contains protein domain (PF01344) - Kelch motif	protease	21808754, 265020, 60170615, 264691
778	20691310 (1555, 1556)	Novel Protein sim. GBank gi 4505461 ref NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)		UNCLASSIFIED	284511
779	80054024 (1557, 1558)	Novel Protein sim. GBank gi 1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	284603
780	85288987 (1559, 1560)	Novel Protein sim. GBank gi 1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]			284907, 284600, 284601, 284602, 284603, 284604, 284605, 284486
781	80250049 (1561, 1562)	Novel Protein sim. GBank gi 1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		UNCLASSIFIED	284905, 284907, 285010, 284600, 284601, 18108362, 18108374, 284556
782	8758529 (1563, 1564)	Novel Protein sim. GBank gi 4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	284605
783	16410791 (1565, 1566)	Novel Protein sim. GBank gi 4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]			285020
784	80051197 (1567, 1568)	Novel Protein sim. GBank gi 4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	284635, 33657023, 28331828, 265017, 284565, 284566
785	56073541 (1569, 1570)	Novel Protein sim. GBank gi 3451335 (AC005525) - F22162.1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 284604
786	20438842 (1571, 1572)	Novel Protein sim. GBank gi 136748 sp P10905 UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA		transport	284603
787	80258364 (1573, 1574)	Novel Protein sim. GBank gi 136748 sp P10905 UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA		UNCLASSIFIED	284593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gij2748079 (AF015310) - BTH1 [Brassica napus]		synthase	264909, 264602, 264603, 264769, 264638
789	17204715 (1577, 1578)	Novel Protein sim. GBank gij2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium salinarum]		UNCLASSIFIED	265007
790	86284408 (1579, 1580)	Novel Protein sim. GBank gij5706378 [dbj]BAA03099.1 - (AB026118) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22278999, 29331824, 264828, 87168559, 265018, 21906785, 21906787, 21906788, 21906789, 265020, 264692, 22278000, 264563
791	84651627 (1581, 1582)	Novel Protein sim. GBank gij5689849 [emb]CAB51885.1 - (AL109883) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			264601, 264605, 264638
792	80058786 (1583, 1584)	Novel Protein sim. GBank gij393194 (L02375) - S-antigen [Plasmodium falciparum]		struct	265021, 264631, 264635, 264556
793	79638730 (1585, 1586)	Novel Protein sim. GBank gij1345408 [dbj]BAA05046 - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264693
794	81839284 (1587, 1588)	Novel Protein sim. GBank gij1050884 [pir]S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	264603, 264604, 264910, 264762, 264908, 264638, 264909, 284757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gij1877334 [emb]CAB07082 - (Z92771) birA [Mycobacterium tuberculosis]		carboxylase	35698423, 264636
796	86669451 (1591, 1592)				60432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gij2995447 [emb]CAA71519 - (Y10495) CDV-1R protein [Mus musculus]		struct	22278998, 264093, 264094, 66714117, 21906787, 21906769, 265020, 265022
798	79865209 (1595, 1596)	Novel Protein sim. GBank gij4487250 [emb]CAB37575 - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		transcript factor	284687, 264768, 264693
799	79557818 (1597, 1598)			hydrolase	264909, 264910, 264638, 264638
800	79970189 (1599, 1600)				
801	80499398 (1601, 1602)	Novel Protein sim. GBank gij2791517 [emb]CAA16054 - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
802	79834598 (1603, 1604)	Novel Protein sim. GBank gij4887211 [gb]AAD32237.1 [AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]		transport	264508, 264511, 265006, 265009, 264769, 264587, 264486
803	20467520 (1605, 1606)				264905, 264693
804	10174239 (1607, 1608)	Novel Protein sim. GBank gij1176152 [sp]P44507 [YHAD_HAEIN - HYPOTHETICAL PROTEIN H10091]		struct	264605
805	79599993 (1609, 1610)			kinase	264510
806	80484113 (1611, 1612)	Novel Protein sim. GBank gij2764612 [emb]CAA04683 - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	transferase	264508, 264769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gij2833311 [sp]Q21828 [YNFCD_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			264764

808	35108817 (1615, 1616)	Novel Protein sim. GBank gij3913092ispq46170JARCO_CLOPE - ARGININE/ORNITHINE ANTIPOPTER		transport	264909, 264602, 21908764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gij3913016isp74309JALF1_SYNY3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264906, 264909, 265007, 264810, 264758, 264600, 264602, 264603, 264605, 264687, 264769, 264689, 264636, 264486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gij401472ispj30863JYAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION	Contains protein domain (PF00248) - Aldo/Keto reductase family	reductase	264389
811	80079280 (1621, 1622)			UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gij146168 (J01617) - glutaminyl- tRNA synthetase [Escherichia coli]		synthase	264805, 264602, 264605, 264682, 264687, 264789, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gij4389652jbjBAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264486, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 264905, 264908, 265007, 33657402, 60433356, 60433438, 264758, 265011, 265017, 265018, 265019, 264369, 264288, 264685, 21906765, 21906767, 265020, 265021, 264692, 65274820, 33857109, 264629, 18108376, 264635, 264638, 60170394, 58182323, 264564 264600
816	19881910 (1631, 1632)	Novel Protein sim. GBank gij1781144[emb]CAB06254] - (Z63866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	264595
817	95293318 (1633, 1634)	Novel Protein sim. GBank gij1477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278998, 60424269, 35686052, 55812038, 21906769, 55811957, 35685917, 33857023, 18108370, 18108374, 55810764, 35686423, 55811576, 264636
818	90938180 (1635, 1636)	Novel Protein sim. GBank gij1001352[jbj]BAA10839] - (D64006) ABC transporter [Synecocystis sp.]		transport	264555
819	80254977 (1637, 1638)	Novel Protein sim. GBank gij1001352[jbj]BAA10839] - (D64006) ABC transporter [Synecocystis sp.]		UNCLASSIFIED	264600, 264602, 264604
820	80059688 (1639, 1640)	Novel Protein sim. GBank gij566814ispj37484YYBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION			
821	79762590 (1641, 1642)	Novel Protein sim. GBank gij3878400[emb]CAA95828] - (Z71264) predicted using GeneFinder; Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST...		UNCLASSIFIED	264910
822	80215310 (1643, 1644)	Novel Protein sim. GBank gij1370076[emb]CAA66887] - (X98235) type I [Drosophila melanogaster]		UNCLASSIFIED	264510, 264594, 264637
823	94992299 (1645, 1646)			struc	264509, 264687, 264691
824	80411171 (1647, 1648)		Contains protein domain (PF01429) - Methyl-CpG binding domain		264910, 264763, 264769, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank glj3025132[sp]P77391YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	284592	
826	11075047 (1651, 1652)	Novel Protein sim. GBank glj3242281[emb]CAA16669] - (AL021646) hypothetical protein RV3202c [Mycobacterium tuberculosis]			284605	
827	80054207 (1653, 1654)	Novel Protein sim. GBank glj3417424[emb]CAA20312] - (AL031281) putative transport protein [Schizosaccharomyces pombe]			284603	
828	95106322 (1655, 1656)	Novel Protein sim. GBank glj4336692[gb]AAD17897] - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 284508, 284905, 284508, 284508, 284908, 284907, 284908, 284909, 284512, 284910, 284591, 284758, 284600, 284768, 284768, 21908768, 35895917, 284691, 284628, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284556, 284639, 83373044, 18108385, 284563, 284566, 284486	
829	81742215 (1657, 1658)	Novel Protein sim. GBank glj3820539 (AF080002) - UDP-N- acetylmutamyl tripeptide synthetase MurC [Heliobacillus mobilis]		UNCLASSIFIED	284758, 284634	
830	20396091 (1659, 1660)	Novel Protein sim. GBank glj1870004[emb]CAB06855] - (Z82539) hypothetical protein RV1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	66714117, 284910, 284639	
831	87112435 (1661, 1662)	Novel Protein sim. GBank glj2500056[sp]Q46267[PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	284602	
832	19536322 (1663, 1664)	Novel Protein sim. GBank glj2497531[sp]Q46078[KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - kinase Pyruvate kinase	UNCLASSIFIED	284600, 284602, 284769, 284689, 284636	
833	20726654 (1665, 1666)	Novel Protein sim. GBank glj28867[sp]P40802[APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR			284768, 263994, 21906767, 284910, 284632, 284635, 284259, 284639, 284693, 83373044, 284758, 35895052, 22279002, 284508, 284905, 284806, 264448, 283972, 284908, 284909	
834	21426782 (1667, 1668)	Novel Protein sim. GBank glj2497531[sp]Q46078[KPYK_CORGL - PYRUVATE KINASE (PK)		UNCLASSIFIED	35895917, 284557	
835	94140482 (1669, 1670)	Novel Protein sim. GBank glj28867[sp]P40802[APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	284595	
836	68126552 (1671, 1672)	Novel Protein sim. GBank glj2498533[sp]Q50598[YOD8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	284687	
837	78450450 (1673, 1674)	Novel Protein sim. GBank glj4557753[re]NP_000372.1[pm]DI1 - midline 1 protein	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	284806	
838	79184203 (1675, 1676)	Novel Protein sim. GBank glj28867[sp]P40802[APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	284687	
839	78841125 (1677, 1678)	Novel Protein sim. GBank glj2498533[sp]Q50598[YOD8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	284806	
840	80059851 (1679, 1680)	Novel Protein sim. GBank glj4557753[re]NP_000372.1[pm]DI1 - midline 1 protein		UNCLASSIFIED	284806	

841	80376318 (1881, 1882)	Novel Protein sim. GBank glt39805[sp]P08045[XFIN_XENLA - XFIN PROTEIN Novel Protein sim. GBank glt2114321[db][BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcription factor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBank glt2114321[db][BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 264558
843	87002847 (1685, 1686)	Novel Protein sim. GBank glt3882325[db][BAA34522.1] - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 26331825, 264908, 264768, 264583
844	17641439 (1687, 1688)	Novel Protein sim. GBank glt2224721[db][BAA20844] - (AB002388) KIAA0380 [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcription factor	265011
845	18346844 (1689, 1690)				264629
846	78863441 (1691, 1692)	Novel Protein sim. GBank glt825679[pt][A36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum		kinase	264907
847	78685348 (1693, 1694)				264909
848	78489365 (1695, 1696)				265020
849	79756367 (1697, 1698)			UNCLASSIFIED	264588
850	78817849 (1699, 1700)	Novel Protein sim. GBank glt3183245[pt]P78061[YC_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBank glt5454130[pt]NP_008280.1[pt]TLN - talin	Contains protein domain (PF01608) - ILWEEQ domain		264488, 52844507, 264489, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264480, 264259, 52845080, 29331822, 29331824, 68714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264107, 264905, 264906, 264907, 264908, 52844045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433356, 33657402, 60433438, 264595, 264758, 264759, 21908754, 33109954, 52844286, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264764, 264683, 18108354, 264288, 264369, 264685, 264768, 264687, 264768, 264769, 21908765, 21908766, 21908767, 21908768, 29148627, 21908769, 29148628, 55811857, 35695917, 265020, 265021, 265022, 60170615, 52844150, 264691, 264692, 33657023, 264693, 263988, 33657109, 27486281, 27486282, 27486284, 27486285, 35695763, 60431802, 18108370, 20281069, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	13032587 (1705, 1706)	Novel Protein sim. GBank gij3402836[embjCAA76082] - (Y18138) 2-enoate reductase [Morbella thermoacetic]		reductase	264636 264568
854	80052438 (1707, 1708)				
855	79641130 (1709, 1710)				
856	11594238 (1711, 1712)			UNCLASSIFIED	264692
857	79210165 (1713, 1714)			UNCLASSIFIED	264591
858	80248910 (1715, 1716)				
859	20296834 (1717, 1718)				265008, 265009, 264601, 264602, 264603, 18108351
860	80041748 (1719, 1720)				264559
861	65857045 (1721, 1722)			UNCLASSIFIED	264489
862	80078487 (1723, 1724)			UNCLASSIFIED	33657023, 264630
863	80578931 (1725, 1726)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			264600
864	94939804 (1727, 1728)	Novel Protein sim. GBank gij5689884[embjCAB52047.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264488, 18108398, 35698286, 264259, 18108351, 264288, 265021
865	80045310 (1729, 1730)	Novel Protein sim. GBank gij4557878[ref]NP_000341.1[pABCR - ATP binding cassette transporter]		UNCLASSIFIED	264259, 264112, 263974 264635, 264600, 264636, 264591, 264602, 264693
866	80162031 (1731, 1732)			transport	264288, 264557, 264558
867	80082402 (1733, 1734)				
868	10075364 (1735, 1736)				264605
869	80062408 (1737, 1738)			UNCLASSIFIED	264909
870	80249651 (1739, 1740)	Novel Protein sim. GBank gij628660[piljS37755 - Adenylyl-transferase - Escherichia coli]		transferase	264605, 264687, 18108374 264601, 264636
871	20378295 (1741, 1742)	Novel Protein sim. GBank gij1708180[sp]Q10602[HEMK_MYCTU - HEMK PROTEIN HOMOLOG gij1708180[sp]Q10602[HEMK_MYCTU - HEMK PROTEIN HOMOLOG (X99384) paladin [Mus musculus]		UNCLASSIFIED	264603
872	95187114 (1743, 1744)	Novel Protein sim. GBank gij1545959[embjCAA67763] - (X99384) paladin [Mus musculus]		UNCLASSIFIED	35698286, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35698052, 264509, 284905, 264908, 264907, 264908, 264909, 284510, 265008, 264511, 264512, 265007, 265008, 265009, 264910, 264591, 60433356, 264598, 52846317, 87168474, 285010, 264602, 264603, 265017, 265018, 264605, 18108351, 264764, 264766, 264768, 52844228, 264789, 21906765, 265021, 264534, 264691, 52645128, 264628, 264629, 35698423, 65274791, 264631, 264632, 264635, 264636, 264556, 264637, 264638, 264639, 60433213, 22278000, 22278002, 264564
873	20189728 (1745, 1746)	Novel Protein sim. GBank gij4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	264595

874	80077692 (1747, 1748)	Novel Protein sim. GBank gll134319 sp P07819 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	264600	
875	86608446 (1749, 1750)	Novel Protein sim. GBank gll481000 p S37594 - mucin - human (fragment)			264259, 264448, 264286, 264557, 87168518	
876	86465157 (1751, 1752)	Novel Protein sim. GBank gll3128283 (AF010496) - Iron(III) dicitrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF000005) - ABC transporter	transport	264907, 264601, 264602, 264605, 265020, 60431602	
877	87802548 (1753, 1754)	Novel Protein sim. GBank gll731074 sp P40349 URB1_ USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF00320) - GATA zinc finger	transcript factor	22278998, 264809, 264369	
878	80187289 (1755, 1756)	Novel Protein sim. GBank gll1351614 sp Q0853 YAED_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I		ATPase_associated	264369, 264555	
879	94328862 (1757, 1758)	Novel Protein sim. GBank gll3875304 emb CAA8434 - (Z74030) predicted using GeneFinder; cDNA EST EMBL-C07608 comes from this gene; cDNA EST EMBL-C08023 comes from this gene; cDNA EST yk4505e9.3 comes from this gene; cDNA EST yk489h8.3 comes from this gene; cDNA EST yk489h8.5 com...			56182575, 28331824, 264508, 264806, 265018, 18108351, 284448, 264683, 21908768, 21908768, 80170815, 33857023, 65274820, 33657109, 18108374, 35895655, 264563	
880	8491135 (1759, 1760)	Novel Protein sim. GBank gll137120 sp P11214 UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF000051) - Kringle domain	cathepsin	264508	
881	11280122 (1761, 1762)	Novel Protein sim. GBank gll2632098 emb CAA75667 - (Y15513) Proctos protein [Drosophila melanogaster]		UNCLASSIFIED	264508	
882	11077011 (1763, 1764)	Novel Protein sim. GBank gll1155088 emb CAA84425 - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264558	
883	79562869 (1765, 1766)	Novel Protein sim. GBank gll1155088 emb CAA84425 - (X94976) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264888	
884	13517921 (1767, 1768)	Novel Protein sim. GBank gll2078027 emb CAB08467 - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264638	
885	80052457 (1769, 1770)	Novel Protein sim. GBank gll2078027 emb CAB08467 - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 18108362	
886	11685138 (1771, 1772)	Novel Protein sim. GBank gll2695834 emb CAA15904 - (AL021006) sucA [Mycobacterium tuberculosis]			264690	
887	94315307 (1773, 1774)	Novel Protein sim. GBank gll5868395 db BAA82981.1 - (AB028952) KIAA1029 protein [Homo sapiens]		dehydrogenase	35586052, 264906, 264600, 264603, 35695917, 35895855, 264638	
888	10083389 (1775, 1776)	Novel Protein sim. GBank gll1881338 db BAA19365 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]		UNCLASSIFIED	264908	
889	20385017 (1777, 1778)	Novel Protein sim. GBank gll1881338 db BAA19365 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]			264603	
890	18904337 (1778, 1780)	Novel Protein sim. GBank gll854005 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			264629	

891	13518879 (1781, 1782)	Novel Protein sim. GBank gi 4959396 gb AAD34331.1 AF11248 - (AF11248) RAD54B protein [Homo sapiens]		UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi 2829688 sp P80808 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE)		transcript factor	22278986, 22278989, 28331828, 35696052, 284908, 284909, 285009, 285011, 284602, 285019, 284766, 21906765, 21906766, 21906769, 285020, 285021, 56528486 284689, 283987
893	79168037 (1785, 1786)	Novel Protein sim. GBank gi 2829688 sp P80808 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE)		synthase	
894	11102240 (1787, 1788)			UNCLASSIFIED	263978
895	80239868 (1789, 1790)			UNCLASSIFIED	264508, 284600, 264555, 264559
896	79747803 (1791, 1792)			UNCLASSIFIED	264632
897	94981923 (1793, 1794)			UNCLASSIFIED	264686, 28331828, 264511
898	87695109 (1795, 1796)				56182575, 60432289, 56182435, 60432229, 55811957, 22279000, 264488 264601
899	11100463 (1797, 1798)			transport	284769, 264691, 284563
900	80499788 (1799, 1800)	Novel Protein sim. GBank gi 1750127 (U66480) - YncC [Bacillus subtilis]			
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi 3122879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)		Contains protein domain (PF01411) - [RNA synthetases class II (A)]	264907, 284602, 264605, 284769, 35695917, 18108376, 284563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi 3355701 emb CAA20001 - (AL031124) 3-isopropylmalate dehydratase large subunit [Streptomyces coelicolor]		Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	264909, 265008, 284602, 284604, 284769, 264689, 264693
903	82060208 (1805, 1806)	Novel Protein sim. GBank gi 2960120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]		Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	35696052, 284905, 284510, 284511, 284512, 264605, 284760, 18108351, 284762, 264687, 284769, 284769, 264688, 21906764, 35695917, 27486262, 35695855, 284634, 284638, 264488 284604
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi 728887 sp P40906 ARGI - COCIM - ARGINASE		Contains protein domain (PF00491) - Arginase family	
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23616.1 AC00716 - (AC00716) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264809
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi 3738200 emb CAA21292 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			264595, 264605
907	87913201 (1813, 1814)			UNCLASSIFIED	60432289, 284601, 284690
908	11754482 (1815, 1816)			UNCLASSIFIED	264638
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi 3865940 gb BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	264602
910	16776205 (1819, 1820)	Novel Protein sim. GBank gi 4589726 gb BAA76883.1 - (AB003137) DnaJ homolog protein [Salix gligiana]		Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	265009

811	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P35685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomal prot	265010, 264604, 60432113
812	20448663 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAO07921.1 - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26895]		hydrolase	284559
813	20469357 (1825, 1826)				
814	79183351 (1827, 1828)	Novel Protein sim. GBank gi 417657 sp Q03804 IR1 CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED reductase	264604 264636
815	87606703 (1829, 1830)	Novel Protein sim. GBank gi 5689571 dbj BAA83069.1 - (AB028040) KIAA1117 protein [Homo sapiens]			18108398, 22278996, 66714117, 264908, 264591, 21808768, 265020, 55811576, 264638
816	78444081 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790 - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
817	20195985 (1833, 1834)				
818	91226795 (1835, 1836)	Novel Protein sim. GBank gi 1655699 emb CAA89032 - (Y07752) pterophorin-S [Volvox carter]		UNCLASSIFIED synthase	264605 264259, 28331826, 264808, 265019, 284448, 265020, 264835, 83373044
819	80436785 (1837, 1838)	Novel Protein sim. GBank gi 5689968 emb CAB52005.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265008, 264512, 264600, 264602, 264604, 264768, 18108370, 264963
820	79606095 (1839, 1840)	Novel Protein sim. GBank gi 1168448 sp Q05813 AMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYL-PROLINE AMINOPEPTIDASE I)		peptidase	264508
821	19856634 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21811.1 - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
822	78982605 (1843, 1844)				
823	86695830 (1845, 1846)	Novel Protein sim. GBank gi 267079 sp P28514 TB86_ARATH - TUBULIN BETA-6 CHAIN		tubulin	265019, 22279002 264907, 265008, 265008, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
824	21431341 (1847, 1848)				264510
825	20630332 (1849, 1850)	Novel Protein sim. GBank gi 2497888 sp Q80963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA2) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264603
826	79397657 (1851, 1852)	Novel Protein sim. GBank gi 3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 263972, 264639
827	37036201 (1853, 1854)			UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gij156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	264605
929	20630336 (1857, 1858)	Novel Protein sim. GBank gij115936[gj]AAD03446.1] - (AF118223) No definition line found [Arabidopsis thaliana]		UNCLASSIFIED	264603
930	5486348 (1859, 1860)	Novel Protein sim. GBank gij4490609[emb]CAB38642.1] - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]			264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gij5459396[emb]CAB50754.1] - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]	Contains protein domain (PF00317) - ribonucleotide reductase	reductase	264486
932	80420613 (1863, 1864)	Novel Protein sim. GBank gij5889523[db]BAA03045.1] - (AB029016) KIAA1093 protein [Homo sapiens]		transport	264508, 264905, 264906, 264909, 264600, 264602, 264603, 264605, 264768, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gij110111[sp]P12978[EBN2_EBV] - EBNA-2 NUCLEAR PROTEIN	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264508, 264686, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22278002
934	80039105 (1867, 1868)				264369, 22278002
935	80063162 (1869, 1870)				
936	80026632 (1871, 1872)	Novel Protein sim. GBank gij845686 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
937	80250273 (1873, 1874)	Novel Protein sim. GBank gij1360669[pri]CGHU1V - collagen alpha 1(V) chain precursor - human		UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
938	80026633 (1875, 1876)	Novel Protein sim. GBank gij2226243[emb]CAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]		synthase	263978
939	11071694 (1877, 1878)			UNCLASSIFIED	264602
940	94144253 (1878, 1880)	Novel Protein sim. GBank gij3560166[emb]CAA20678] - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2		264600
941	11398414 (1881, 1882)				264805, 264906, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264596, 264758, 264760, 264683, 264766, 264768, 264769, 33657023, 33657109, 264828, 264629, 264630, 264635, 264638, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264586, 18108391
942	19484122 (1883, 1884)	Novel Protein sim. GBank gij4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264593
943	80080258 (1885, 1886)			UNCLASSIFIED	264760
944	80216098 (1887, 1888)	Novel Protein sim. GBank gij2494764[sp]Q50729[GUA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]			264600, 264687, 264689, 264563
945	80052477 (1889, 1890)	Novel Protein sim. GBank gij732353[sp]P39606[YWCH_BACSU - HYPOTHETICAL 36.8 KD PROTEIN IN OXO-VPR INTERGENIC REGION]	Contains protein domain (PF00818) - ice nucleation protein repeat	synthase	264511, 264603
946	78248402 (1891, 1892)			UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
					265017

947	81802698 (1893, 1894)	Novel Protein sim. GBank gll2896770[emb]CAA17247] - (AL021898) hypothetical protein Rv2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264605, 264769, 264689, 264693
948	88165538 (1895, 1896)	Novel Protein sim. GBank gll2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		lgi	18108398, 56182575, 22278997, 22278999, 60432049, 26331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486285, 263972, 55811576, 264638, 60170394, 264566
949	88081786 (1897, 1898)	Novel Protein sim. GBank gll4507985[ref]NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcription factor	29331825, 21908764, 27486261, 21908766, 52844288, 33657349, 87188518, 56994075, 265020, 265021, 87188559, 52844150, 264637
950	78485872 (1899, 1900)	Novel Protein sim. GBank gll1079461[pr]S43865 - cytochrome b, type II - polio (fragment)	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gll5420387[emb]CAB46079.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gll5305702[gb]AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	264910, 264691
953	10186003 (1905, 1906)	Novel Protein sim. GBank gll2495642[sp]Q47142 YFHS_ECOLI - HYPOTHETICAL 41.6 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	264510
954	8893326 (1907, 1908)	Novel Protein sim. GBank gll2360965 (AF018253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	95313410 (1908, 1910)	Novel Protein sim. GBank gll5454064[ref]NP_008319.1 pSIP1 - SYT interacting protein	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264782, 264763, 264764, 264766, 264686, 264767, 264887, 264768, 264769, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 264563, 264564, 264605
956	80064224 (1911, 1912)	Novel Protein sim. GBank gll2052129[emb]CAB08155] - (Z94752) rifM [Mycobacterium tuberculosis]			
957	80058206 (1913, 1914)	Novel Protein sim. GBank gll1709787[sp]Q00451 PRF1_LYCES - 38.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264603, 18108362
958	80038446 (1915, 1916)	Novel Protein sim. GBank gll2131050[emb]CAB09260] - (Z95844) opcA [Mycobacterium tuberculosis]		UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gll2129478[pr]S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264602, 264692
960	37815406 (1919, 1920)	Novel Protein sim. GBank gll2129478[pr]S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11398318 (1923, 1924)				264593

963	80580374 (1925, 1926)					UNCLASSIFIED	264510, 264288, 264555, 264558, 264559, 264488
964	78832019 (1927, 1928)	Novel Protein sim. GBank gij4588622[jdbj BAA76833.1] - (AB023208) KIAA0989 protein [Homo sapiens]				UNCLASSIFIED	264112, 264910, 264689
965	91229485 (1929, 1930)	Novel Protein sim. GBank gij5420387[embj CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]				UNCLASSIFIED	264488, 265017, 264448, 264634, 264558, 83373044
966	95292815 (1931, 1932)					UNCLASSIFIED	264808, 264592, 264586, 264604, 264768, 21908784, 264692, 264693, 264629, 264638, 264760
967	78255708 (1933, 1934)	Novel Protein sim. GBank gij1731207[sp Q11156 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3			Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	
968	78560289 (1935, 1936)	Novel Protein sim. GBank gij2661836[embj CAA75187] - (Y14964) putative transport protein [Methylophilus methylotrophus]				transport	264693
969	78918470 (1937, 1938)	Novel Protein sim. GBank gij5419878[embj CAB46422.1] - (AL098747) hypothetical protein [Homo sapiens]			Contains protein domain (PF00098) - Zinc finger, C2H2 type	dna_ma_bind	35698288, 264685, 264688, 35695917, 264692, 18108374, 264635
970	85085947 (1939, 1940)					UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 22278999, 29147620, 264828, 265006, 265007, 265008, 265009, 18108348, 33108954, 265010, 265011, 18108351, 264288, 21908767, 21906768, 18108370, 18108374, 18108377, 264630, 264635, 18108380, 83373044, 18108387, 18108388
971	78919770 (1941, 1942)					UNCLASSIFIED	265007, 265020, 22278002
972	20710704 (1943, 1944)						264557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gij1723119[sp P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174					264604
974	80057103 (1947, 1948)					UNCLASSIFIED	264565
975	10186018 (1949, 1950)					UNCLASSIFIED	264510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gij3881459[embj CAA82988.1] - (Z68753) predicted using GeneFinder: Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D64777 comes from this gene; cDNA EST EMBL:D64777 comes from this ge...				UNCLASSIFIED	264508, 264906, 264758, 264632, 264639, 264563
977	10355349 (1953, 1954)	Novel Protein sim. GBank gij549456[sp Q05335 XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3				UNCLASSIFIED	264906
978	80025927 (1955, 1956)						
979	80447820 (1957, 1958)	Novel Protein sim. GBank gij3171904[embj CAA75869] - (Y15908) DIA-12C protein [Homo sapiens]				UNCLASSIFIED	264600, 264602, 264603, 264604
980	80025928 (1959, 1960)					UNCLASSIFIED	264767, 264768, 265006, 265007, 264906
981	80089550 (1961, 1962)	Novel Protein sim. GBank gij3599940 (AF017368) - [actogenital dysplasia protein 2 [Mus musculus]				UNCLASSIFIED	264600, 264602, 264605
						UNCLASSIFIED	264692, 264555, 264558, 264557, 264559

982	80195670 (1983, 1984)	Novel Protein sim. GBank gl 295020 emb CAA71575 - (Y10545) fused-ccdB [Escherichia coli]		UNCLASSIFIED	264404
983	90995041 (1985, 1986)	Novel Protein sim. GBank gl 476389 pir JB43402 - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56182575, 264908, 264909, 265007, 265008, 264758, 265010, 55811150, 33657023, 264634, 264557, 264558
984	20466878 (1987, 1988)	Novel Protein sim. GBank gl 3451504 emb CAA07660.1 - (A007747) hypothetical protein BbLPSt.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	UNCLASSIFIED	264605
985	85481368 (1988, 1970)				56182435, 264600
986	87102888 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)				264809
988	19858681 (1975, 1976)			UNCLASSIFIED	264600
989	88083329 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057748 (1979, 1980)	Novel Protein sim. GBank gl 5725508 gb AAD48080.1 AF06015 - (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M12B) family zinc metalloprotease	oxidase	264259, 264908, 265009, 264910, 264596, 264369, 264288, 264766, 264628, 264635, 264566
991	10108140 (1981, 1982)			UNCLASSIFIED	264909
992	79845694 (1983, 1984)	Novel Protein sim. GBank gl 2105049 emb CAB08835 - (Z85436) hypothetical protein RV3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)	Novel Protein sim. GBank gl 3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	264907
994	11080590 (1987, 1988)				264602
995	94321811 (1989, 1990)	Novel Protein sim. GBank gl 5106572 gb AAD39760.1 AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 65274572, 22278996, 264490, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432229, 60431735, 33657402, 264595, 264758, 21908754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21908765, 21908768, 21908789, 55811957, 264692, 264693, 264629, 35898423, 55811576, 35895855, 264638, 264555, 264556, 264558, 83373044, 22278002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gl 2911719 (AC004227) - KIA0011LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 263978, 55811957, 56526488, 87168518, 264910, 264906, 264565, 264566, 264693, 264766
997	80503347 (1993, 1994)	Novel Protein sim. GBank gl 2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35696286, 22278997, 22278999, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264688, 264769, 265021, 264585, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gl 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			264595

999	11766047 (1997, 1998)	Novel Protein sim. GBank gij2506697[sp]P46480[YFCA_HAEIN - HYPOTHETICAL PROTEIN H10198]		UNCLASSIFIED	284682
1000	20727844 (1999, 2000)			UNCLASSIFIED	264602
1001	85673131 (2001, 2002)	Novel Protein sim. GBank gij2224689[db][BAA20833] - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	60432049, 264907, 264908, 264511, 264603, 264683, 264684, 264687, 264689, 28148627, 21908769, 264692, 18108385, 22279000 265009, 264369, 265020
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gij586121[sp]P37709[TRHY_RABIT - TRICHOHYALIN]		struct	
1003	17833491 (2005, 2006)				265019
1004	16314887 (2007, 2008)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 8]			264635
1005	79617144 (2008, 2010)	Novel Protein sim. GBank gij114073[sp]P07672[APT_ECOLI - ADENINE PHOSPHORIBOSYL TRANSFERASE (APRT)]		UNCLASSIFIED	264508
1006	37815429 (2011, 2012)				
1007	79820871 (2013, 2014)	Novel Protein sim. GBank gij4062979[db][BAA36210.1] - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	264259
1008	88094444 (2015, 2016)	Novel Protein sim. GBank gij2808807[emb]CAA04607.1] - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		synthase	264905
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gij3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	265007, 264602, 264605, 264760, 264636
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gij3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	264102, 284288
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gij2342847[gb]AAB86591.1] - (U90653) DHHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	264592
1012	85284456 (2023, 2024)	Novel Protein sim. GBank gij3413411[emb]CAA20272] - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35896052, 264905, 264784, 264788, 35895917, 264629
1013	86095772 (2025, 2026)				35896052, 264905, 264600, 264601, 284602, 284605, 264762, 264768, 264768, 264689
1014	86608828 (2027, 2028)			UNCLASSIFIED	284591, 21908768 28331824, 265019, 265020

1015	85418879 (2028, 2030)	Novel Protein sim. GBank gij4158985 (AF063095) - SELIL [Mus musculus]	Contains protein domain (PF00040) - Fibronectin type II domain	struct	22278894, 22278895, 56884075, 22278896, 22278899, 264259, 29331825, 29331828, 264807, 58182435, 264510, 264591, 264593, 60433358, 264594, 55812038, 264758, 21908754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21906765, 21906766, 21906767, 21906768, 55811957, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35686423, 264630, 22279000, 284585
1016	78558694 (2031, 2032)	Novel Protein sim. GBank gij2508989 [P41407]ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	284886, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gij5103943 [dbj]BAA79259.1 - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gij4493973 [emb]CAB39032.1 - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w). Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278896, 28148627, 264563
1019	11703607 (2037, 2038)			UNCLASSIFIED	264686
1020	80234432 (2039, 2040)				264508, 264509, 264512, 264600, 264762, 264769, 264688, 18108370, 264638, 264639, 264486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gij4633607 [gb]AAD26859.1AF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gij1781230 [emb]CAB06277.1 - (Z83667) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35696052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11398341 (2045, 2046)	Novel Protein sim. GBank gij3777495 (U92083) - calcium transporting ATPase [Pichia angustia]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	264593
1024	80057128 (2047, 2048)			UNCLASSIFIED	52646842, 33657402, 33657023, 18108378, 55811576, 264631, 264558, 264557, 264559, 18108388, 264566
1025	78844200 (2048, 2050)	Novel Protein sim. GBank gij3483045 [emb]CAA20556.1 - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	264693
1026	80025948 (2051, 2052)	Novel Protein sim. GBank gij1174922 [sp]Q02322 [UVRD_HAEIN - DNA HELICASE II]		helicase	264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gij4757728 [re]NP_004886.1pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	265017

1028	20287928 (2055, 2058)	Novel Protein sim. GBank gij2791409[emb]CAA16003] - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	264600
1029	94665090 (2057, 2058)			UNCLASSIFIED	264595
1030	88095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374
1031	95289117 (2061, 2062)			UNCLASSIFIED	264905, 264906, 264909, 264595, 264692, 264630, 264634, 264638
1032	84673275 (2063, 2064)	Novel Protein sim. GBank gij4503895[ref]NP_000145.1[pGALK - galactokinase 1]		UNCLASSIFIED	264689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gij2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35696052, 264908, 264510, 18108354, 264687, 264769, 264689, 60431602, 18108385, 264486
1034	79245937 (2067, 2068)	Novel Protein sim. GBank gij405895 (U00007) - methionyl- tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264906
1035	79956355 (2069, 2070)			UNCLASSIFIED	264892
1036	85804988 (2071, 2072)			UNCLASSIFIED	264905, 66712502, 264908, 264768
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 264908, 60433438, 265019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gij790819 (L39891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLATLH2 domain	UNCLASSIFIED	264604, 264634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gij2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263967
1040	80026940 (2079, 2080)	Novel Protein sim. GBank gij2352095 (U97022) - DNA topoisomerase I [Fenvidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	UNCLASSIFIED	264595
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gij3256535[db]BAA29218.1] - (AF000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]	Kinase		264907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gij2058299[emb]CAA66953] - (X88309) ARJ protein [Drosophila melanogaster]			264605
1043	80057136 (2085, 2086)	Novel Protein sim. GBank gij1870187[emb]CAA70125] - (Y08821) msik [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter		264565, 264567
1044	80025952 (2087, 2088)	Novel Protein sim. GBank gij5689890[emb]CAB52053.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	265006, 264602, 265017
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gij854085[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]	helicase		264686
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gij4210471[db]BAA74535.1] - (AB018033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gij3413419[emb]CAA20278] - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain	UNCLASSIFIED	264687
1048	79186400 (2095, 2096)	Novel Protein sim. GBank gij5051636[db]AAD38326.1]AF07372 - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264905, 264634
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gij5051636[db]AAD38326.1]AF07372 - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264688
1050	79471521 (2099, 2100)			UNCLASSIFIED	264688

1051	60475471 (2101, 2102)				UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442862 (2103, 2104)	Novel Protein sim. GBank gi 3123275 sp P35136 SERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases		dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2108)	Novel Protein sim. GBank gi 5441319 emb CAB46717.1 - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]				264686, 18108374, 29331824, 83373044, 21908754, 52645156, 66182435, 264689, 29331827, 27486281, 35696052, 21908765, 35696423, 21908788, 56182575, 21908769, 55811957, 87168518, 35696288, 22278987, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264908, 52644150, 264908, 264288, 29331822, 52645080, 264766
1054	78580225 (2107, 2108)				UNCLASSIFIED	264686
1055	80584138 (2109, 2110)	Novel Protein sim. GBank gi 5052508 gb AA038584.1 AF14560 - (AF145609) BcDNA:GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/IDEAH box helicase		helicase	264907, 264602, 264681, 264288, 21908769, 33657108, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gi 3021676 gb BAA25358 - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]			mapolymerase	264908
1057	85687216 (2113, 2114)	Novel Protein sim. GBank gi 1226281 (U50308) - No definition line found [Caenorhabditis elegans]			UNCLASSIFIED	264682
1058	80378578 (2115, 2116)					264764
1059	94662754 (2117, 2118)	Novel Protein sim. GBank gi 1170016 sp P46808 GREA_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREa (TRANSCRIPT CLEAVAGE FACTOR GREa)			transcriptfactor	35696052, 35695855, 265009, 264636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (UGT)			glycoprotein	29146499, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gi 90254 pir J1A28334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse			phosphatase	264634
1062	38567937 (2123, 2124)	Novel Protein sim. GBank gi 3334200 sp Q49954 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)			dehydrogenase	264593
1063	9460481 (2125, 2126)	Novel Protein sim. GBank gi 2499988 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)				264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gi 82654 pir J1A0086 - 10K zein precursor - maize				265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. GBank gij120898jpirj[S70682 - glycosyltransferase homolog - Bordetella pertussis]	transferase	264600, 264602, 264689
1066	17896878 (2131, 2132)	Novel Protein sim. GBank gij12506362jspiP15042jDNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))	synthase	265009
1067	10132178 (2133, 2134)	Novel Protein sim. GBank gij14007669jembjCAA22355j - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	reductase	264909 264688, 18108362, 264558, 264600, 264760
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264604
1069	83002954 (2137, 2138)	Novel Protein sim. GBank gij120304jspiP15832jFLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)	UNCLASSIFIED	264604, 264760
1070	82101892 (2139, 2140)	Novel Protein sim. GBank gij1750387 (U81281) - glutamate synthase large subunit [Pseudomonas aeruginosa]	synthase	264602
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1072	82356540 (2143, 2144)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	synthase	264909 264906
1073	78814400 (2145, 2146)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1074	80105992 (2147, 2148)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1076	80477284 (2151, 2152)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1078	20288874 (2155, 2156)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1080	11767188 (2159, 2160)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1081	94747080 (2161, 2162)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768
1082	81490656 (2163, 2164)	Novel Protein sim. GBank gij14589484jdbjBAA76770.1j - (AB023143) KIAA0926 protein [Homo sapiens]	UNCLASSIFIED	264687, 264688, 21908764, 35698052, 35698517, 35698555, 264600, 264601, 264602, 265008, 264605, 264608, 264609, 264690, 264906, 264762, 264628, 264768

1083	87448717 (2165, 2166)	Novel Protein sim. GBank gll1722945[sp]Q10523[Y01N_MYCTU - HYPOTHETICAL 44.8 KD PROTEIN CY427.23		UNCLASSIFIED	60424179, 264905, 264906, 264510, 60432229, 264759, 67168474, 264605, 264768, 264689, 18108384, 18108376, 35695855, 264636 264769
1084	37793308 (2167, 2168)	Novel Protein sim. GBank gll418384[sp]P32057[WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1085	86475388 (2169, 2170)	Novel Protein sim. GBank gll1899190 (U80204) - haat shock protein 60 [Tsukamurella tyrosinosolvens]	Contains protein domain (PF00118) - eph TCP-1/cpr60 chaperonin family		60432229, 264687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gll1172856[sp]P46176[RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomal prot	264486
1087	79603976 (2173, 2174)	Novel Protein sim. GBank gll4160199[emb]CAA154311 - (AL008583) dJ327 J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHROMatin Organization Modifier) domain	helicase	29331827, 264693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gll2883155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	264905, 264601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gll4981768[sp]AAD36280.1[AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264768, 264689, 21908764, 35695917, 265020, 32833986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gll4007680[emb]CAA23368 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gll2495582[sp]P77239[YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252286 (2183, 2184)	Novel Protein sim. GBank gll2860098[emb]CAA17998.1 - (AL022121) ntb [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III	nuclease	264566 264769, 35695917, 35695855, 264600, 264602, 264603, 264605, 18108351
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gll1007642[db]BAA10373 - (D64002) dGTP triphosphohydrolase [Synecocystis sp.]		UNCLASSIFIED	264686
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gll4585587[emb]CAB40855.1 - (AL049628) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	264906, 265007, 264595, 264600, 264602, 264603, 264604, 264605, 264762, 264768, 264769, 264636, 264558, 18108387, 60432113, 264482, 264486
1095	87457250 (2189, 2190)				
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gll11500[sp]P18206[BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)]		synthase	264600, 264602, 264603, 264604, 264605, 35695917, 264692, 264631
1097	79239560 (2193, 2194)			UNCLASSIFIED	265019
1098	70168424 (2195, 2196)	Novel Protein sim. GBank gll114135[sp]P08205[JARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)]		synthase	264687

1099	38523838 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (M1G- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603	
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gi 3023255 sp Q64420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)	desaturase		264259, 264636	
1101	80481857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	264769	
1102	79777614 (2203, 2204)					
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi 1806596 U81788 - kinesin-73 [Drosophila melanogaster]		UNCLASSIFIED	264910, 264909	
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2835448 AF048976 - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		STRUCT	264757	
1105	80255121 (2209, 2210)					
1106	79314110 (2211, 2212)					
1107	80470018 (2213, 2214)					
1108	80440816 (2215, 2216)					
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gi 1173421 sp P43416 SECY_STRSC - PREPROTEIN TRANSLUCASE SECY SUBUNIT Novel Protein sim. GBank gi 2995310 emb CAA18338 - (AL022288) putative ATP-dependent helicase [Streptomyces coelicolor]		UNCLASSIFIED	264568	
1110	80503554 (2219, 2220)					
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622038 AE000868 - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]				
1112	95010088 (2223, 2224)					
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gi 3218378 emb CAA19628 - (AL023862) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	264908	
1114	14988014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir S54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse				
1115	11785583 (2229, 2230)					
1116	78841152 (2231, 2232)					
				dehydrogenase	264636	
				UNCLASSIFIED	264686	
					264908	

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gij3255985[embjCAA94089] - (Z70200) U5 anRNP-specific 200KD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108392, 264488, 263394, 264489, 18108398, 56182575, 22278995, 22278998, 35698286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 66714117, 29331825, 29331828, 60432289, 29331827, 29331828, 35698052, 33656970, 28146498, 264508, 264805, 264509, 264908, 264907, 264908, 66712502, 264909, 52844045, 56182435, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55612038, 264596, 264758, 264759, 21906754, 33109954, 33657084, 265011, 87188599, 264600, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55611150, 264681, 264762, 18108351, 264448, 264682, 264764, 264683, 264288, 264389, 264684, 264685, 264786, 264787, 264886, 264687, 264788, 264789, 264888, 18108359, 264889, 21906785, 21906786, 21906787, 21906788, 21906789, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264690, 264691, 33657023, 264682, 264693, 65274620, 33657108, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 264691
1118	78563328 (2235, 2236)			UNCLASSIFIED	264691
1119	78842463 (2237, 2238)			UNCLASSIFIED	264807
1120	78480463 (2238, 2240)	Novel Protein sim. GBank gij5420387[embjCAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	78471718 (2241, 2242)	Novel Protein sim. GBank gij1844450 (U87884) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264683, 264632, 18108388
1122	78456246 (2243, 2244)			UNCLASSIFIED	264839, 264563
1123	78637119 (2245, 2246)	Novel Protein sim. GBank gij98800[pri]S17768 - 3-dehydroquinase synthase (EC 4.6.1.3) - Mycobacterium tuberculosis		synthase	264683, 27486285
1124	78811596 (2247, 2248)			UNCLASSIFIED	264809
1125	78757861 (2248, 2250)			UNCLASSIFIED	264910
1126	78756914 (2251, 2252)	Novel Protein sim. GBank gij136154[sp]P03943[VG, BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)]		eph	264805, 264809, 264910
1127	11800930 (2253, 2254)			UNCLASSIFIED	264882
1128	8384885 (2255, 2256)	Novel Protein sim. GBank gij5002704[embjCAB44358.1] - (AJ242630) DNA polymerase I [Methylobacterium sp. DMA]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gij5689485dbj BAA03026.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)	Novel Protein sim. GBank gij4981328gjb AAD35881.1 AE00174 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	Novel Protein sim. GBank gij1841552 (U89335) - unknown [Homo sapiens]		UNCLASSIFIED	35696286, 22278998, 29331828, 264603, 284805, 264559
1132	82062248 (2263, 2264)			UNCLASSIFIED	22278998, 264906, 265009, 264600, 284602, 264604, 264605, 264760, 32833986, 18108374
1133	17290437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gij453917 emb CAB39700.1 - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264600, 264602, 264603, 18108376
1136	78842052 (2271, 2272)	Novel Protein sim. GBank gij4982454gjb AAD39931.1 AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264808
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gij4972746gjb AAD34768.1 - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - TPR Domain	collagen	22278998, 22278999, 35696052, 264907, 265009, 60433356, 264596, 265010, 264448, 264682, 264767, 264689, 265020, 264892, 55811578, 35695855, 264631, 264632, 22279002
1138	78841163 (2275, 2276)	Novel Protein sim. GBank gij731607 sp P38739 HCB8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR		struct	264906
1139	78633561 (2277, 2278)	Novel Protein sim. GBank gij3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264693
1140	39480358 (2279, 2280)			UNCLASSIFIED	264593
1141	78638019 (2281, 2282)			UNCLASSIFIED	285019, 264693
1142	19635848 (2283, 2284)			UNCLASSIFIED	264631
1143	87782158 (2285, 2286)	Novel Protein sim. GBank gij3928000 emb CAA05880 - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 264908, 264600, 264632, 87168518
1144	80088988 (2287, 2288)			UNCLASSIFIED	264635, 264636, 264907, 264593, 264908, 264596, 264909
1145	14610262 (2289, 2290)			UNCLASSIFIED	264112
1146	82062082 (2291, 2292)			UNCLASSIFIED	264769, 264689, 35696286, 264760, 264905, 264488, 264559
1147	80071761 (2293, 2294)				264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank gij2499003 sp P76422 THID_ECOLI - PHOSPHOMETHYL-PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)	kinase		264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gij2896734 emb CAA17213.1 - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]			264581

11150	81325074 (2289, 2300)	[Novel Protein sim. GBank gjl2995085 (AF011337) - putative E1-E2 ATPase [Mus musculus]			ATPase_associated	264486, 35696286, 264807, 264908, 264909, 264910, 264593, 264598, 264758, 264764, 264768, 264788, 264693, 264628, 80431850, 264564, 264566, 264587
11151	80070874 (2301, 2302)	[Novel Protein sim. GBank gjl4324655]gbjAAD16978j - (AF108181) DNA polymerase III alpha subunit [Streptomyces coelicolor]			polymerase	264595
11152	80235547 (2303, 2304)	[Novel Protein sim. GBank gjl3874275]lembjCAB07311.1j - (Z92825) predicted using GeneFinder: Similarity to Yeast low affinity glucose transporter HXT4 (PS:32467): cDNA EST EMBL:C12555 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thi...			glycoprotein	264488, 22278988, 264805, 264629, 264486
11153	80027783 (2305, 2306)	[Novel Protein sim. GBank gjl4240315]dbjBAA74936.1j - (AB020720) KIAA0913 protein [Homo sapiens]			UNCLASSIFIED	264910, 264555, 264557
11154	93002995 (2307, 2308)	[Novel Protein sim. GBank gjl586855]sp37617jATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZNI(II)-TRANSLLOCATING P-TYPE ATPASE)			UNCLASSIFIED	265008
11155	78411088 (2309, 2310)	[Novel Protein sim. GBank gjl418480]spj32139jYIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION			UNCLASSIFIED	264680, 264636
11156	57147843 (2311, 2312)	[Novel Protein sim. GBank gjl2496481]spj050724jY08S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C		Contains protein domain (PF00122) - E1-E2 ATPase	transport	264803
11157	95287711 (2313, 2314)	[Novel Protein sim. GBank gjl1139408]dbj[BAA11490] - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]			UNCLASSIFIED	264906, 264907, 264758, 264768, 264769, 264689, 18108374, 35685855
11158	82454817 (2315, 2316)	[Novel Protein sim. GBank gjl1139408]dbj[BAA11490] - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]			UNCLASSIFIED	264687
11159	78186451 (2317, 2318)	[Novel Protein sim. GBank gjl1139408]dbj[BAA11490] - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]			UNCLASSIFIED	264687
11160	91220893 (2319, 2320)	[Novel Protein sim. GBank gjl1139408]dbj[BAA11490] - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]			UNCLASSIFIED	264687
11161	7417143 (2321, 2322)	[Novel Protein sim. GBank gjl2443342]dbj[BAA22380] - (D88764) alpha 2 type I collagen [Rana catesbeiana]			UNCLASSIFIED	264359
11162	79635357 (2323, 2324)	[Novel Protein sim. GBank gjl4503375]re]NP_001376.1jppPYS - dihydropyrimidinase			UNCLASSIFIED	264693
11163	79563168 (2325, 2326)	[Novel Protein sim. GBank gjl5082554]gbjAAD38607.1jAF14563 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]			UNCLASSIFIED	264359
11164	79650829 (2327, 2328)	[Novel Protein sim. GBank gjl5082554]gbjAAD38607.1jAF14563 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]			UNCLASSIFIED	264359
11165	80481888 (2329, 2330)	[Novel Protein sim. GBank gjl4589476]dbj[BAA76766.1j - (AB023139) KIAA0922 protein [Homo sapiens]			UNCLASSIFIED	264359
11166	88096456 (2331, 2332)	[Novel Protein sim. GBank gjl4589476]dbj[BAA76766.1j - (AB023139) KIAA0922 protein [Homo sapiens]			UNCLASSIFIED	264359

1167	79963862 (2333, 2334)	Novel Protein sim. GBank gij2580433[dbj BAA23138] - (D76414) ppGpp hydrolase [Staphylococcus aureus]		kinase	264488
1168	86094678 (2335, 2336)			UNCLASSIFIED	264259, 29331827, 56182435, 60433438, 265019, 33657023, 35695655, 264586
1169	11805403 (2337, 2338)			UNCLASSIFIED	264681
1170	21632244 (2339, 2340)			UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gij2772914 (AF028249) - procollagen D [Mytilus edulis]		UNCLASSIFIED	264556
1172	78610113 (2343, 2344)	Novel Protein sim. GBank gij4757846[ref NP_004317.1 pBCL9 - B-cell CLL/lymphoma 9]		UNCLASSIFIED	55810764, 35696052, 264634, 264488
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gij2584053[dbj BAA22946] - (AB007832) Bm trachealless [Bombyx mori]			264508, 264906, 264907, 264809, 264591, 264632, 264638, 264639
1174	20293077 (2347, 2348)	Novel Protein sim. GBank gij2911027[emb CAA17520] - (AL021858) mmsA [Mycobacterium tuberculosis]		dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gij118333[sp P23234 DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE)]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	264601
1176	80252845 (2351, 2352)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00586) - AIR synthase related protein	synthase	264509, 264905, 264593, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gij118791[sp P28643 FABG_CUPLA - 3-OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)]	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gij5031697[ref NP_005594.1 pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase associated	65274572, 18108398, 22278998, 22278999, 28331826, 284508, 264908, 264828, 33857402, 33109954, 264769, 21806765, 21906766, 21906768, 55811957, 33657023, 264629, 55811576, 35698423, 264638, 264556, 56182323, 60432113, 22278000, 22278002, 264603
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gij2960090[emb CAA17988.1] - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00486) - Bacterial extracellular solute-binding proteins, family 5	transport	
1180	11794446 (2359, 2360)	Novel Protein sim. GBank gij2558614[emb CAA04787] - (AJ001493) dehydroquininate dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	264638
1181	17946382 (2361, 2362)			UNCLASSIFIED	265017
1182	81494264 (2363, 2364)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proleophosphoglycan [Leishmania major]			265007, 265009, 264564, 264909, 264693
1183	79574044 (2365, 2366)	Novel Protein sim. GBank gij4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]			264689, 35698423, 264638, 18108385
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gij2128478[pir J551939 - chitinase (EC 3.2.1.14) precursor - beet	UNCLASSIFIED		264602
1185	79491185 (2369, 2370)		glycoprotein		263967

1188	20224012 (2371, 2372)				UNCLASSIFIED	264559	
1187	79248834 (2373, 2374)				UNCLASSIFIED	28331825, 265017, 18108351	
1186	79831387 (2375, 2376)	Novel Protein sim. GBank gi 2986039 (AF054525) - hypothetical protein [Synecococcus PCC7002]			UNCLASSIFIED	264905, 264908	
1189	79609367 (2377, 2378)					264682	
1190	79830569 (2378, 2380)				UNCLASSIFIED	285018	
1191	60310105 (2381, 2382)				UNCLASSIFIED	264600, 264605, 264764, 36895855, 264638, 264486	
1192	13521641 (2383, 2384)			Contains protein domain (PF01581) - FMRFamide related peptide family		264638	
1193	11103584 (2385, 2386)				UNCLASSIFIED	263978	
1194	78893947 (2387, 2388)	Novel Protein sim. GBank gi 854085 (emb CAA58337) - (X83413) U88 [Human herpesvirus 8]			UNCLASSIFIED	265007, 265008	
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gi 1790277 (AE000459) - putative oxidoreductase [Escherichia coli]			UNCLASSIFIED	264605	
1196	13000868 (2391, 2392)					264689	
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gi 2487360 (sp Q50715) (MDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)		Contains protein domain (PF00571) - CBS domain		264594	
1198	95290101 (2395, 2396)					264603	
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gi 1709525 (sp P54873) (PK1_DICD1 - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)				264258, 264757, 33108954, 21908768	
1200	98468880 (2398, 2400)						
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gi 2499877 (sp P70845) (BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)			UNCLASSIFIED	264910	
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gi 606342 (U18997) - ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]			cathepsin	264766, 264769	
1203	82125373 (2405, 2408)				ribosomalprol	264600, 264558	
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gi 2500728 (sp Q59912) (SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT			UNCLASSIFIED	264768, 264769, 35695817, 264910, 264760, 264908, 264907, 264628, 264908, 264909, 264768	
1205	80053961 (2409, 2410)					264905, 264769, 264638	
1206	80241865 (2411, 2412)				UNCLASSIFIED	264566	
1207	79841192 (2413, 2414)				UNCLASSIFIED	264556, 264557, 264558	
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gi 2645560 (AF027954) - Bcl-2 related ovarian killer protein [Rattus norvegicus]		Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family		29331824, 264909, 265021, 18108370	
					apoptosis	28331824, 39331825, 28331827, 265007, 264784, 264683, 264769, 264688, 264689	

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gll1175033[sp]P44388[X]YLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	56426884 (2419, 2420)				
1211	94665655 (2421, 2422)	Novel Protein sim. GBank gll421095[pir]S30688 - hypothetical protein o246 - Escherichia coli		UNCLASSIFIED	264907, 264693
1212	79187929 (2423, 2424)	Novel Protein sim. GBank gll380625[emb]CAB07858] - (293785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01882 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this gene	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transferase	264591, 264592, 264595
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gll226292[pir]1505375A - vir gene [Bordetella pertussis]			264689, 263987
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gll5728285[gb]AAD48396.1[AF12616] - (AF126162) HERV-H LTR associating protein 2 [Homo sapiens]		kinase	264909
1215	80050108 (2429, 2430)	Novel Protein sim. GBank gll2326739[emb]CAB10953] - (Z89268) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	264808
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gll417328[sp]P33038[MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYL-PYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE) (EPT)		UNCLASSIFIED	265009, 264601, 264602, 264603, 33657109
1217	95011344 (2433, 2434)			transferase	264604
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gll1805460[dbj]BAA09022] - (D50453) homologue of succinate semialdehyde dehydrogenase GabbD of E. coli [Bacillus subtilis]		UNCLASSIFIED	264805, 264907, 264908, 264591, 264766, 264891, 264693, 264629, 264630, 264636,
1219	91216252 (2437, 2438)			dehydrogenase	264564 264601
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gll4240315[dbj]BAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]			56181686, 29331822, 60432289, 264601, 264692, 264629
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gll2143886[pir]152523 - nucleoporin p82 homolog - rat (fragment)		oncogene	52644507, 264805, 264908, 265008, 265019, 265020, 52644150, 33657023, 264693,
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gll730805[sp]P39663[SPHR_SYNP7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR		UNCLASSIFIED	33657182, 35695763, 264634, 22279000, 22279002, 264482
1223	11615647 (2445, 2446)		Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	264768, 265020, 264908
1224	80432845 (2447, 2448)	Novel Protein sim. GBank gll1172627[sp]P46546[PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - kinase		264593 264768, 18108376, 264636, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gij2105050[emb]CAB08836] - (Z95436) hypothetical protein RV3844c [Mycobacterium tuberculosis]			284768
1226	80237518 (2451, 2452)			polymerase	284805, 284512, 284688
1227	79422138 (2453, 2464)	Novel Protein sim. GBank gij1708768[sp]P98133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]		UNCLASSIFIED	284808, 284637, 284639
1228	79209027 (2455, 2456)	Novel Protein sim. GBank gij1653901[dbj]BAA18811] - (D90817) acriflavine resistance protein [Synecocystis sp.]	Contains protein domain (PF00873) - AcrB/AcrD/AcrF family		284605, 284634
1229	94328135 (2457, 2458)			UNCLASSIFIED	87168474, 265011, 87168559, 284681, 284689, 284693, 65274820, 18108374
1230	80048357 (2459, 2460)	Novel Protein sim. GBank gij116230[sp]P28589[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family		284909, 284605, 18108388
1231	78843141 (2461, 2462)			UNCLASSIFIED	284808
1232	78853104 (2463, 2464)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]		transport	284808
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij116298[sp]P20730[CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]		UNCLASSIFIED	265017, 284564
1234	78242168 (2467, 2468)	Novel Protein sim. GBank gij728671[sp]P40280[H2A_MAIZE - HISTONE H2A]	Contains protein domain (PF00125) - histone Core histone H2A/H2B/H3/H4		265008, 265010, 18108381
1235	78914423 (2469, 2470)				284634, 284762
1236	81827147 (2471, 2472)			UNCLASSIFIED	285018, 5581150, 284565, 284757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gij387513[emb]CAA94750] - (Z70750) similar to actin binding domain; cDNA EST EMBL: T00093 comes from this gene; cDNA EST EMBL: D34443 comes from this gene; cDNA EST EMBL: D37508 comes from this gene; cDNA EST EMBL: D64247 comes from this gene; cDNA EST EMBL: ...			284758, 284601, 284766, 284687, 18108372, 284555, 284559
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gij3885470 (AF061443) - G protein-coupled receptor LGR4 [Rattus norvegicus]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	284259, 28331822, 29331824, 35696032, 284508, 284906, 52844045, 52846317
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij4007990[gbj]AAC85339] - (AF084383) DOK protein [Mus musculus]		oncogene	284288, 284769, 284693, 284632, 284634, 284558, 87168518, 284583
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1176192[sp]P45420[YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLTF-NANT INTERGENIC REGION PRECURSOR]			284509, 284511, 284759, 284760, 284764, 284557
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij121383[sp]P18904[GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)]	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	284769
1242	78775890 (2483, 2484)				284601, 284604, 284638
					284906, 284807, 284908, 284634

1243	78779458 (2485, 2488)	Novel Protein sim. GBank gij3355671[embjCAA19071] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695817, 35695855, 265009, 264508, 264908
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gij2970646 (AF051845) - Xin. [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gij4586338[dbjBAA76357.1] - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - cytochrome C and Quinol oxidase polypeptide I	UNCLASSIFIED	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gij3581849[embjCAA20805] - (AL031541) putative phenylalanine-4RNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264584
1247	80064831 (2483, 2484)	Novel Protein sim. GBank gij2821684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	80070353 (2495, 2496)	Novel Protein sim. GBank gij1352403[epiP09467]F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (O-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108382, 264258, 26331826, 264106, 264508, 264907, 264828, 265009, 80433356, 264757, 264758, 21908754, 265010, 265011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gij2781407[embjCAA16001] - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]	transport		264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2498, 2500)	Novel Protein sim. GBank gij112785[epiP05100]3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	78850448 (2501, 2502)				
1252	78458087 (2503, 2504)				
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gij5870170[gbjAAD46816.1]AF16131 - (AF161317) NRAMP manganese transport protein MnaA [Salmonella typhimurium]	UNCLASSIFIED	glycoprotein	264908, 264683, 263976, 264600, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gij103160[pirjS22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)]		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21908767, 55811957, 264692, 264556, 264639
1255	78189728 (2509, 2510)				
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gij2985353[embjCAA04608.1] - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	264636
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gij3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	60432289, 264600, 264605, 264764, 264687, 264769, 264689, 27486265, 18108374, 18108376
1258	20708150 (2515, 2516)				264094, 265019
1259	80186012 (2517, 2518)				
1260	80084606 (2519, 2520)				
				UNCLASSIFIED	264602, 263978
				UNCLASSIFIED	264906, 264448, 264808
				UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gl 568951 dbj BAA83039.1 - (AB029010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	28331824, 284806, 284809, 284788, 284789, 284689, 284693, 284639, 18108384, 284583, 284634
1262	13504588 (2523, 2524)	Novel Protein sim. GBank gl 95100 pir S21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	
1263	20710987 (2525, 2526)	Novel Protein sim. GBank gl 3550958 (AF004940) - CDO [Rattus norvegicus]		struct	284602, 284634
1265	80253578 (2529, 2530)			UNCLASSIFIED	284563
1266	78914604 (2531, 2532)			UNCLASSIFIED	284766, 284636, 284638, 284567
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gl 1085002 pir S55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	284259, 21808754, 284369
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gl 4886445 emb CAB43370.1 - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278995, 56994075, 60424269, 28331827, 284109, 284512, 285007, 285008, 285009, 284595, 33109954, 33657084, 87188559, 284600, 285018, 285019, 284369, 284688, 21806767, 285020, 52844150, 284691, 33657023, 33657348, 18108374, 284556, 18108385, 60432113, 22279002, 284488
1269	78821848 (2537, 2538)	Novel Protein sim. GBank gl 3334791 emb CAA18939 - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	284508, 284905, 284806, 284687, 284693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gl 2651634 sp Q50591 YOD1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	285010, 284601
1271	79840499 (2541, 2542)			ATPase associated	35886052, 284908
1272	79482878 (2543, 2544)				284686, 284689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gl 1655665 emb CAB03731 - (Z81389) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	284509, 284639
1274	95010802 (2547, 2548)			UNCLASSIFIED	
1275	20730763 (2548, 2550)	Novel Protein sim. GBank gl 123726 sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)	Contains protein domain (PF00183) - Hsp90 protein	eph	284905, 284808, 284809, 284768, 284602
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gl 2129478 pir S51838 - chitinase (EC 3.2.1.14) precursor - beetle		UNCLASSIFIED	284369
1277	20438195 (2553, 2554)			UNCLASSIFIED	284558
1278	11088365 (2555, 2556)	Novel Protein sim. GBank gl 1175473 sp P44555 YAAJ_HAEIN - HYPOTHETICAL PROTEIN H10183		UNCLASSIFIED	284603
1279	21058758 (2557, 2558)	Novel Protein sim. GBank gl 1929513 (U64318) - ATP synthase subunit beta [Moorelia thermocellae]		synthase	284605
1280	79310958 (2559, 2560)	Novel Protein sim. GBank gl 4938504 emb CAB43862.1 - (AL078465) putative protein [Arabidopsis thaliana]		struct	283976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gll1136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF000047) - immunoglobulin domain	UNCLASSIFIED	29331825, 29331828, 264766, 83373044
1282	87537695 (2563, 2564)	Novel Protein sim. GBank gll3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gll3261721 (embjCAB07057) - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20638325 (2567, 2568)	Novel Protein sim. GBank gll3929022 (AF057696) - LspB [Haemophilus ducreyi]			284604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gll417154 (spjP33126) HS82_ORYSA - HEAT SHOCK PROTEIN 82	Contains protein domain (PF00183) - eph		264766, 264689, 263987
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gll2078004 (embjCAB08451) - (Z95207) gorA [Mycobacterium tuberculosis]	reductase		264605, 264639
1287	80417530 (2573, 2574)				
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gll5353510 (gbjAAD42161.1) AF08891 - (AF088916) emilin precursor [Homo sapiens]	UNCLASSIFIED		265011, 264602, 264766, 264687, 264769, 264689, 18108370, 264636, 18108385, 284583
1289	11813847 (2577, 2578)		Contains protein domain (PF00386) - collagen C1q domain		35688032, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264764, 264288, 264685, 264768, 264687, 264768, 264769, 265020, 265021, 264534, 264682, 18108370, 264628, 18108374, 35688423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264567, 264488, 18108391
1290	18526027 (2579, 2580)	Novel Protein sim. GBank gll1169995 (spjP46023) GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR	UNCLASSIFIED		264637
1291	80470266 (2581, 2582)	Novel Protein sim. GBank gll2072674 (embjCAB08305) - (Z95120) rhIE [Mycobacterium tuberculosis]	7 transmembrane receptor (rhodopsin family)		264563
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gll1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1293	80067536 (2585, 2586)		Contains protein domain (PF01530) - Zinc finger, C2HC type	transcription factor	264092, 264259, 29331822, 28331824, 264508, 264908, 264909, 264512, 265008, 265009, 264591, 265018, 264369, 264288, 264686, 264768, 264693, 18108374, 264632, 58182323, 264639, 83373044, 22278002, 284482, 264563
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gll2129173 (spjPjF64453) - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Melhanococcus jannaschii		UNCLASSIFIED	265008, 55812038, 264369, 264556
1295	11686651 (2589, 2590)	Novel Protein sim. GBank gll5441778 (embjCAB46803.1) - (AL096611) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]	biolindap		264602, 264605, 264760, 18108351, 264689, 33657023, 264559
			dehydrogenase		264689

1286	11887804 (2581, 2592)	Novel Protein sim. GBank gl 4882191gb AAD36686.1(AE00180 - (AE001805) DNA-directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease	UNCLASSIFIED	264591, 264638
1287	78639300 (2593, 2594)	Novel Protein sim. GBank gl 1943770 (U97181) - F53F10.1 gene product [Caenorhabditis elegans]			264693
1288	84239508 (2595, 2596)	Novel Protein sim. GBank gl 3445181 (AC005498) - R31865_2 [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	struct	18108348, 265017
1289	80253378 (2597, 2598)	Novel Protein sim. GBank gl 4062973dbj BAA36204.1 - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	UNCLASSIFIED	transcriptfactor	264488, 264906, 264909, 22278002, 264586
1300	80084867 (2599, 2600)				264605
1301	17939814 (2601, 2602)				264806
1302	95416188 (2603, 2604)				85658542, 265020
1303	8684121 (2605, 2606)				264908
1304	78371186 (2607, 2608)			UNCLASSIFIED	264508
1305	19905699 (2609, 2610)				264566
1306	13069230 (2611, 2612)	Novel Protein sim. GBank gl 3242273emb CAB07017 - (Z92668) hypothetical protein Rv0238c [Mycobacterium tuberculosis]	UNCLASSIFIED		264636
1307	82201029 (2613, 2614)	Novel Protein sim. GBank gl 1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	UNCLASSIFIED	264907, 264592, 264764
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gl 95819ipr S16288 - ferric enterobactin transport protein IepC - Escherichia coli		reductase	264555
1309	79263011 (2617, 2618)	Novel Protein sim. GBank gl 5459220emb CAB48893.1 - (AL098837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]	transport		264806, 18108354
1310	20466319 (2619, 2620)		UNCLASSIFIED		264605
1311	87613142 (2621, 2622)				35688286, 28331827, 264908, 265008, 264764, 264766, 264688, 21908767, 21908769, 35695917, 264691, 264693
1312	88081720 (2623, 2624)	Novel Protein sim. GBank gl 4455118gb AAD21084 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_bind	22278895, 22278898, 22278899, 264905, 264908, 265011, 265017, 265019, 264687, 21906768, 265020, 265021, 33657023, 22278002, 264584
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gl 4929733gb AAD34127.1(AF15189) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - Ribosomal protein S16	ribosomalprot	22278898, 22278899, 264259, 20281089, 29148498, 264508, 264908, 68712502, 60433356, 60433436, 265011, 265017, 264683, 264288, 21906765, 21906767, 29148627, 21906768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22278000, 264583, 18108390
1314	56928053 (2627, 2628)				264693
1315	84357182 (2629, 2630)	Novel Protein sim. GBank gl 2589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264691

1316	95361609 (2631, 2632)	Novel Protein sim. GBank gij5689407[dbj BAA82987.1] - (AB028950) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181880, 20281171, 28331822, 29331824, 60424269, 28331825, 35696052, 52844045, 284591, 60432228, 265018, 265019, 55811150, 56181562, 21908765, 21908767, 21908768, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 35695855, 18108387, 87168518, 60432113, 22279002, 284584
1317	88055167 (2633, 2634)	Novel Protein sim. GBank gij483757[gb AAD30541.1]AF134918 semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264083, 264906, 264908, 264369, 264684
1318	95322893 (2635, 2636)	Novel Protein sim. GBank gij4680204[gb AAD27667.1]AF114171 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 285011, 285017, 18108359, 18108362, 56182323, 18108385, 22279000
1319	94238546 (2637, 2638)				264908, 264909, 265008, 265008, 264592, 265019, 284766, 56181582, 18108368, 284628, 284629, 18108377, 284638
1320	86603567 (2639, 2640)	Novel Protein sim. GBank gij4240183[dbj BAA74870.1] - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696286, 55812038, 265018, 21906768, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gij4886505[emb CAB43377.1] - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcript factor	60432049, 28331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 284764, 284766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gij5262591[emb CAB45736.1] - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331828, 264908, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gij5459516[dbj BAA82407.1] - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264258, 28331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21906766, 21906767, 35695917, 265020, 264693, 65274781, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gij503171[ref NP_005704.1]pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278996, 22278998, 28331828, 264905, 284907, 29331830, 264908, 264510, 265008, 264595, 264759, 21908754, 285018, 264288, 264768, 264769, 21906768, 265022, 18108378, 264631, 264632, 264634, 264636, 284638, 264583, 284584, 264565, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gij3294501 (U64857) - similar to the DPTUKunltz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696286, 264805, 264806, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85658542, 264760, 264768, 264769, 264691, 35696423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gij1397275 (U61947) - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635

1327	85322897 (2653, 2654)	Novel Protein sim. GBank gi 728632 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF00278) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278986, 22278987, 22278999, 284081, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284105, 284905, 56182435, 264112, 265008, 265009, 21906754, 265010, 265011, 265017, 265018, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21906767, 21906769, 29148629, 265020, 264690, 264691, 264692, 264693, 263967, 33857109, 33857182, 27486282, 33857349, 18108370, 18108374, 55810764, 35695855, 264634, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264567
1328	87753483 (2655, 2656)			UNCLASSIFIED	264488, 22278997, 29331826, 264695, 18108351, 264766, 22279002, 264482, 264587
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi 4878224 gb AAD26969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi 437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264595, 264598, 56528486
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi 4589586 db BAA76815.1 - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264688, 21906765, 55811857, 265020, 33657023, 33657109, 263973, 55811576, 35696423, 35695855, 56182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gi 5459516 db BAA82407.1 - (AB028821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 22278996, 56984075, 22278998, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 21908754, 87168559, 265018, 265019, 264448, 264288, 264369, 264686, 21906765, 21908766, 21906767, 21906768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gi 5689527 db BAA83047.1 - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433358, 60433438, 55812038, 265010, 264639, 56528486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi 2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	264805
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi 4240285 db BAA74921.1 - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21908754, 87168559, 265017, 264288, 21906765, 21906767, 21908768, 21908769, 265020, 33657109, 27486284, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87767890 (2671, 2672)	Novel Protein sim. GBank gij465445ip33465jVNUA_PRIVKA - PROBABLE NUCLEAR ANTIGEN			264509, 264905, 264512, 264764, 264683, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gj15689471dbjBAA83019.1j - (AB028880) KIAA1067 protein [Homo sapiens]	UNCLASSIFIED		56182575, 56894075, 22278988, 22278989, 264092, 264259, 60432289, 29331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433356, 55812038, 33657084, 265011, 265017, 265018, 265019, 264682, 264448, 264683, 264389, 264688, 264689, 21908766, 21908769, 265020, 264691, 27488281, 20281089, 18108379, 55811576, 35895855, 58182323, 60432113, 22279002, 264587
1338	80366114 (2675, 2676)		UNCLASSIFIED		29331822, 265010, 264288, 264689, 18108370, 35695855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gj1176422 (U43194) - rhophilin [Mus musculus]	UNCLASSIFIED		35886052, 264909, 264688, 264558, 264558
1340	88316311 (2679, 2680)				264905, 264907, 87168559, 264764
1341	86101485 (2681, 2682)	Novel Protein sim. GBank gj15018564jembjCAB44507.1j - (AL035542) dJ894E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like protein)) [Homo sapiens])		Contains protein domain (PF000001) - 7 transmembrane receptor (rhodopsin family)	264681, 264685, 264686, 264692 264629
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gj4557543jrefjNP_001384.1pECM2 - extracellular matrix protein 2		Contains protein domain (PF00560) - Leucine Rich Repeat	264910, 264686, 264534
1343	80082862 (2685, 2686)				263978
1344	20562559 (2687, 2688)	Novel Protein sim. GBank gj12144101prij155210 - tricarboxylate carrier - rat (fragment)	glycoprotein		264608, 60170394
1345	81225546 (2689, 2690)	Novel Protein sim. GBank gj13881052jembjCAA19523j - (AL023843) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk248a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk248a12.5 comes...	kinase	Contains protein domain (PF000059) - Eukaryotic protein kinase domain	22278988, 264907, 264681, 264685, 264689, 265020, 264693, 22279000, 22279002, 264568
1346	80255717 (2691, 2692)				
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gj4504379jrefjNP_003658.1pHG38 - orphan G protein- coupled receptor HG38	glycoprotein	Contains protein domain (PF00560) - Leucine Rich Repeat	264906, 264908, 264909, 265006, 264910, 265011, 265017, 264764, 264766, 264767, 264769, 264631, 264634, 264638, 264667, 264486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gj13399720dbjBAA32100j - (AB010899) peptidylarginine deiminase type IV [Rattus norvegicus]	UNCLASSIFIED		264486, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264558, 264557, 264558, 22279002, 264486

1349	81225548 (2687, 2698)	Novel Protein sim. GBank glij2144101 prj 55210 - tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	52646842, 35686286, 22278996, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 284508, 284905, 284906, 284907, 284908, 284909, 264511, 265008, 264512, 264910, 60170831, 264591, 60433438, 264757, 21906754, 265017, 265018, 264605, 264760, 264762, 264288, 264768, 264889, 21906765, 21906766, 21906767, 21906768, 55811957, 35685917, 265020, 264534, 284691, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35698423, 60170384, 22278000, 22278002, 264583, 264584
1350	87083138 (2689, 2700)			UNCLASSIFIED	52646842, 264259, 29331825, 284808, 264511, 264604, 264288, 21906769, 265020, 33657182, 33657349, 18108374, 35685955, 264555, 264558, 18108385, 22278002, 264488
1351	87361327 (2701, 2702)	Novel Protein sim. GBank glij4887239 gb AAD32246.1 - (AF084584) BAW protein [Fugu rubripes]		UNCLASSIFIED	264806, 264807, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264683, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank glij2144101 prj 55210 - tricarboxylate carrier - rat (fragment)			35686286, 60424269, 264905, 264508, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264598, 55811386, 265011, 264605, 55811150, 264762, 264764, 264766, 52644229, 56181562, 35685917, 265022, 33657023, 264693, 35685783, 60431528, 264629, 283978, 35686423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264583, 264584, 264588
1354	95350845 (2707, 2708)	Novel Protein sim. GBank glij4889108 gb AAD27763.1 AF07703 - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264906, 265008, 33657402, 21908754, 265011, 87168559, 264684, 264369, 264769, 264689, 21908765, 21908768, 52644150, 33657023, 264692, 264693, 18108374, 83373044, 87168518, 22278000
1355	88260188 (2708, 2710)	Novel Protein sim. GBank glij1469189 db BAA09487 - (D50828) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 264259, 68714117, 264511, 21908754, 265010, 264769, 264689, 21908765, 21908768, 21908769, 264532, 27486262, 264629, 264636, 264556, 264638, 264639, 264482, 264484

1356	95313981 (2711, 2712)	Novel Protein sim. GBank gjl113865 (U40342) - ninein [Mus musculus]		struct	18108397, 22278995, 22278996, 22278998, 284094, 29331828, 284905, 285008, 285007, 285008, 285010, 285017, 285018, 285019, 284764, 18108354, 284689, 21906785, 285022, 18108384, 35698423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gjl897683[emb]CAA90330] - (Z50026) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		284258, 29331822, 28331825, 264510, 87168559, 285018, 264448, 264288, 21906785, 21906788, 21906788, 285021, 284693, 18108376
1358	38718455 (2715, 2716)	Novel Protein sim. GBank gjl556219 (L36831) - transcription regulator [Mus musculus]			284757
1359	87771843 (2717, 2718)			UNCLASSIFIED	284907, 284908, 284510, 284511, 284512, 18108351, 284764, 284534, 33657023, 18108374, 284634, 284638, 284638, 284639, 18108385, 284488, 284587
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gjl2598282[emb]CAA75612] - (Y15417) acetate--CoA ligase [Coprinus cinereus]		synthase	60432289, 284605
1361	87583527 (2721, 2722)	Novel Protein sim. GBank gjl5688443[db]BAA83005.1] - (AB028976) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35696286, 22278997, 22278999, 284259, 29331828, 284508, 284509, 284905, 284907, 284908, 285007, 265009, 33109954, 21908754, 87168474, 285011, 284761, 284683, 284288, 284768, 284769, 284689, 21906788, 285020, 285021, 33657023, 55811576, 35698423, 284634, 60432113, 22278002, 284482, 284486
1362	95287861 (2723, 2724)	Novel Protein sim. GBank gjl5689411[db]BAA82889.1] - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	eph	58182575, 58181688, 60432049, 284259, 29331822, 58182181, 29331827, 35698052, 29331828, 284905, 284908, 284908, 284595, 55812038, 85658542, 55811150, 284681, 284288, 284389, 58181562, 60431528, 55810784, 35698423, 60431850, 284558
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gjl1130484 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTPase activating protein for Arf	UNCLASSIFIED	284488, 29331826, 284907, 284687, 284689, 284693
1364	88178488 (2727, 2728)				
1365	83003108 (2728, 2730)	Novel Protein sim. GBank gjl4589562[db]BAA76803.1] - (AB023176) KIAA0859 protein [Homo sapiens]		oncogene	60432289, 60433356, 60433438, 87168559, 284603, 18108351, 21906788, 35698423, 60432113
1366	87003282 (2731, 2732)	Novel Protein sim. GBank gjl1084844[pr]S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	284766

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gij489408[emb]CAB43240.1] - (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52846842, 52846385, 22278995, 56994075, 35698286, 22278998, 22278998, 284259, 29331824, 66714117, 29331825, 60432289, 35696052, 264805, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265009, 60170831, 33657402, 55812038, 21808764, 265011, 87188559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264369, 264688, 264767, 264689, 21908765, 21908766, 21908768, 21908769, 55811957, 265020, 265021, 265022, 264534, 60170815, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35698423, 35695855, 264635, 264555, 264637, 264556, 52844332, 60170394, 264558, 18108381, 18108385, 56526486, 22278000, 264563, 264587
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gij484561[sp]P35289[RB15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 28331827, 35696052, 264508, 264905, 264908, 264908, 264908, 264510, 265007, 264910, 60433438, 264758, 85658542, 87188559, 264600, 264601, 264760, 264764, 264765, 264768, 52844229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52844332, 264558, 264639, 83373044, 264563, 264586, 264486, 264567, 265008, 60432229, 60433356, 33657084, 21908784, 21908769, 264555, 264639, 264559, 264587
1369	86534033 (2737, 2738)	Novel Protein sim. GBank gij2062702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	
1370	95318910 (2739, 2740)	Novel Protein sim. GBank gij5031823[ref]NP_005823.1[prKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278998, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265018, 264764, 264766, 264768, 21908767, 35695917, 18108362, 35696423, 264632, 264635, 264638, 264555, 264638, 264558, 264639, 18108385, 65274727, 264404, 264583, 264558, 264488
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gij5032203[ref]NP_005714.1[prTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264805, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695855, 264558, 22278002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gl 840708 dbj BAA08334 - (D50886) trans-aldolase [Trypanosoma cruzi]		collagen	263978	264769, 21806765, 21806767, 22278989, 264691, 284810, 55812038, 265010, 264681, 264684
1373	80498421 (2745, 2746)			UNCLASSIFIED		264807, 264510, 265007, 264512, 265008, 60432229, 264688, 85274781, 264555, 264556, 264557, 83373044, 60432113
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gl 111876 pir JC1241 - beta-interferon-induced protein - rat		interferon		52844507, 52645156, 52846842, 52846366, 56102575, 56181686, 22278988, 56984075, 35898286, 22278987, 22278988, 22278989, 264259, 29331822, 52845080, 29331824, 29331825, 60432229, 29331826, 29331827, 29331828, 35898052, 33656970, 284805, 284509, 264906, 284807, 284808, 29331830, 264808, 265006, 264511, 265007, 265008, 265009, 33657402, 60433356, 52846317, 33108954, 33657084, 52844286, 87188474, 87188559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264288, 264389, 264766, 52844229, 21806765, 21806768, 21806767, 21806768, 21806769, 55811957, 35895917, 265020, 265021, 52844150, 33657023, 264693, 65274620, 52845129, 33657109, 27486281, 33657349, 27486265, 35895763, 18108378, 55810784, 35898423, 35895855, 264630, 264631, 264634, 264636, 264555, 264638, 18108385, 87188518, 60432113, 22278000, 22278002, 264563, 264564, 264566, 264567, 264766, 264769, 35695917, 22278987, 264691, 264259, 29331822, 284693, 35898052, 264508, 284508, 284905, 264906, 264828, 264908, 264629, 18108372, 264809, 264510, 264511, 264512, 265008, 264630, 264631, 284910, 264632, 264634, 264635, 264636, 284591, 284592, 264637, 284638, 284558, 284639, 33657402, 264595, 18108385, 56528486, 265010, 265011, 264600, 264583, 284762, 264564, 264565, 264784, 264488, 264766
1375	94356942 (2749, 2750)	Novel Protein sim. GBank gl 5649176 gb AAD03500.2 - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase		
1376	87398050 (2751, 2752)	Novel Protein sim. GBank gl 136350 sp P28968 VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED		
1377	86864242 (2753, 2754)	Novel Protein sim. GBank gl 1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated		29331824, 264581, 265019, 264686, 264769, 55811957, 284693, 22279002

1378	87595071 (2765, 2756)	Novel Protein sim. GBank gij4107015[dbj BAA36283] - (AB001772) PEM-5 [Clona savigny]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264389, 264288, 29148627, 55811957, 264881, 18108368, 33657109, 18108368, 264635, 263881, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gij3252872 (AF035820) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627862 (2759, 2760)	Novel Protein sim. GBank gij4837737[gb AAD30662.1] - (AF096834) germ cell specific Y-box binding protein [Homo sapiens]	nucL_rept		264510, 264512, 265009, 264288, 264564
1381	88178658 (2761, 2762)	Novel Protein sim. GBank gij4731580[gb AAD28508.1] (AF125384) L82A [Drosophila melanogaster]	UNCLASSIFIED		87168559, 265017, 264628, 22278002
1382	94847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433356, 85858542, 265017, 265018, 264685, 264768, 21908768, 35695917, 33657023, 27486281, 27486282, 35695763, 35695955, 87168518, 22278002
1383	87860588 (2765, 2766)			UNCLASSIFIED	18108396, 264692
1384	86915895 (2767, 2768)			UNCLASSIFIED	264488, 264508, 264509, 264905, 264908, 264908, 264909, 264511, 264512, 264910, 264760, 18108351, 264766, 264769, 35695855, 264630, 264636, 264559, 264638, 264483, 264564, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gij2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]	UNCLASSIFIED		35686052, 55811386, 264888, 21908765, 265020, 33657023, 18108385
1386	81013049 (2771, 2772)	Novel Protein sim. GBank gij2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]	Inf		60432289, 29331826, 264908, 264807, 56162435, 265011, 264881, 60170615, 33657023, 83373044, 264568
1387	87787958 (2773, 2774)	Novel Protein sim. GBank gij4160304[emb CAA10600] - (AJ132192) HS1 binding protein 3 [Mus musculus]	UNCLASSIFIED		264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gij4895164[gb AAD32753.1] (AC007231) putative disease resistance protein [Arabidopsis thaliana]	glycoprotein		65274572, 22278999, 264259, 29331826, 29331827, 35698052, 264509, 264807, 264908, 264909, 265008, 265008, 60170831, 33657402, 60433438, 264596, 21908754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 264682, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22278000

1389	91256016 (2777, 2778)	Novel Protein sim. GBank gi 5689387 dbj BAA82977.1 - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29148499, 264908, 68712502, 55812038, 285017, 265018, 265019, 18108351, 264369, 21906765, 21906768, 21906767, 21906768, 265020, 265021, 264692, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22279000, 264563, 264564, 52645156, 52646365, 264259, 52645080, 29331825, 29331828, 264808, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181562, 52644229, 21906765, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486261, 27486284, 85274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1390	84111916 (2779, 2780)	Novel Protein sim. GBank gi 3702295 (AC005783) - R33083_1 [Homo sapiens]	peptidase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gi 1348910 sp P28650 PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP--ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		52646842, 65274572, 22278994, 22278995, 35688286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35686052, 29331828, 33656870, 264907, 52644045, 265008, 265007, 265009, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906764, 21906767, 35685917, 265020, 265021, 33657109, 52645129, 27486261, 27486282, 27486265, 33657349, 35685763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264638, 52644332, 18108362, 18108385, 87168518, 60432113, 22279000, 264484, 264568, 18108391
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gi 726286 (U23394) - mSin3A [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1393	80408472 (2785, 2786)				
1394	15028819 (2787, 2788)				
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gi 2274845 dbj BAA21534 - (D88481) N-WASP [Rattus rattus]		UNCLASSIFIED	264629
				UNCLASSIFIED	265009, 18108381

1398	95363253 (2791, 2792)	Novel Protein sim. GBank gij2135904 pij 54610 - pH-EIF1 - human			22278997, 22278999, 264259, 29331825, 60432289, 29331828, 29140498, 29140499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264602, 265017, 265018, 265019, 18108354, 52644228, 18108358, 21906767, 29148627, 21908768, 21908769, 29148628, 29148784, 265021, 265022, 18108358, 18108374, 56182323, 18108385, 264563, 264567, 35686286, 264907, 66712502, 264510, 35685917, 264692, 264693, 35699423, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 285018, 265019, 264682, 264768, 21906787, 265020, 33657023, 27488281, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1397	87631317 (2793, 2794)			UNCLASSIFIED	
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gij5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]			264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 285018, 265019, 264682, 264768, 21906787, 265020, 33657023, 27488281, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gij2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264768, 18108370, 264555, 264557
1400	95418084 (2799, 2800)	Novel Protein sim. GBank gij283920 pij 527939 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264769, 21908768, 21908787, 55811957, 264691, 264692, 264628, 264629, 55811576, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226376 (2801, 2802)	Novel Protein sim. GBank gij3256185 emb CAA15485 - (AL008635) dJ510H18.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 264809, 264758, 264768, 21908769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gij1515427 (U57523) - nei homolog [Homo sapiens]	Contains protein domain (PF00008) - Igf EGF-like domain	igf	264805, 264907, 264908, 264909, 264112, 264693, 33657109, 264634
1403	94147833 (2805, 2806)	Novel Protein sim. GBank gij5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21908765, 21908769, 264693, 55811576, 65274791, 60432113
1404	80835393 (2807, 2808)			UNCLASSIFIED	65274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433436, 265017, 264693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X63413) U88 [Human herpesvirus 6]			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264908, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264784, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264486, 264567, 264807, 264605
1406	87812369 (2811, 2812)	Novel Protein sim. GBank gi 624076 gb AAC96425.1 - (U42560) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (BX); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramedum buraria Chlorella virus 1]	collagen		
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gi 2827866 (AF015037) - endooligopeptidase A related protein; EOPA related protein [Ornitholagus cuniculus]	UNCLASSIFIED		35696286, 22278999, 264094, 264259, 88714117, 29331826, 29331827, 29331828, 29146498, 264107, 264908, 265008, 265008, 264810, 60433438, 265011, 265017, 18108351, 264448, 264288, 264686, 21908765, 21908769, 264692, 33657109, 18108370, 264628, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 80432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gi 2564853 (AF030001) - unknown [Mus musculus]	oncogene	Contains protein domain (PF00008) - EGF-like domain	264488, 264489, 35696286, 264109, 264508, 264805, 264509, 264906, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264801, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264688, 21906767, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264583, 264564, 264565, 264566, 264567, 264693
1409	86644385 (2817, 2818)	Novel Protein sim. GBank gi 2662165 gb BA23714 - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gi 2493790 sp Q60994 ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)	complement	Contains protein domain (PF00388) - C1q domain	29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264789, 21906767, 263974, 264631, 264566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gij3123155isp191343YM3M_CAEEL - HYPOTHETICAL 49.0 KO TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - Kinase receptor WD domain, G-beta repeat	22278995, 22278997, 22278999, 29331822, 60432289, 29331828, 284907, 265017, 265018, 284682, 21906787, 21906788, 21906789, 265020, 284690, 284691, 33657023, 33657108, 27486264, 284628, 263972, 284634, 284558, 18108385 284757
1412	84380919 (2823, 2824)	Novel Protein sim. GBank gij387912 emb CAA84370 - (Z70310) predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S37771), cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	UNCLASSIFIED	
1413	85416558 (2825, 2826)	Novel Protein sim. GBank gij387912 emb CAA84370 - (Z70310) predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S37771), cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - homeobox Ank repeat	56994075, 29331822, 35896052, 29331828, 29331830, 284908, 52844045, 284510, 52844296, 85658542, 87168474, 285017, 265018, 284681, 284687, 21906788, 35895917, 265020, 52844150, 284692, 283987, 27486264, 35895783, 284638, 18108387, 284566
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gij3252881 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	UNCLASSIFIED	284682, 284683, 265022, 284636
1415	94320948 (2829, 2830)	Novel Protein sim. GBank gij1871187 (U90439) - unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00560) - Leucine Rich Repeat	52846365, 56182575, 22278994, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52844045, 284113, 284511, 33657402, 284757, 21906754, 55811388, 285017, 265018, 285019, 284761, 284683, 284369, 284288, 284686, 284689, 21906788, 21906787, 29148627, 21906789, 55811957, 265020, 285021, 284690, 33657023, 65274620, 52845129, 27486262, 27486264, 60431528, 284629, 35895855, 56182323, 284559, 60432113, 284404, 22279002, 284482

1416	94325677 (2831, 2832)	Novel Protein sim. GBank gi 5106557 gb AAD39749.1 AF123052 - (AF123052) MILL seplin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278996, 35698286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29146498, 284905, 264907, 284908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52644229, 264688, 264689, 21906765, 21906766, 21906767, 29148827, 21906768, 55811957, 29148829, 295020, 52644150, 18108361, 33657023, 18108382, 18108368, 264628, 18108370, 264629, 18108374, 18108379, 55811576, 65274791, 264634, 264636, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000 264107, 264448
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi 4858835 dbj BAA78095.1 - (AB027570) suppressor of potassium transport defect 3 (Rattus norvegicus)	ATPase_associated	
1418	87594276 (2835, 2836)			
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi 2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]	UNCLASSIFIED	264259, 264908, 265010, 52644229, 21908764, 21906768, 264690, 264639, 18108388
1420	87298628 (2839, 2840)	Novel Protein sim. GBank	struct	264259, 60432289, 265006, 87168474, 264288
1421	94146986 (2841, 2842)	gi 5174421 ref NP_006023.1 pCPNE - copine VI (neuronal) (Z68635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	ATPase_associated kinase	29331824, 265007, 264563 18108358, 18108386, 18108397, 21908768, 18108398, 21906767, 56182575, 21908768, 21908789, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27486261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 68712502, 263972, 55811576, 35696423, 35695855, 264512, 285007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264486, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gi 4505939 ref NP_000928.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)			mapolymerase	56994075, 35696286, 87168559, 55811957, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)				UNCLASSIFIED	284686, 264489, 264692, 264594, 264603, 285018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gi 437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]		Contains protein domain (PF00620) - RhoGAP domain	struct	28331822, 28331825, 28331827, 29146488, 264905, 264908, 264908, 264908, 265007, 264910, 265009, 33109554, 265010, 87168559, 265018, 264766, 264887, 21908765, 21908766, 21908767, 21908768, 29146827, 55811957, 29146829, 265021, 264691, 264692, 56526486, 22278002, 264593
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gi 100788 pir S14959 - proline- rich protein - wheat			UNCLASSIFIED	285007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gi 2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386) [Caenorhabditis elegans]			UNCLASSIFIED	284488, 60424178, 35698286, 22278897, 22278998, 22278999, 264259, 60432049, 28331822, 28331825, 28331827, 56182435, 264910, 60433356, 60433438, 21806754, 265018, 264288, 21908765, 21908766, 21908767, 21908768, 265020, 265022, 33657109, 18108370, 18108378, 264558, 83373044, 18108385, 56526486, 22278002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gi 5616074 gb AAD45616.1 AF06194 - (AF061943) protale- derived STE20-like kinase PSK (Homo sapiens)		Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	22278994, 56994075, 22278897, 28331828, 28331830, 264828, 265006, 265007, 265008, 265009, 264883, 264288, 18108354, 21908765, 21908768, 29146829, 33657023, 18108374, 35698855, 83373044, 22278002, 264584
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gi 138350 sp P28868 VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR			glycoprotein	56181686, 264259, 284907, 265007, 265009, 264595, 265010, 264688, 65274620, 264629, 65274791, 22279002, 264568
1429	87886889 (2857, 2858)				UNCLASSIFIED	284112, 264595, 265017, 265019, 21806765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gi 1181619 db BAA11565 - (D82384) a variant of TSC-22 [Gallus gallus]				264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21908767, 85274620, 55811576, 264639, 87168518, 22278002
1431	80428081 (2861, 2862)	Novel Protein sim. GBank gi 5420389 emb CAB4680.1 - (AJ243460) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gi 414797 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]			phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29146828, 263889
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gi 2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]		Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	284259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)				UNCLASSIFIED	264682, 264691

1435	84708213 (2869, 2870)	Novel Protein sim. GBank gij3970850[dbj BAA34788.1] - (AB015330) HRIHFB2007 [Homo sapiens]		transcriptfactor	22278997, 22278998, 22278999, 60432049, 264259, 28331822, 28331824, 66714117, 28331826, 33656970, 264508, 264905, 66712502, 29331830, 264908, 265007, 265008, 264910, 265009, 60433358, 60433438, 264508, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906787, 21906788, 21906789, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108378, 55811576, 264636, 60170394, 56182323, 264559, 83373044, 87188518, 60432113, 22278000, 22278002, 264563, 264482, 264565
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gij3183977[emb CAA39515] - (X56044) protein HIF9C [Mus musculus]		UNCLASSIFIED	263378, 264557, 264559
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gij2496887[sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 66714117, 28331826, 264907, 56182435, 265009, 18108351, 264692, 264693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gij1905908 (AD0000092) - hypothetical human serine-threonine protein kinase R31240.1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264488, 264508, 264908, 264909, 264757, 264600, 264601, 264605, 264768, 264769, 264690, 35698423, 264558, 264563, 264568
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gij3876289[emb CAA94892] - (Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]	Contains protein domain (PF00450) - Serine carboxypeptidase	cathepsin	264489, 18108394, 65274572, 56182575
1440	87423643 (2879, 2880)	Novel Protein sim. GBank gij2662165[dbj BAA23714] - (AB007802) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 28331822, 28331824, 60432289, 28331826, 28331827, 28331828, 35696052, 33656970, 264107, 264508, 264509, 264907, 66712502, 28331830, 56182435, 264511, 265008, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264638, 56182323, 83373044, 18108387, 87188518, 60432113, 22279000, 264486
				UNCLASSIFIED	264487, 264259, 264906, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

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[illegible]

1464	87620482 (2827, 2828)	Novel Protein sim. GBank gl 3874447 emb CAB02772 - (Z81039) predicted using Genefinder; cDNA EST EMBL:701209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 35696052, 20281100, 284905, 29331830, 264909, 265007, 33857402, 21806754, 265017, 265018, 264682, 264684, 264369, 264288, 264766, 21906765, 21906766, 21906767, 21906769, 35695917, 264691, 33657023, 284692, 35696423, 35695855, 264630, 264631, 264639, 264585
1465	87425192 (2828, 2830)	Novel Protein sim. GBank gl 4598598 dbj BAA76821.1 - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	264488, 22278994, 56894075, 60432049, 264598, 56182181, 60432288, 29331827, 52844045, 284511, 265007, 265008, 264598, 55812038, 55811388, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33857182, 55811576, 264557, 18108382, 60432113
1466	87606227 (2931, 2932)	Novel Protein sim. GBank gl 2246532 (U83872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264512, 285017, 264689, 264558
1467	87614328 (2933, 2934)			strud	264683, 264636
1468	85342882 (2935, 2936)	Novel Protein sim. GBank gl 450724 trf NP_003137.1 pSSRP - structure specific recognition protein 1			22278998, 264758, 265018, 265019, 21906769, 265020, 33857108, 22278002
1469	79236174 (2937, 2938)	Novel Protein sim. GBank gl 1806596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108368, 18108374, 18108381, 18108382, 18108384, 18108388
1470	84890482 (2939, 2940)	Novel Protein sim. GBank gl 5649170 gb AAD43131.2 AF15909 - (AF159092) syld709813 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264581, 60432229, 60433356, 264595, 60433438, 264758, 33109854, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264369, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87168518, 60432113, 264404, 22279002, 264482, 264567, 264487
1471	87626842 (2941, 2942)	Novel Protein sim. GBank gl 3976148 emb CAB01750 - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL:701651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331822, 29331824, 29331825, 264628, 264603, 264689, 264693, 18108374, 55811576

1472	87756616 (2943, 2944)	Novel Protein sim. GBank g 4680707 pb AD27743.1 AF13298 - (AF13298) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	264805, 18108351, 21906765, 264486
1473	87791609 (2945, 2946)	Novel Protein sim. GBank specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - MHC Nucleosome assembly protein (NAP)		18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 66714117, 29331825, 29331826, 35686052, 264906, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264766, 21906769, 55811957, 265021, 264681, 264693, 264629, 55811576, 264634, 264636, 56182323, 22278002, 264566, 264486
1474	85800989 (2947, 2948)	Novel Protein sim. GBank g 2494890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		264488, 35695917, 35698286, 264692, 33657023, 264693, 33657109, 35696052, 264508, 264905, 264906, 264907, 264629, 264908, 264909, 35698423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264558, 264557, 264639, 264758, 60432113, 264604, 264605, 264565, 264566, 264764, 264488, 264885, 264766, 264681, 264682, 264288, 264568
1475	86871835 (2949, 2950)			UNCLASSIFIED	
1476	87548855 (2951, 2952)	Novel Protein sim. GBank g 4757752 ref NP_004664.1 pANGP - angiotensin 3	Contains protein domain (PF00041) - Fibronectin type III domain Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	60424179, 56181686, 29331824, 60424269, 29331826, 35696052, 264508, 264805, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812036, 265011, 264601, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35698423, 264634, 264635, 264636, 60431850, 264555, 264636, 264557, 264639, 18108382, 18108388, 60432113, 22278002, 264259, 264107, 264805, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1477	87774279 (2953, 2954)	Novel Protein sim. GBank g 2498308 sp Q80870 DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED	
1478	11754412 (2955, 2956)				264686

1479	91640140 (2857, 2858)	Novel Protein sim. GBank gi 5499741 gb AAD43978.1 AF15296 - (AF15296) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 68714117, 294908, 264807, 56182435, 265006, 60170831, 33657402, 284758, 33108954, 21906754, 265017, 265018, 284448, 284288, 264767, 264687, 52644228, 21906784, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486261, 27486282, 33657349, 18108370, 60431528, 263876, 55811576, 264556, 264557, 60170394, 87168518, 284404, 22278000, 22279002, 264563, 264482
1480	84312412 (2859, 2860)	Novel Protein sim. GBank gi 3550456 emb CAA06329.1 - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35698286, 56994075, 22278996, 22278997, 22278998, 22278999, 264091, 264259, 35698052, 29146499, 264103, 264105, 264108, 284907, 52844045, 284112, 265007, 265008, 265009, 60433356, 60433438, 264598, 33109954, 33657084, 52844286, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 284769, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52844150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 284566, 284089, 264486
1481	87021442 (2881, 2882)	Novel Protein sim. GBank gi 4836807 gb AAD30586.1 AF14679 - (AF14679) PFT27 [Mus musculus]		MHC	265006, 265007, 265010, 18108374
1482	85320442 (2863, 2864)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF12292) Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	284808, 284910, 264758
1483	94115503 (2865, 2866)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 285007, 55812038, 33109954, 265017, 264288, 21906788, 21906789, 264636, 18108380, 87168518, 22279000
1484	94131544 (2867, 2868)	Novel Protein sim. GBank gi 1911774 pbls 180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35698288, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906768, 29148827, 33657023, 27486282, 18108374, 35698423, 83373044, 60432113
1485	80184441 (2869, 2870)	Novel Protein sim. GBank gi 580128 gb AAD42883.1 AF15511 - (AF15511) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	284369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gij4569516jdbjBAA76780.1] - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00068) - Eukaryotic protein kinase domain	kinase	56182575, 22278989, 264908, 264907, 21906754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gij5019275jembjCAB44431.1] - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]		synthase	21906754, 264486
1488	87732026 (2975, 2976)	Novel Protein sim. GBank gij5712131jblAAD47379.1jAF12049 - (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	fgf	264686, 264768, 264689, 264692, 264693, 264509, 264906, 264907, 18108370, 264908, 264629, 264908, 264510, 265006, 264512, 265007, 265008, 265009, 264555, 264556, 284557, 264558, 264762, 264564, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gij2487303jplQ82786jFPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21906767, 22278989, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35896423, 35895855, 265007, 265008, 265009, 83373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87380127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170615, 33657109, 35695855, 264635, 60170394, 56526486, 22278002, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gij295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gij1656005 (U71205) - rii [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278988, 29331822, 264907, 66712502

1493	81677215 (2985, 2986)	Novel Protein sim. GBank gij5689515[dbj]BAA83041.1] - (AB028012) KIAA1089 protein [Homo sapiens]	UNCLASSIFIED	264488, 52846365, 65274572, 56182575, 22278994, 35698286, 56994075, 22278999, 60432049, 29331824, 29331828, 35686052, 264508, 264805, 264806, 52844045, 264809, 58182435, 265006, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264682, 264685, 264686, 52844229, 21906765, 21906768, 21906768, 21906769, 265020, 265021, 60170815, 52844150, 33657023, 18108364, 18108365, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35685763, 18108370, 264629, 18108374, 52844332, 56182323, 87168518, 22279002, 264584, 264586, 264587
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gij728632[sp]P39189[ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII]	kinase	264807, 265009, 264789, 18108370, 55811576, 264639, 264565, 264488
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gij4589589[dbj]BAA76816.1] - (AB023189) KIAA0972 protein [Homo sapiens]	transcript factor	22278997, 264259, 264806, 264907, 265008, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264583, 264565, 264566, 264486, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	35686286, 264808, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gij3674925[emb]CAA92591] - (Z68286) Similarly to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:TO1018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene;...	kinase	264910, 264758, 265011, 264764, 264288, 264690, 264634, 264635, 56526486
1498	80934938 (2995, 2996)	Novel Protein sim. GBank gij728636[sp]P39183[ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII]	oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148827, 29148829, 18108374, 264637, 264638, 264567
1499	86451589 (2997, 2998)	Novel Protein sim. GBank gij2570198 (U54556) - microfilarial sheath protein SHP3 [Litomosoides sigmodontis]	glucoamylase	263978, 264566
1500	80499388 (2999, 3000)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein precursor [Boreogadus saida]	UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein precursor [Boreogadus saida]	UNCLASSIFIED	264559
1502	80206141 (3003, 3004)			264508, 264112, 264604, 264684, 52844150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gij3900855 (AC004874) - similar to N-acetylglucosaminyltransferase; similar to Q07537 (PID:g1171899) [Homo sapiens]	transferase	29331822, 265007, 264369

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1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC006585 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52846365, 52846842, 65274572, 22278894, 35698288, 58994075, 264259, 52845080, 29331822, 29331825, 35696052, 29331830, 52844045, 58182435, 265008, 60433358, 60433438, 55812038, 21906754, 52846317, 52844296, 87168474, 87168559, 264448, 52844229, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52844150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486284, 27486285, 35695763, 18108376, 35698423, 35695855, 52844332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163538 (3029, 3030)	Novel Protein sim. GBank (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33368 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin		
1516	88073539 (3031, 3032)	Novel Protein sim. GBank gi 488015 (L27479) - X123 [Homo sapiens]		UNCLASSIFIED	265008, 58182323, 22278002
1517	87783325 (3033, 3034)	Novel Protein sim. GBank gi 3415134 (AF082024) - Phyb1 [Pimpinella brachycarpa]			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi 28838 p P39195 ALU0_HUMAN - III ALU SUBFAMILY SX WARNING ENTRY IIII	tm7		66714117, 284508, 284509, 264905, 264510, 284910, 264591, 264595, 264288, 264766, 284769, 18108374, 264638, 264638, 264486 264569, 264489, 60432049, 265009, 33657402, 264598, 21908754, 265019, 264369, 21908765, 21908768, 21908769, 264691, 65274620, 33657182, 27486261, 18108374, 264557, 264639, 87168518, 22278002
1519	94328689 (3037, 3038)	Novel Protein sim. GBank gi 526268 emb CAB45771.1 - (AL080188) hypothetical protein [Homo sapiens]			
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi 2662161 db BAA23712 - (AB007800) HH-0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	18108392, 60432049, 264259, 29331824, 265007, 60433358, 265010, 21908768, 264636
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi 5052351 gb AAD38518.1 AF13542 - (AF13542) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleotidyl transferase	synthase	18108394, 264259, 66714117, 265011, 284603, 265019, 18108364, 35698423, 284557, 264558, 18108388 29331824, 265018, 265020, 265021
1522	78960587 (3043, 3044)	Novel Protein sim. GBank gi 3776567 (AC005388) - Strong similarity to F2187.33 gi 2809284 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]		UNCLASSIFIED	65274572, 21908768, 264693
1523	91005151 (3045, 3046)			UNCLASSIFIED	
1524	80203723 (3047, 3048)			UNCLASSIFIED	264112, 21906754, 263974
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi 4759040 ref NP_004283.1 PRIN1 - ras inhibitor		UNCLASSIFIED	264683, 264687, 264688, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264586, 55812036, 264605, 264683, 21906785, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gi 2792498 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 97168559, 265017, 264288, 21906766, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278895, 22278897, 264259, 66712502, 264586, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gi 406663 gb AAD20053 - (AF131828) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263884, 56182575, 22278895, 35696286, 22278897, 264259, 29331822, 60432289, 29331827, 35696052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264768, 18108357, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 60432113, 22279002, 264583, 264584, 264488, 264587
1530	95012785 (3059, 3060)	Novel Protein sim. GBank gi 2828710 (AF043642) - malin cyclophilin [Rattus norvegicus]			264488, 264489, 35696286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264488
1531	95419351 (3061, 3062)	Novel Protein sim. GBank gi 1905974 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - Kinase PDZ domain (Also known as DHR or GLGF).		56182575, 35696286, 264087, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264568

1532	85716224 (3063, 3064)	Novel Protein sim. GBank gjl3874716[emb]CAA91265] - (Z68484) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264689
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gjl1490324[emb]CAB01543] - (Z78141) unknown [Mus musculus]	struct			29331824, 28148499, 264807, 284112, 265008, 265011, 265017, 265018, 264762, 18108351, 263967, 20281148, 18108374, 263981, 264566
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gjl81286[pri]S22697 - extensin - Volvox carter (fragment)	UNCLASSIFIED			264905, 264807, 264768, 264637
1535	90936732 (3069, 3070)					65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 29148499, 265008, 265008, 60170831, 60433438, 33109854, 87188559, 265018, 18108357, 21908768, 29148629, 265021, 265022, 18108377, 56182323, 60432113, 22278000, 22279002
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gjl106024[pri]B32891 - finger protein 2, placental - human	transcript factor	Contains protein domain (PF00098) - Zinc finger, C2H2 type		264686, 18108357, 18108384, 21908767, 21908768, 29148629, 35686286, 265020, 265021, 52844150, 264693, 68714117, 29331825, 29331826, 284508, 264805, 20281149, 264809, 18108374, 35686423, 35695855, 265009, 264634, 264636, 264638, 18108385, 56526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	95354556 (3073, 3074)	Novel Protein sim. GBank gjl3876332[emb]CAB02096] - (Z78754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426112.5 comes from this gene; cDNA EST yk342110.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 56182575, 60432049, 264259, 29331828, 265008, 265007, 60433356, 60433438, 284601, 18108351, 264448, 264369, 264288, 33657023, 65274820, 33657109, 60432113
1538	85724828 (3075, 3076)	Novel Protein sim. GBank gjl403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds], gene product [Gallus gallus]	kinase	Contains protein domain (PF00059) - Eukaryotic protein kinase domain		18108394, 18108397, 264809, 265008, 265009, 265010, 18108351, 264638, 18108362, 18108385, 18108388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gij3218411 emb CAA19575.1 - (AL023859) SPBC19C7.07c, putative tRNA splicing endonuclease gamma subunit, len:284aa, similar eg. to YAR008W, YAH0_YEAST, P39707, YAR008W, tRNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:268, E(1):6.4e-2...		nuclease	22278994, 22278998, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 60424268, 29331825, 60432288, 29331826, 29331827, 29331828, 35696052, 33656970, 56182435, 265009, 33657402, 60433356, 60433436, 55812038, 21906754, 87188558, 265017, 265018, 265019, 18108351, 264288, 52644229, 16108359, 21906764, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486261, 18108370, 18108376, 35696423, 55811576, 65274791, 264558, 56182323, 60170394, 83373044, 87188518, 60432113, 22279000, 22279002, 264566
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gij5052634 gb AAD38647.1 AF145672 BcDNA.GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317848 (3081, 3082)	Novel Protein sim. GBank gij5052349 gb AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 284259, 29331822, 35696052, 264508, 284509, 264905, 264907, 264908, 264511, 284512, 264910, 264582, 264781, 264782, 264446, 264764, 264288, 264687, 21906769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 284628, 18108374, 264632, 264634, 264635, 264638, 18108385, 264563, 264564, 264585, 264586, 264486
1542	90837649 (3083, 3084)	Novel Protein sim. GBank gij505702 gb AAD41779.1 AF12668 - (AF126687) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52844150, 18108388, 264636, 18108391, 18108382
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gij728632 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		nuclease	264106, 33109854, 265019, 264683, 35695917, 264690, 264692, 33657109
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gij3493182 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	mup_recpt	35696286, 56994075, 22278999, 35696052, 60433358, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87168518, 22279000
1545	85757673 (3089, 3090)	Novel Protein sim. GBank gij1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP-P22082) in a region of giv-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	79476589 (3091, 3092)			UNCLASSIFIED	264905, 264566
1547	86999584 (3093, 3094)	Novel Protein sim. GBank gij266132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	264259, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811578, 18108380, 264563

1548	94233065 (3095, 3098)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	28331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gi 5689519 dbj BAA3043.1 - (AB028014) KIAA1091 protein [Homo sapiens]		eph	60424179, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 28331822, 56182181, 29331824, 35886052, 264905, 264906, 264908, 264909, 265006, 264511, 265008, 60431735, 60433358, 21908754, 55811386, 87188559, 265017, 265018, 265019, 55811150, 264682, 264288, 264359, 56181562, 264769, 21908765, 21908769, 21908769, 55811957, 265020, 264681, 33657109, 60431528, 35696423, 35695855, 56528486, 60432113, 22279002, 264563, 264568
1550	95201807 (3099, 3100)	Novel Protein sim. GBank gi 544483 sp P3350 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	im7	65274572, 60432289, 265008, 264910, 652011, 265017, 265019, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank gi 4758566 ref NP_004788.1 pHS6S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278989, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21908754, 265018, 265019, 264681, 264764, 264766, 264688, 264769, 21908769, 264692, 35695763, 264835, 264555, 264556, 264557, 264638, 264558, 264563
1552	87817114 (3103, 3104)			UNCLASSIFIED	264259, 29331828, 66712502, 264764, 264288, 264686, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gi 4589570 dbj BAA76807.1 - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	- dehydrogenase	56182575, 35696286, 26146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264893, 33657109, 18108374, 35696423, 85274781, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233089 (3107, 3108)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	- transferase	35696286, 22278997, 264259, 28331822, 28331824, 28331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265019, 264681, 264369, 264686, 264767, 264768, 21906765, 21908769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gij2257495[dj]BAA21392] - (AB004534) p1015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331828, 35698052, 264508, 264805, 264808, 264907, 264908, 52644045, 264909, 264910, 60432228, 60433359, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21908785, 35695917, 265022, 264691, 33657023, 35698423, 35698555, 264635, 264555, 264636, 264638, 264639, 18108385, 56526488
1556	91228268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35698423, 265018, 264632, 264682, 29331822, 265020, 265011, 60432289, 264509, 264908, 264907, 264908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264768, 264690, 263978, 264634, 264635, 264639, 264584, 264486, 22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 264448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 29331822, 60432288, 35696052, 264259, 29331822, 264763, 21908784, 264107, 264110, 21906754, 33109954, 87168559, 264760, 264763, 21908784, 21908785, 21906768, 265021, 264690, 35695855
1557	87840809 (3113, 3114)	Novel Protein sim. GBank gij3329811 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zif-C3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 264448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 29331822, 60432288, 35696052, 264259, 29331822, 264763, 21908784, 264107, 264110, 21906754, 33109954, 87168559, 264760, 264763, 21908784, 21908785, 21906768, 265021, 264690, 35695855
1558	94840376 (3115, 3116)	Novel Protein sim. GBank gij5360105[jb]AAD42871.1[AF155105] putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			264908, 264603, 264638
1559	88224885 (3117, 3118)	Novel Protein sim. GBank gij112808[sp]P02750[A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 264763, 21908784, 264107, 264110, 21906754, 33109954, 87168559, 264760, 264763, 21908784, 21908785, 21906768, 265021, 264690, 35695855
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gij3880146[emb]CAA92704] - (Z88319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71617 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	264908, 264603, 264638
1561	86609159 (3121, 3122)				
1562	83358682 (3123, 3124)				
1563	85508694 (3125, 3126)				
1564	87786371 (3127, 3128)	Novel Protein sim. GBank gij1169287[sp]P45953[JACDV_RAT - ACYL-CoA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED UNCLASSIFIED - dehydrogenase	264510, 264594, 263967, 264910, 264764, 264768, 18108394, 35698286, 264259, 29331822, 60432289, 35698052, 29331828, 264508, 66712502, 264908, 56182435, 265007, 264810, 80170831, 21908754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21908765, 21908768, 265021, 60170615, 264692, 35698423, 35698555, 264557, 56182323, 60432113, 22278002, 264482

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gll128726[sp]P05307[PDI_BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI)] (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264689, 18108398, 55811857, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264835, 264636, 264591, 264555, 264582, 264637, 264593, 264584, 264595, 264586, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gll3880445[emb]CAA20328[- (AL031266) VM106R.1 [Caenorhabditis elegans]		inf	22278996, 22276999, 264259, 29331822, 29331824, 60432289, 29331827, 68712502, 264908, 265008, 18108351, 52644228, 21908765, 21908767, 21908768, 21908769, 33657109, 264555, 264639, 264482
1567	84988006 (3133, 3134)	Novel Protein sim. GBank gll4928699[gb]AAD34110.1[AF15187] CGI-115 protein [Homo sapiens]		UNCLASSIFIED	56182375, 21908769, 264692
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gll4827063[ref]NP_005072.1[pZNF1 - Zinc finger protein 142 (clone pHz-49)]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21908767, 21908768, 264691, 264693, 22278000, 22278002
1569	90938668 (3137, 3138)	Novel Protein sim. GBank gll5689451[db]BAA83009.1[- (AB028880) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 284905, 56182435, 265007, 265019, 264764, 21908765, 21908769, 55811857, 60170615, 52844150, 264692, 33657023, 33657109, 18108377, 264563, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gll1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gll4507731[ref]NP_001061.1[pTUBG - tubulin, gamma polypeptide]	Contains protein domain (PF00091) - Tubulin/FisZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21908765, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384
1572	61201664 (3143, 3144)			UNCLASSIFIED	35696052, 264805, 264908, 264908, 264910, 264758, 264766, 35695917, 264637
1573	80207068 (3145, 3146)			UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gl[4758334]refJNP_004256.1[pFADS - delta-8 fatty acid desaturase]	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278999, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 285008, 264910, 265009, 264591, 21908754, 265011, 265019, 18108351, 284682, 264763, 264764, 18108354, 264368, 264288, 264685, 264766, 264686, 264768, 264688, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 264690, 264691, 264693, 20281089, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22278002, 264563, 264568
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gl[3881810]emb[CAA94856] - (Z70763) similar to EF-hand calcium binding protein; cDNA EST EMBL:CO8700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265008, 265008, 265009, 265010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811957, 265020, 265021, 60170815, 264691, 33657023, 33657109, 60431528, 85274791, 35695855, 18108385, 60432113, 22278002, 264482
1576	95314019 (3151, 3152)	Novel Protein sim. GBank gl[2773185] (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]	UNCLASSIFIED	UNCLASSIFIED	264559, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265008, 264910, 21908754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264638, 83373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gl[2489130]sp[P70315]WASP_MOUSE - WISKOTT- ALDRICH SYNDROME PROTEIN HOMOLOG [WASP]		UNCLASSIFIED	264511, 265011, 264681, 264368, 264686, 264688, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gl[2978255]dbj[BAA25190] - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	264259, 29331826, 265017, 264689, 264693, 60432113
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gl[4324682]gbj[AAD16986] - (AF108674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	35698288, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518 22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gl[2088838] (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21908764, 55811957, 35695917, 264692, 55811578, 264637, 56182323, 264559, 83373044, 60432113

1582	95368052 (3163, 3164)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 60432289, 29331827, 264509, 264905, 264906, 264907, 264908, 264910, 264782, 264288, 264768, 264769, 264632, 264555, 264639, 58526486, 22278000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gij5578958[emb]CAB51351.1] - (AL050306) dJ475B7.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170931, 33657402, 264682, 21906766, 35895855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gij5551815[gb]AAD44482.1] - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	60424179, 52646842, 65274572, 56182576, 22278995, 35896286, 22278998, 22278998, 264259, 29331822, 56182181, 60424269, 60432289, 29331827, 29331828, 35896052, 26146488, 66712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33857402, 60433438, 55812038, 21906754, 55811386, 52644296, 87188474, 87188559, 265018, 265018, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35895917, 265020, 265021, 265022, 52844150, 33657023, 33657108, 18108374, 55810764, 55811576, 35896423, 65274791, 35895855, 56182323, 83373044, 18108387, 87188518, 60432113, 22278002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gij4240132[db]BAA74846.1] - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	phosphatase	35896286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 265006, 265007, 265008, 60433356, 33109854, 87188474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264829, 263972, 18108383, 18108388, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gij3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			285017, 265018, 264688, 33657023, 263978, 264638, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264907, 264908, 264511, 264810, 264591, 264594, 264628, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gij1077573[pr]J52680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	284259, 29331828, 264905, 265008, 264758, 21906754, 264781, 264782, 21906765, 21906769, 60170915, 52644150, 33657109, 35895855, 56182323, 18108385
1589	80880553 (3177, 3178)	Novel Protein sim. GBank gij213756[pr]J48746 - semaphorin C - mouse (fragment)		UNCLASSIFIED	65274572, 264480, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264586, 265011, 264686, 21906766, 21906768, 55811957, 27460285, 264639, 18108385, 56526486, 60432113

1590	9531825 (3179, 3180)			UNCLASSIFIED	264489, 2227898, 264259, 29331824, 29331825, 29331826, 29331827, 265006, 60433356, 21906754, 265017, 265018, 265019, 264448, 264765, 264288, 52844229, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 27486285, 35695763, 56528488, 60432113, 22278000, 22279002, 264564
1591	66877160 (3181, 3182)	Novel Protein sim. GBank		MHC	
1592	87882533 (3183, 3184)	gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator			
1593	94891601 (3185, 3186)			UNCLASSIFIED	264259, 264905, 29331830, 264595, 265017, 264448, 264288, 264690, 264629, 87166518
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA87060 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35686423, 22278000, 264565, 264567
1595	79819425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments Integral membrane proteins	UNCLASSIFIED	264488, 29331827, 264905, 264906, 264807, 264908, 264909, 264910, 264592, 264593, 264757, 264802, 264604, 264760, 264681, 264288, 264766, 264768, 29148629, 35695917, 264692, 264628, 264629, 264630, 264632, 264634, 264635, 264636, 264638, 264563, 264584, 264566
1596	78933928 (3191, 3192)	Novel Protein sim. GBank		UNCLASSIFIED	29331826, 264908, 55811957
1597	86971857 (3193, 3194)	gi 5257114 gb AAD41244.1 AF094480 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450	UNCLASSIFIED	29146498, 264758, 263867
1598	87862839 (3195, 3196)	Novel Protein sim. GBank			264092, 29331824, 264508, 264682, 264369, 264686, 264630, 264563
1599	87849829 (3197, 3198)	Novel Protein sim. GBank gi 4506797 ref NP_000324.1 pSCAT - sphinocerbellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	264259, 264634
1600	80056002 (3199, 3200)			UNCLASSIFIED	52645080, 29331824, 29331826, 264511, 265009, 265011, 264605, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108385
1601	15023246 (3201, 3202)			UNCLASSIFIED	29331826, 264603, 264681, 264563
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	284635
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283820 pir S27839 - lensin - chicken			29146499, 264112, 264762, 18108351, 29148627, 263974
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 476883 gb AAD29633.1 AF11682 - (AF116827) unknown [Homo sapiens]	collagen		264490, 29331824, 264807, 264909, 264511, 265008, 264592, 265010, 265011, 264762, 264764, 264369, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
			ATPase associated		263977

1605	91221129 (3208, 3210)			struct	264905, 264509, 264908, 264907, 264908, 264909, 264904, 264768, 264768, 264892, 264693, 33657108, 264629, 35695855, 264635, 264638, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gi 4505313 ref NP_003784.1 pmym - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	struct	22278998, 22278999, 264258, 33657402, 265017, 18108351, 264448, 21808787, 21906769, 52644150, 264891, 87168518
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gi 5174473 ref NP_005888.1 p PPI - Intracisternal A particle- promoted polypeptide		transcriptfactor	264689
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gi 2224629 dbj BAA20802 - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED	264094, 264808, 264807, 264809, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	84311572 (3217, 3218)	Novel Protein sim. GBank gi 4884073 emb CAB43213.1 - (AL049934) hypothetical protein [Homo sapiens]			52644507, 52645158, 52646365, 52646842, 56182575, 22278994, 5694075, 35696288, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 28331828, 35696052, 33658970, 264508, 264509, 264907, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21808754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 21908785, 21908786, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657108, 52645129, 27486261, 27486282, 35695763, 264628, 18108370, 18108376, 35698423, 264638, 52644332, 18108387, 87168518, 22279000, 264563, 264488
1610	85488200 (3219, 3220)	Novel Protein sim. GBank gi 263920 pir S27839 - tensin - chicken		UNCLASSIFIED	264593, 264757, 55812038, 265018, 265020, 264681, 264682, 264693, 264631, 264634, 264635, 264555, 22279000, 264554
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gi 107284 pir A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - EGF-like domain	peroxidase	35698286, 21908765, 264691, 35698423
1612	85748031 (3223, 3224)	Novel Protein sim. GBank gi 3874846 emb CAA94337 - (Z70307) Similarly to B. subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:CO9951 comes from this gene; cDNA EST EMBL:CO8265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264508, 18108370, 18108387, 264488
1613	82247354 (3225, 3226)			UNCLASSIFIED	264759

1614	81228634 (3227, 3228)	Novel Protein sim. GBank gi 4680673 gb AAD27726.1 AF132951 CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 56182323, 83373044, 264568 22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264891, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1615	86121808 (3229, 3230)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1 - (AB028987) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264891, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi 3878260 emb CAB01696 - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EMBL:C08081 comes from this gene; cDNA EST comes from this gene; cDNA ...	UNCLASSIFIED		264486, 52644507, 52645158, 52646355, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 33656970, 264905, 264909, 264594, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644229, 21906764, 264889, 21906765, 21906766, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 18108376, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518 35696052, 264905, 264509, 264907, 264808, 264510, 264511, 264764, 264766, 264768, 264689, 264693, 18108374, 264635, 264636, 264638
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gi 466053 sp P34679 Y041_CAEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHC zinc finger domain	peptidase	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264891, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi 4240231 dbj BAA74894.1 - (AB020678) KIAA0871 protein [Homo sapiens]		struct	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264891, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1619	95354560 (3237, 3238)	Novel Protein sim. GBank gi 5031763 ref NP_005515.1 PHYR - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcript factor	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264891, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi 151047 sp P45843 SCRT_DRONE - SCARLET PROTEIN		UNCLASSIFIED	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264891, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002

1621	87076708 (3241, 3242)	Novel Protein sim. GBank gi 3822553 (AF088788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00822) - SPRY domain	UNCLASSIFIED	264910 - 18108392, 65274572, 18108388, 22278986, 22278997, 22278999, 29146498, 29146499, 294905, 284808, 284909, 284828, 52844045, 284592, 60433358, 21806764, 284602, 285017, 284389, 21908788, 55811957, 285021, 60170615, 284635, 284557, 60170394, 83373044, 18108385, 22279000, 22279002, 284568
1622	84741739 (3243, 3244)	Novel Protein sim. GBank gi 3875666 emb CAB05478 (Z83104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL: D33665 comes from this gene; cDNA EST EMBL: D36540 comes from this gene; cDNA EST yk240/8.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...	ribosomalprot	UNCLASSIFIED	18108398, 284259, 284909, 56182435, 87168474, 284448, 21806788, 35895817, 284691, 87168518, 284583
1623	87778106 (3245, 3246)	Novel Protein sim. GBank gi 731088 sp P40389 UV22_SCHPO - UV-INDUCED PROTEIN UV122		UNCLASSIFIED	68714117, 28331825, 284908, 265008, 264758
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gi 3875666 emb CAB05478 (Z83104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL: D33665 comes from this gene; cDNA EST EMBL: D36540 comes from this gene; cDNA EST yk240/8.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...		UNCLASSIFIED	284489, 22278994, 22278995, 22278996, 35896286, 22278997, 22278998, 22278999, 284092, 284259, 29331824, 29331825, 29331827, 29331828, 284102, 284106, 284508, 33857084, 285017, 265018, 18108351, 284683, 284369, 284288, 21806765, 21908766, 21908767, 21908769, 35895917, 265021, 284691, 65274820, 18108368, 263972, 18108376, 35898423, 284631, 284634, 22279000, 22279002
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gi 4589822 dbj BAA76833.1 (AB023206) KIAA0989 protein [Homo sapiens]	kinase		52844507, 52845156, 52846365, 52846842, 22278994, 58994075, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 68714117, 29331826, 60432289, 29331827, 29331828, 35898052, 284908, 66712502, 284909, 285008, 285009, 60432229, 60433356, 60433438, 21808754, 52846317, 52844296, 285011, 87168559, 284804, 265018, 284448, 284369, 284288, 264766, 52844229, 284689, 21908765, 21908768, 35895917, 285021, 285022, 52844150, 33857023, 65274620, 27486261, 27486262, 27486285, 35895763, 263972, 52844332, 60170394, 87168518, 60432113, 284587
1626	84734369 (3251, 3252)	Novel Protein sim. GBank gi 5878070 gb AAD46844.1 AF16090 - (AF160904) BcDNA, HL05936 [Drosophila melanogaster]			284288, 264686, 284767, 22279002
1627	83388773 (3253, 3254)	Novel Protein sim. GBank gi 3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264288
1628	85708459 (3255, 3256)		eph		

1629	84983841 (3257, 3258)	Novel Protein sim. GBank gij4240175[dbj BAA74866.1] - (AB020650) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87779027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 264693, 264634, 22278002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gij1915892[emb CAA69995] - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811857, 264259, 33657023, 264693, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 264638, 264637, 56182323, 264559, 264758, 18108385, 264583, 264764, 264766
1632	87871682 (3263, 3264)	Novel Protein sim. GBank gij2558501[dbj BAA22696] - (D83850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264769, 264681, 264692, 29148499, 264509, 264905, 264907, 284511, 284512, 264482, 264681, 264763, 264682, 264683
1633	87773683 (3265, 3266)				264488, 264259, 264907, 264908, 264909, 264628, 264629, 264631
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gij4887229[gb AAD32244.1]AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	265007, 264637, 22278002
1635	84232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35896052, 52644045, 264511, 265008, 265009, 265010, 265011, 265018, 265019, 264448, 264369, 21908765, 21908768, 265021, 264690, 264482
1636	80413227 (3271, 3272)	Novel Protein sim. GBank gij4557511[ref NP_001339.1]pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED	22278995, 264594, 264763, 265020
1637	80070435 (3273, 3274)			kinase	264558
1638	87101854 (3275, 3276)	Novel Protein sim. GBank gij3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			21906765, 21906767, 22278998, 35696286, 22278999, 264259, 264692, 264693, 29331824, 33657109, 264508, 264906, 18108370, 264629, 265007, 33657402, 21906754, 264602, 264604, 264764, 264683, 264566, 264288
1639	94322184 (3277, 3278)	Novel Protein sim. GBank gij5420389[emb CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35896052, 264908, 56182435, 264112, 265006, 265008, 264757, 264758, 55811386, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21906767, 55811957, 264691, 33657023, 65274620, 18108370, 55810764, 55811576, 264558, 264639, 83373044, 18108385, 87108518

1840	94143185 (3278, 3280)	Novel Protein sim. GBank gij2842469jemb CAA16847.1 - (AL021747) hypothetical protein (Schizosaccharomyces pombe)		UNCLASSIFIED	56182575, 56994075, 35698286, 60432049, 60432289, 29331827, 35698052, 52844045, 56182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52844229, 21908765, 21908768, 21908768, 35695917, 265021, 60170815, 52844150, 33657023, 33657109, 33657349, 18108374, 35698423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1841	87625160 (3281, 3282)			UNCLASSIFIED	29146489, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1842	94312557 (3283, 3284)	Novel Protein sim. GBank gij1575333 (U60416) - myr 8 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain		22278989, 29147620, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264889, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52844332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564
1843	94131768 (3285, 3286)				29331825, 29331827, 29331828, 21806754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1844	88095125 (3287, 3288)			UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1845	85013858 (3289, 3290)			UNCLASSIFIED	264685, 264693
1846	95382681 (3291, 3292)	Novel Protein sim. GBank gij1076802 pir S49915 - extensin like protein - maize		UNCLASSIFIED	22278994, 56994075, 35698288, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486281, 27486265, 33657349, 60432113, 264563, 264564
1847	94278428 (3293, 3294)	Novel Protein sim. GBank gij5002573jemb CAB44338.1 - (Y17466) alpha-N-acetylglactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264906, 264908, 264359, 21908768, 60170615, 264639, 22279000
1848	87842088 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264886, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385

1648	85347628 (3297, 3298)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278996, 22278997, 22278998, 60432049, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284905, 264907, 66712502, 264908, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264581, 264583, 60433438, 264596, 55812038, 21906754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52644229, 264688, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35696423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264482, 264555, 264566, 264487, 265011, 264802, 21906767, 18108374, 18108377, 18108385
1650	87418539 (3289, 3300)	Novel Protein sim. GBank gij3647335[emb]CAA21059] - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			
1651	91639773 (3301, 3302)	Novel Protein sim. GBank gij4884278[emb]CAB43247.1] - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 28331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264686, 21906765, 21906768, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695855, 264556, 264637, 264557, 264559, 83373044, 56526488, 22279000, 22279002, 264564, 22278997, 28146498, 58182435, 21906754, 264368, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002
1652	86588622 (3303, 3304)	Novel Protein sim. GBank gij1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00189) - struct PH domain		
1653	94255983 (3305, 3306)	Novel Protein sim. GBank gij3776054[emb]CAA06273] - (AJ004989) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - glycoprotein Immunoglobulin domain		
1654	79756471 (3307, 3308)		UNCLASSIFIED		18108396, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264908, 265006, 265008, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108384, 65274791, 18108384, 60432113, 264567, 33657109, 264565

1655	86689346 (3308, 3310)	Novel Protein sim. GBank gjl3355717[embjCAA73496] - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52644507, 35686288, 22278998, 22278999, 29331824, 29331825, 29331826, 33656970, 284908, 52844045, 284511, 284910, 52646317, 284288, 52844228, 33657023, 33657108, 52844332, 284557, 56182323, 56526486, 60432113
1656	79862297 (3311, 3312)	Novel Protein sim. GBank gjl1890141[dbjBAA18947] - (D83208) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771984 (3313, 3314)	Novel Protein sim. GBank gjl4557845[refjNP_001524.1]pHNP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00078) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	- dna_ma_bind	29331827, 265009, 21806766, 21906767, 285020, 265022, 33657109, 284636, 59526486, 264482
1658	87773778 (3316, 3318)	Novel Protein sim. GBank gjl3877072[embjCAA87060] - (Z48037) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52646385, 35686288, 22278998, 22278997, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 284805, 284908, 52644045, 265008, 60433356, 284757, 60433436, 21806754, 265011, 18108351, 284448, 264368, 284288, 264766, 264768, 21908765, 21908767, 21908768, 21908769, 29148628, 265021, 265022, 18108362, 263989, 263971, 18108374, 35686423, 18108383, 22278000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gjl538218[pirjIS38038] - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21908766, 21908767, 21908768, 87168518, 22278998, 265020, 22278999, 87168559, 264603, 265017, 264631, 265018, 265019, 22278002, 264482, 264635, 264565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gjl2487012[spQ10010]YSV4_CAEEL - HYPOTHETICAL 26.6 KO PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	284488, 35686288, 284259, 35686052, 284508, 264509, 264805, 264806, 284807, 284908, 284909, 284510, 284511, 265006, 265007, 264512, 265008, 284910, 264592, 264598, 265010, 264600, 264802, 265017, 265018, 264605, 264760, 284764, 264288, 264766, 264686, 284768, 264769, 264689, 21908766, 356865917, 284690, 33657023, 264693, 33657109, 264628, 35686423, 35686555, 264634, 284635, 284555, 284636, 284637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 284564, 264565, 284566, 284488, 284567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278988, 264259, 29331824, 29331826, 29331827, 29331828, 284509, 68712502, 29331830, 284908, 52644045, 265007, 264512, 60433356, 60433438, 55812038, 21908754, 285019, 264448, 264766, 264768, 264769, 21908788, 21908769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264563, 264564, 264565, 264567 18108392, 29331822, 29331828, 20281100, 264106, 265008, 265007, 265008, 18108348, 21908766, 18108365, 18108368, 18108374, 83373044, 18108385
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730502 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PFT27			52845156, 56182575, 22278984, 22278985, 35696286, 22278986, 56984075, 22278997, 22278988, 22278989, 264269, 29331822, 29331826, 29331827, 29331828, 33656970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33108954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21908765, 21908768, 21908767, 21908768, 21908769, 265021, 265022, 264691, 33657023, 264693, 263987, 33657109, 264630, 52844332, 83373044, 87168518, 80432113, 22278900
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi 4884136 emb CAB43275.1 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - kinase WW domain		264488, 263994, 35696286, 29331824, 35696052, 264508, 264509, 284905, 264908, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264769, 21908764, 21908765, 21908767, 35695917, 265021, 264534, 60170815, 264690, 264691, 264692, 33857109, 33657182, 264628, 18108370, 264628, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 284566, 264486
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi 3043692 db BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	

1665	91226652 (3329, 3330)	Novel Protein sim. GBank gij1083506iprj[S50065 - sialoadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	264486, 29331826, 29331828, 264509, 264908, 264907, 264909, 264510, 264511, 264910, 264592, 264593, 264595, 264758, 264596, 264600, 264760, 264762, 264764, 264766, 264768, 264828, 264630, 264634, 264636, 83373044, 264584, 264566, 264567, 264486
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gij3913431spjO42643jDDX8_SCHPO - PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	56994075, 22278989, 264259, 29331824, 29331826, 29331827, 29146498, 265009, 33108954, 87168559, 265019, 264288, 264688, 21908767, 21908769, 264691, 33857182, 18108370, 18108374, 18108385, 22279002
1667	91226655 (3333, 3334)	Novel Protein sim. GBank gij5689535jdbj[BAA83051.1] - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	264259, 29331822, 29331828, 264905, 264908, 264908, 264510, 265009, 264595, 264758, 265011, 87168559, 265017, 265018, 265019, 264448, 264766, 264686, 21908765, 21908767, 21908769, 265020, 265021, 60170615, 264690, 264692, 264693, 18108368, 18108370, 263972, 55810764, 264555, 83373044, 80432113, 22279000, 22279002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gij2076894jgbj[AAB53983.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE_bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	kinase	66714117, 264508, 264509, 264906, 264907, 264908, 264511, 264910, 264764, 264687, 264689, 33657109, 35696423, 35695855, 264632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gij3875371jembj[CAB85414.1] - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor UZAF 65 KD subunit: cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D68829 comes fr...	UNCLASSIFIED	29331825, 33108954, 264369, 264767, 264689, 33657109, 83373044
1670	87628009 (3339, 3340)		UNCLASSIFIED	264258, 26331824, 29331827, 60433438, 265022, 264636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gij462451spjP34244jKKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	kinase	35696286, 22278987, 29331825, 264909, 21906754, 265017, 265018, 265019, 264682, 264683, 264768, 264688, 21906766, 21906767, 21906768, 21908769, 264691, 264555, 264556, 22279000, 264566
1672	86291834 (3343, 3344)	Novel Protein sim. GBank gij1814270 (U74566) - double-stranded RNA specific adenosine deaminase [Rattus norvegicus]	deaminase	264908, 264909, 264632, 18108381

1673	88085137 (3345, 3346)	Novel Protein sim. GBank gjl2070894[gbjAAB53983.1]- (AF002197) short region of weak similarity to protein Kinase C; contains similarity to Pfam domain PF00130 (DAG_PE_bind). Score=10.0, E-value=0.0034, N=1 (Caenorhabditis elegans)	Contains protein domain (PF00130) - kinase Phorbol esters/diacylglycerol binding domain (C1 domain)	264488, 264569, 18108394, 56994075, 22278996, 264259, 35696052, 264508, 264905, 264509, 264608, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264784, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33657023, 284692, 284693, 33657109, 284628, 284629, 18108374, 35696423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 284565, 264566, 264567, 264488
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gjl5262467[embjCAB45683.1]- (AL080062) hypothetical protein [Homo sapiens]	kinase	29331822, 28331824, 264906, 52644045, 60433356, 87168559, 264448, 264288, 264388, 264691
1675	87606466 (3348, 3350)	Novel Protein sim. GBank gjl3128366 (AF010496) - 50S ribosomal protein 19 [Rhodobacter capsulatus]	UNCLASSIFIED	56181688, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 66712502, 284764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35696423, 35695855, 284637, 264639, 18108385, 264564
1676	95358086 (3351, 3352)	Novel Protein sim. GBank gjl4164085[gbjAAD05327]- (AF111091) latrophilin 3 splice variant bbar [Bos taurus]	UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gjl3327046[dbjBAA31591]- (AB014516) KIAA0916 protein [Homo sapiens]	UNCLASSIFIED	264908
1678	88668829 (3355, 3356)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	UNCLASSIFIED	29331824, 264102
1679	81214106 (3357, 3358)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	UNCLASSIFIED	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35696286, 29331824, 265006, 265007, 265008, 265009, 18108348, 285011, 18108351, 264683, 18108354, 18108358, 18108359, 21906765, 29148627, 29148628, 264690, 18108361, 18108362, 18108364, 18108365, 18108366, 284626, 18108379, 35696423, 35695855, 284635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	81005372 (3359, 3360)	Novel Protein sim. GBank gjl2394478 (AF024500) - No definition line found [Caenorhabditis elegans]	transport	65274372, 22278994, 22278998, 66714117, 29331827, 56182435, 21906754, 265018, 284288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gjl5689537[dbjBAA83052.1]- (AB029023) KIAA1100 protein [Homo sapiens]	UNCLASSIFIED	22278996, 29331822, 264908, 264563, 264604, 265019, 264683, 5611857, 264690, 33657023, 35696423, 83373044, 284563
1682	86042710 (3363, 3364)		UNCLASSIFIED	264909, 285017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263694, 35698286, 35698052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264756, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264369, 264766, 264768, 35695917, 264692, 33657109, 35698423, 35695955, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80083409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gi 1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase	UNCLASSIFIED	60424179, 52846842, 22278994, 35698286, 22278998, 264259, 52845080, 28331824, 29331826, 265007, 33657084, 265018, 264881, 264448, 264883, 264369, 264889, 21908765, 21908767, 21908768, 21908769, 265021, 264692, 65274620, 33657109, 27466262, 264635, 52644332, 56182323, 22278000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gi 2244707 dbj BAA21115.1] - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264805, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264585, 264489, 264587
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gi 4680679 gb AAD27728.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264808, 264907, 264908, 264510, 265008, 265007, 264910, 264558, 18108381, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gi 4240193 dbj BAA74875.1] - (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264569, 35698286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gi 3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - cadherin	cadherin	264369, 21908766, 264692, 264639, 87168518
1691	68095223 (3381, 3382)	Novel Protein sim. GBank gi 2773208 (AF039713) - No definition line found [Caenorhabditis elegans]	Cadherin domain		264768, 33657108, 29331827, 29148629, 264510, 264106, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264807, 264908, 33657023, 264567, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gi 121271 sp P02207 GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331828, 264508, 264905, 264907, 264595, 265010, 265011, 21908768, 33657023, 264629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gij5453932[ref]NP_006225.1[pOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 10 kDa subunit	mapolymerase	35698286, 22278996, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331828, 35698052, 29146499, 284905, 284908, 52844045, 264511, 285008, 285007, 265009, 264592, 60433356, 21806754, 265010, 265011, 18108351, 264763, 264682, 284448, 264683, 284288, 264768, 264689, 21806768, 60170815, 264691, 264692, 264693, 18108370, 18108374, 263978, 35698423, 35698555, 264556, 18108381, 18108385, 87188518, 264482, 264486 284634
1695	84718325 (3389, 3390)	Novel Protein sim. GBank gij4680670[gb]AAD2729.1[AF13285 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gij4220517[emb]CAA22890] - (AL035358) hypothetical protein [Arabidopsis thaliana]			
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gij505652 (U10362) - GP36b glycoprotein [Homo sapiens]		glycoprotein	22278997, 264259, 265010, 18108351, 264764, 21908766, 18108370 264682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gij5052031[gb]AAD38411.1[AF155739 - (AF155739) axotropilin [Mus musculus]			
1699	87424793 (3397, 3398)				56994075, 22278998, 22278999, 264509, 33657402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29146627, 21908769, 29148829, 265020, 265022, 33657023, 284556, 87168518, 22279002 35698286, 284635
1700	87859161 (3399, 3400)	Novel Protein sim. GBank gij543344[pil]S41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED nuc_rept	28331824, 52644045, 265008, 265009, 263969, 263971
1701	86570488 (3401, 3402)			UNCLASSIFIED	264092, 264110, 263977
1702	87795092 (3403, 3404)	Novel Protein sim. GBank gij3877439[emb]CAA96852] - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		MHC	22278995, 22278997, 264082, 29146498, 29148498, 264107, 264508, 264907, 264110, 264112, 265009, 60170831, 21906754, 265011, 265017, 264762, 18108351, 264288, 21806765, 35695917, 265021, 60170615, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263978, 35695855, 264555, 263981, 60170394, 18108385, 56528486, 87168518, 60432113
1703	79568651 (3405, 3406)	Novel Protein sim. GBank gij451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264909, 265017, 264628, 264629, 264638
1704	86622978 (3407, 3408)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	264389
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gij4519621[dbj]BAI75870.1] - (AB017614) OASIS protein [Mus musculus]			264569, 35696286, 264907, 265010, 264687, 264768, 264692, 264693, 264636, 264586
1706	87790987 (3411, 3412)	Novel Protein sim. GBank gij3123034[epi]15011Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21906768, 21908769, 265022, 264691, 264556, 22279000

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gl 4321684 gb AAD15797 - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108398, 22278997, 264259, 28147620, 29331826, 29146498, 264905, 264908, 265008, 264593, 264595, 264759, 264596, 265018, 264760, 18108351, 264764, 264766, 264889, 264693, 18108370, 35698423, 55811576, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gl 5174597 ref NP_005947.1 pMT-HF - 5,10-methyltetrahydrofolate dehydrogenase, 5,10-methyltetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - synthase Formate-tetrahydrofolate ligase		56192575, 22278998, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 265009, 60170831, 33657402, 33108954, 87168559, 265019, 18108351, 264448, 21908765, 21908767, 21908768, 29148627, 29148629, 29148784, 60170815, 52844150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563
1709	80222583 (3417, 3418)			UNCLASSIFIED	264107, 55811857, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)	Novel Protein sim. GBank gl 5031735 ref NP_005760.1 pHEC - N-acetylglucosamine 6-O-sulfotransferase		UNCLASSIFIED	264556
1711	81013729 (3421, 3422)	Novel Protein sim. GBank gl 5454168 ref NP_008453.1 pXAP4 - HBV associated factor		sulfotransferase	65274572, 29331824, 29331826, 264768, 60431528, 35698423, 60432113, 264563
1712	96330184 (3423, 3424)	Novel Protein sim. GBank gl 5454168 ref NP_008453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	kinase	56994075, 264093, 264259, 29331822, 264909, 29331824, 29331827, 284107, 264110, 264511, 264582, 265011, 265018, 264683, 264686, 264689, 265020, 33657023, 263987, 33657109, 263974, 35698423, 35695855, 264630, 264636, 264558, 264566
1713	84143453 (3425, 3428)	Novel Protein sim. GBank gl 160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278995, 264508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 264757, 21908765, 265020, 265021, 264692, 56528486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gl 5689537 dbj BAA83052.1 - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	264509, 264905, 264906, 264807, 264908, 264909, 264910, 264591, 265011, 264766, 264768, 264769, 264691, 264692, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 264564
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gl 458946 dbj BAA76761.1 - (AB012808) mBOCT [Mus musculus]	transport		56182575, 29331824, 60432289, 264109, 264809, 265007, 264600, 265019, 264686, 265020, 264683, 55811576, 264558, 60432113, 22279002

1717	87503223 (3433, 3434)	Novel Protein sim. GBank gi 2765411 emb CAA74749 - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264559, 264258, 29331826, 29331826, 29331826, 29331826, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265008, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264766, 264688, 18108357, 35695917, 264690, 264692, 264693, 264628, 264628, 35696423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391
1718	87032628 (3435, 3436)	Novel Protein sim. GBank gi 2833262 sp Q14899 Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264682, 264684, 264688, 264689, 21908765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22279002
1719	94315258 (3437, 3438)	Novel Protein sim. GBank gi 4505187 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108388, 65274572, 35696286, 22278987, 60432049, 56182181, 66714117, 60432228, 29331826, 35696052, 29331828, 264906, 29331830, 56182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264600, 264601, 285017, 264448, 264764, 264286, 264769, 21906766, 21908769, 55811957, 265020, 265021, 52844160, 33657023, 33657109, 33657182, 27486282, 33657349, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 58182323, 264559, 264584, 264486, 56182575, 22278989, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21908754, 265011, 264801, 264760, 264762, 264288, 264766, 264686, 18108357, 264689, 21908765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 85274781, 264630, 20281071, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 56182323, 87168518
1720	94853063 (3438, 3440)	Novel Protein sim. GBank gi 2129478 pf S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	22278994, 22278999, 29331822, 265006, 265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906766, 21908768, 21908769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108385, 264486
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi 4886461 emb CAB43381.1 - (AL050260) hypothetical protein [Homo sapiens]		UNCLASSIFIED	56984075, 28331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gi 5889375 db BAA82968.1 - (AB030644) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - kinase Tudor domain		

1723	95358181 (3445, 3446)	Novel Protein sim. GBank gij4426962[gb AAD20633] - (AF126082) Art-like 2 binding protein BART1 (Homo sapiens)	UNCLASSIFIED	264488, 264687, 264769, 21906767, 21906768, 56182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33657023, 29331822, 29331824, 29331825, 60432289, 33657182, 33656870, 33657349, 29146499, 264508, 264907, 18108370, 264628, 264808, 264909, 18108374, 55811578, 264510, 265008, 264511, 265007, 264910, 264632, 264591, 60432228, 264582, 60433356, 264584, 60433438, 264595, 83373044, 55812038, 33109954, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264583, 264448, 264682, 264586, 264784, 264288, 264587, 264486, 264369, 264766
1724	87713808 (3447, 3448)	Novel Protein sim. GBank gij2340162 (AF005083) - dsRBP. ZFa [Xenopus laevis]	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264636, 264555, 264558, 264558, 264559
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gij3152682 (AF084604) - KE03 protein [Homo sapiens]	homebox	35696286, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264780, 18108351, 264681, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35698423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264586
1726	85754255 (3451, 3452)	Novel Protein sim. GBank gij4889348[gb AAD27861.1]AF13256 - (AF132562) BcDNA.LD14270 [Drosophila melanogaster]	UNCLASSIFIED	29146498, 264683, 264689
1727	85286382 (3453, 3454)		UNCLASSIFIED	264903, 265011, 264689, 21906768

1728	95348515 (3455, 3456)	Novel Protein sim. GBank gij4406549[gb AAD20027] - (AF131738) Unknown [Homo sapiens]	UNCLASSIFIED	60424179, 18108397, 56182575, 22278895, 56994075, 35696286, 22278987, 22278998, 22278999, 264094, 60432049, 264259, 28331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696032, 264905, 264906, 264907, 29331830, 66712502, 284908, 56182435, 284511, 265008, 265009, 60432229, 60433356, 33657402, 80433438, 264759, 21906754, 87169474, 265010, 265011, 87168559, 265017, 265018, 265019, 55611150, 284681, 284448, 264682, 284783, 264683, 264288, 264684, 264389, 264685, 264768, 264687, 264769, 21906784, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 284535, 264891, 264892, 33657023, 264893, 33657109, 18108370, 264628, 263872, 264629, 18108374, 18108376, 55810784, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56526486, 87168518, 60432113, 22278000, 22279002, 264564, 264566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 8]	UNCLASSIFIED	284906, 264907, 264908, 284511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)	Novel Protein sim. GBank gij631600[pir S47094] - hypothetical protein - rabbit	UNCLASSIFIED	28331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264784, 264629
1731	88266088 (3461, 3462)	Novel Protein sim. GBank gij4240231[dbj BAA74894.1] - (AB020678) KIAA0871 protein [Homo sapiens]	UNCLASSIFIED	52646842, 264807, 264909, 56182435, 55811386, 87168559, 265018, 265019, 294760, 52644229, 55811576
1732	81216878 (3463, 3464)	Novel Protein sim. GBank gij1575756 (U70674) - m-Numb [Mus musculus]	struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265018, 21906768, 21906769, 35695917, 265020, 265021, 264636, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank gij1575756 (U70674) - m-Numb [Mus musculus]	Contains protein domain (PF00640) - Phosphotyrosine interaction domain (PTB/PTD)	264907, 264910, 33657402, 265010, 264681, 284683, 264684, 264686, 264769, 264691, 264692, 264693, 264628, 264636, 264558
1734	87785261 (3467, 3468)			264693

1735	88318838 (3469, 3470)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016		284488, 18108394, 18108398, 22278998, 60432048, 264259, 29331822, 264808, 285008, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 284882, 18108354, 284769, 284689, 21906785, 21908768, 21908769, 29148829, 29148784, 265021, 265022, 52644150, 18108384, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264593, 18108390
1736	95362884 (3471, 3472)	Novel Protein sim. GBank gi 4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED		284480, 264259, 86714117, 66712502, 56182435, 285008, 285008, 284910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 284639, 284584
1737	88165548 (3473, 3474)	Novel Protein sim. GBank gi 2143607 pir S56895 - B/K protein - rat	Contains protein domain (PF00168) - C2 domain	Kinase	29331822, 29331830, 284591, 265011, 265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi 2225941 emb CAA69714 - (Y08460) Mdes protein [Mus musculus]	UNCLASSIFIED		284808, 284809, 265008, 284910, 264566
1739	87328576 (3477, 3478)		UNCLASSIFIED		35686052, 264603, 264557
1740	83592938 (3479, 3480)	Novel Protein sim. GBank gi 4809 emb CAA44309 - (X62452) YCR801 [Saccharomyces cerevisiae]	UNCLASSIFIED	traffic	264604, 21906764, 18108364, 264628, 35685855, 264638
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi 4883888 gb AAD31695.1 AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	60432289, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21906769, 285020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi 4505193 ref NP_003667.1 pMLD - membrane fatty acid (lipid) desaturase	UNCLASSIFIED		264808, 264910, 264758, 265011, 264631, 264638, 264566
1743	88986475 (3485, 3486)				285017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED		22278998, 264508, 264907
1745	20290075 (3489, 3490)		UNCLASSIFIED		264558
1746	84328110 (3491, 3492)	Novel Protein sim. GBank gi 731756 sp P38873 YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-IK1 INTERGENIC REGION [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	65274791, 264639, 264559
1747	94324333 (3493, 3494)		transcript factor		52646842, 29331824, 28331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264389, 284769, 264689, 35685917, 60170615, 264691, 33657023, 65274791, 35685855, 60170394, 22279000, 264482

1748	88003580 (3495, 3498)	Novel Protein sim. GBank gij450451 ref NP_001530.1 pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00864) - eph DnaJ central domain (4 repeats)	264489, 56182575, 29331824, 56182435, 264112, 265007, 265019, 264764, 21906788, 265020, 264691, 55811578, 264635, 264555, 264556, 264557, 264559 264106
1749	83363091 (3497, 3498)	Novel Protein sim. GBank gij5650780 gb AAD45948.1 AF15196 - (AF151968) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00815) - Regulator of G protein signaling domain	33657402, 264288, 52644150, 263974, 83373044
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gij4896884 gb AAC28444.2 - (AF065164) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]		
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gij2780161 dbj BAA24184 - (AB010054) outer arm dynein light chain 2 [Anthracidaris crassispina]	Contains protein domain (PF00560) - Leucine Rich Repeat	265010, 264369
1752	88456530 (3503, 3504)	Novel Protein sim. GBank gij3915482 sp P74346 G29_S1NY3 - HYPOTHETICAL 38.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - RNA pseudouridylylase synthase	264510, 264593, 264682, 21908765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gij2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acyltransferase	56994075, 22278986, 264908, 60170831, 264682, 264784, 264369, 264288, 264685, 264687, 21908766, 264692, 264693, 65274620, 65274791, 35685855, 264637, 264584
1754	86095323 (3507, 3508)	Novel Protein sim. GBank gij731421 sp P38981 YEH4_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION	transport	264488, 35686286, 264509, 264908, 264807, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264604, 264762, 264763, 264685, 264766, 264691, 264628, 35686423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264584, 264585, 264586, 264587 264686
1755	76470282 (3509, 3510)	Novel Protein sim. GBank gij1176422 (U43194) - rhophilin [Mus musculus]	UNCLASSIFIED	
1756	92862614 (3511, 3512)	Novel Protein sim. GBank gij4432860 gb AAD20708 - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]		52646842, 22278984, 22278985, 56984075, 22278986, 22278987, 264259, 29331822, 60432289, 28331827, 33656970, 265006, 265009, 60432229, 60433356, 60433436, 33109954, 21908754, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87168518, 80432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gij5441615 emb CA846856.1 - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	22278987, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21906768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612871 (3515, 3518)	Novel Protein sim. GBank gjl3881040jemb[CAA16403] - (AL021497) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265009, 264591, 33657402, 33109854, 87168474, 264600, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657108, 264629, 18108374, 35995855, 264632, 52844332, 22279002, 264563
1759	36994372 (3517, 3518)			UNCLASSIFIED	264759
1760	87328716 (3518, 3520)	Novel Protein sim. GBank gjl5262748jemb[CAB45688.1] - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432049, 35896052, 284805, 264908, 264907, 264908, 264909, 265006, 265009, 264910, 60432229, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811957, 35895817, 264690, 284692, 264628, 264628, 55811576, 35898423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 264486
1761	87408586 (3521, 3522)	Novel Protein sim. GBank gjl127749sp[P10569]MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264810, 264885, 264886
1762	85319887 (3523, 3524)	Novel Protein sim. GBank gjl3169158 (AC004770) - BC268730_2 [Homo sapiens]	Contains protein domain (PF00173) - desaturase Heme-binding domain in cytochrome b5 and oxidoreductases		22278998, 264259, 264905, 284807, 60170831, 265010, 265011, 265017, 264448, 21908765, 21908766, 21908767, 21908768, 265021, 264680, 33857109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gjl4809028jgb[AAD30062.1] - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181686, 29331825, 35896052, 264905, 264908, 264909, 264763, 264682, 264769, 35895817, 265022, 33657023, 18108374, 35898423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gjl360869pirj[CGHU1V - collagen alpha 1(V) chain precursor - human]	Contains protein domain (PF01410) - collagen Fibrillar collagen C-terminal domain		22278998, 264259, 35896052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264286, 21908766, 21908767, 29148627, 35895917, 264691, 33657023, 60432113, 22279002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gjl486808pirj[S35503 - finger protein neutralized - fruit fly (Drosophila melanogaster)]		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264810, 265009, 21906754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108359, 21908768, 21908767, 29148627, 29148629, 35895917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	85081201 (3531, 3532)	Novel Protein sim. GBank gi2489087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	52645156, 87168559, 60170815, 33657023, 264693, 33657109, 27486261, 264555, 83373044
1767	87755988 (3533, 3534)	Novel Protein sim. GBank gi1476443 emb CAA18263.1 - (AL022239) dJ1042K10.4 (novel protein) [Homo sapiens]		UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)	Novel Protein sim. GBank gi115204 sp P00736 C1R, HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin	UNCLASSIFIED	26331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)			UNCLASSIFIED	264563
1770	95413144 (3539, 3540)			complement	264468, 264768, 264769, 56182575, 55811957, 264690, 264691, 35696052, 264905, 264509, 264906, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264764, 264684, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi3914181 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLSUBUNIT 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00516) - TPR Domain	transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22279000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi4959442 gb AAD34351.1 AF12136 - (AF121360) DNZDHCANEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHHC zinc finger domain		22278998, 29331828, 33109954, 265018, 265019, 264764, 21806765, 265020, 265021, 264556
1773	84116824 (3545, 3546)	Novel Protein sim. GBank gi3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel	65274572, 56182575, 22278998, 35696286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265008, 265007, 265008, 60170831, 60433438, 264758, 55811386, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526486, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi2495899 sp Q15034 V032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21806754, 265017, 21906767, 21906768, 21806769, 265020, 264691, 264636, 56182323, 22279002

1776	85359330 (3549, 3550)	Novel Protein sim. GBank gi 1469199 dbj BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182576, 56994075, 35696286, 22278997, 29331822, 29331826, 60432289, 29331828, 35696052, 29331830, 66712502, 264828, 58182435, 264511, 265007, 265009, 60170831, 60432228, 60433438, 55812038, 21806754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 264448, 264288, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35698423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1778	84133756 (3551, 3552)	Novel Protein sim. GBank gi 4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gi 3218939 sp P87115 YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.08C IN CHROMOSOME 1	nuc1_recpt		56994075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21806769, 35695917, 264690, 33657023, 35695783, 60431528, 35698423, 55811576, 35695855, 22279000, 22279002, 264564
1778	94651624 (3555, 3556)	Novel Protein sim. GBank gi 3875648 emb CAA91454.1 - (Z68561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...	UNCLASSIFIED		29331826, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gi 4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]	UNCLASSIFIED		29148627, 35696286, 29147620, 265006, 265007, 265008, 18108385, 65274727, 264482, 264369, 264766
1780	87023487 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264908, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gi 729225 sp P41237 CTXN_RAT - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264286, 264768, 264769, 264635, 264636, 264637, 264639, 264583
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gi 2257543 dbj BAA21436 - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]	interferon		264768

1784	95197083 (3567, 3568)	Novel Protein sim. GBank gi 755048 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	35696286, 264259, 35696052, 264508, 264905, 264906, 264907, 66712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264762, 264763, 264764, 264388, 264766, 264687, 264768, 264688, 21008768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35696423, 264631, 264632, 264633, 264637, 264638, 264639, 18108385, 22279000, 22279002, 264555, 264556, 264486, 55274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 264908, 66712502, 56182435, 264511, 265007, 60433356, 55811150, 264683, 264369, 264687, 52644229, 21808767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695855, 264555, 65274727, 22279002
1785	95357475 (3568, 3570)	Novel Protein sim. GBank gi 4589552[dbj][BAA78798.1] - (AB023171) KIAA0954 protein [Homo sapiens]	UNCLASSIFIED	264908, 35696423, 264636
1786	85298485 (3571, 3572)	Novel Protein sim. GBank gi 117788[sp]P26770[CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)]	UNCLASSIFIED	
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gi 3877175[emb]CAA90338.1] - (Z50028) cDNA EST yk321h9.5 comes from this gene; cDNA EST EMBL:D88896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264905, 264908, 264909, 264595, 264764, 264766, 264692, 60431528, 264629, 264636, 264564, 264566
1788	91228779 (3575, 3576)		UNCLASSIFIED	264488, 83373044
1789	88094529 (3577, 3578)	Novel Protein sim. GBank gi 2088669 (AF003130) - F58A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264636
1790	82489734 (3579, 3580)			35696052, 264905, 264908, 264907, 264908, 264909, 265008, 264910, 264758, 265011, 265019, 264764, 264766, 264769, 264628, 264635

1781	95187269 (3581, 3582)	Novel Protein sim. GBank gij2114321dbj BAAZ00371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF000047) - glycoprotein Immunoglobulin domain	284488, 284686, 284687, 284768, 18108394, 284769, 18108397, 284259, 284681, 284692, 33657023, 284693, 284508, 284905, 284908, 284628, 284907, 284629, 284908, 284909, 284510, 285008, 284511, 285008, 284630, 285009, 284631, 284910, 284632, 284634, 284635, 284555, 284636, 284592, 284637, 284593, 284638, 18108381, 284639, 284758, 285010, 285011, 284602, 22279000, 284604, 284760, 284584, 284681, 284762, 284585, 284763, 284683, 284566, 284764, 284288, 284684, 284567, 18108354, 18108391, 284685, 284766
1782	87792680 (3583, 3584)	Novel Protein sim. GBank gij4337106 gb AAD180821 - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - UNCLASSIFIED G-patch domain	22278997, 284259, 284508, 265007, 33657402, 87188558, 284389, 33657023, 35895855, 20281071, 284559, 18108387, 87168518
1783	95337877 (3585, 3586)	Novel Protein sim. GBank gij5578331 gb AAD45504.1 AF145732 - (AF145732) endoplasmic reticulum alpha-mannosidase I [Homo sapiens]	Contains protein domain (PF01532) - ATPase associated Glycosyl hydrolase family 47	65274572, 22278995, 22278996, 22278997, 22278998, 284083, 284259, 28331824, 68714117, 60432288, 28331827, 28331828, 284103, 284105, 28331830, 285007, 284910, 285009, 60170831, 60433356, 21806754, 285010, 285017, 285019, 284681, 284682, 284288, 52644229, 21806765, 21806768, 21808767, 21808768, 21806769, 265020, 285021, 285022, 60170615, 52844150, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 60432113, 22279000, 284482, 284564
1784	87759806 (3587, 3588)	Novel Protein sim. GBank gij4914804 emb CAB43677.1 - (AL050369) hypothetical protein [Homo sapiens]	Contains protein domain (PF01788) - UNCLASSIFIED Putative snoRNA binding domain	18108394, 22278995, 22278998, 284259, 28331822, 28331824, 28331825, 28146498, 28146499, 284508, 284905, 52844045, 284112, 285006, 285008, 284910, 60433356, 284757, 55812038, 87168474, 265011, 285017, 18108351, 284763, 284448, 284683, 284369, 21808765, 21808768, 21808767, 21808769, 28148784, 35695917, 80170815, 33657023, 284629, 18108374, 18108376, 35898423, 35895855, 284556, 284557, 284638, 284558, 18108385, 284564, 284632, 284635, 284636, 284595, 284596, 284907, 284566, 284909
1785	79747856 (3589, 3590)		UNCLASSIFIED	284907, 284566, 284909
1786	88599488 (3591, 3592)	Novel Protein sim. GBank gij585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)	glycoprotein	284488, 284907, 284908, 284584, 284595, 284766, 284687, 21806765, 21806767, 284628, 284630, 284559

1787	91223210 (3593, 3594)	Novel Protein sim. GBank gll1842111 (U87586) - decoy (Arabidopsis thaliana)		ribosomalprot	22278996, 22278997, 22278998, 22278999, 28331822, 264910, 60170831, 21908754, 52644228, 21908768, 21908769, 21908769, 3595917, 265022, 52644150, 264691, 33657023, 263987, 33657109, 22278900
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gll2832906(dbjlBAA24608.1) - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 28331828, 60432289, 28331828, 33656970, 265008, 60432229, 264757, 60433438, 21908754, 33657084, 87168559, 265017, 18108351, 264682, 264448, 264288, 21908765, 21908768, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22278900, 264488
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gll5689541(dbjlBAA33054.1) - (AB029026) KIAA1102 protein [Homo sapiens]	eph		264808, 21908754, 21908767, 21908769, 265020, 33657023, 264692, 264693, 264404, 22278900
1800	87080116 (3599, 3600)	Novel Protein sim. GBank gll4680679(gb AAD27729.1 AF132954) CGI-20 protein [Homo sapiens]	UNCLASSIFIED		204691, 264556, 264566
1801	95060723 (3601, 3602)	Novel Protein sim. GBank gll134920(splP21897)SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			52844045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gll4680679(gb AAD27729.1 AF132954) CGI-20 protein [Homo sapiens]			35686286, 66714117, 264508, 264509, 56182435, 264512, 18108351, 264688, 55811857, 264692, 55811576, 35695855, 264488
1803	95060725 (3605, 3606)	Novel Protein sim. GBank gll4680679(gb AAD27729.1 AF132954) CGI-20 protein [Homo sapiens]			264688, 264488, 264687, 264488, 264788, 264789, 264689, 21908769, 35696286, 35695917, 264259, 264691, 264692, 264693, 20281088, 18108384, 35696052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 68712502, 264908, 264909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264586, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264584, 264448, 264565, 264763, 264683, 264764, 264566, 264288, 264486, 264567, 264785, 264766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gij3878914[emb]CAA8538.1] - (Z74043) predicted using Ganefinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk34314.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278998, 264805, 264808, 264809, 264810, 21806754, 264766, 21806765, 21806768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264584, 264586
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gij5453644[ref]NP_008461.1 pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644228, 35696423, 264636, 60432113
1806	94133782 (3611, 3612)	Novel Protein sim. GBank gij4589678[dbj]BAA78857.1] - (AB023230) KIAA1013 protein [Homo sapiens]	struct		264094, 264105, 264908, 35698423, 265008, 265007, 265008, 264559, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264808, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gij4684079[emb]CAB43235.1] - (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		284488, 35696286, 66714117, 35696052, 68712502, 264592, 60433436, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35696423, 35695855, 56182323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gij1916927 (U87865) - putative G protein [Mus musculus]	UNCLASSIFIED		284594, 55811150, 264686, 29148829, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88096318 (3619, 3620)	Novel Protein sim. GBank gij1352944[sp]P47178 YJ8P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		284488, 35696052, 264805, 264806, 264807, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264686, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264583, 264566, 264486, 264567
1811	86086272 (3621, 3622)	Novel Protein sim. GBank gij2134984[pir]j137275 - death-associated protein kinase (EC 2.7.1.-) - human	Contains protein domain (PF00023) - kinase Ank repeat		264488, 264259, 264508, 264509, 264805, 264806, 264807, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	79245772 (3623, 3624)				29331822, 29331824, 265019, 18108351, 21908769

1813	88080972 (3625, 3626)	Novel Protein sim. GBank gi 5051638 gb AAD38326.1 AF07372 - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 264259, 29331824, 68714117, 29331828, 35886052, 284509, 264805, 264908, 264907, 264908, 66712502, 264909, 265007, 264910, 264991, 264993, 55812038, 265011, 265018, 264760, 264682, 264764, 264683, 264369, 264766, 264768, 264769, 21906766, 21906786, 264691, 264693, 18108374, 35695855, 264634, 264635, 264637, 264639, 264558, 22279000, 22279002, 264568
1814	88178047 (3627, 3628)	Novel Protein sim. GBank gi 3643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35686286, 22278898, 264082, 264094, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29331827, 29331828, 264105, 264107, 52644045, 56182435, 265009, 60432229, 60433356, 87168474, 87168559, 264369, 264288, 21906765, 35685917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 264638, 56528486, 264482
1815	85298473 (3629, 3630)	Novel Protein sim. GBank gi 117788 sp P2670 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		struc1	22278898, 264508, 264509, 264907, 264908, 264910, 265011, 264760, 264768, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi 1176823 sp P41846 YO86_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264509, 264907, 264908, 264909, 265008, 264591, 265011, 265017, 264687, 264689, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264635, 264557, 264564, 264567, 264488, 22278897, 22278899, 60432048, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644228, 21906765, 21906767, 21906768, 52644150, 33637023, 33657109, 27486262, 18108370, 18108374, 60170394, 56182323, 22279002
1817	88095288 (3633, 3634)	Novel Protein sim. GBank gi 376637 emb CAA21428 - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	264488, 22278897, 22278899, 60432048, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644228, 21906765, 21906767, 21906768, 52644150, 33637023, 33657109, 27486262, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3638)	Novel Protein sim. GBank gi 367812 emb CAA94370 - (Z70310) predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S3771): cDNA EST EMBL:TO1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	35686286, 60433356, 264758, 264369, 264886, 21906769, 264893, 264632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi 5031865 ref NP_005771.1 p.HFP - lipoma HMGI(C fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432229, 265017, 265018, 265019, 264448, 264288, 21906768, 21906769, 265020, 18108381, 18108384, 22279000, 22279002, 264567

1820	87769455 (3639, 3640)				284905, 284907, 284594
1821	80431510 (3641, 3642)				284907, 284768, 283978
1822	91221523 (3643, 3644)	Novel Protein sim. GBank gll4884130[emb]CAB43272.1] - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278998, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 35698052, 29331828, 284908, 29331830, 60170831, 284591, 284593, 60433356, 264596, 265017, 265019, 18108351, 264763, 284683, 21906765, 21906767, 21906768, 21906769, 35695817, 265020, 265021, 33657023, 18108384, 18108370, 35695855, 22278000, 22279002
1823	85522330 (3645, 3646)			UNCLASSIFIED	264488, 264259, 264511, 264288, 264768, 284693, 35696423, 264634, 18108385, 264486
1824	86612025 (3647, 3648)	Novel Protein sim. GBank gll477072[pt]A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264807, 264908, 264808, 264511, 264631, 264634, 264635, 264637, 264638, 264639, 264758, 264568
1825	87430125 (3649, 3650)	Novel Protein sim. GBank gll3036803[emb]CAA18493] - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60432049, 264910, 264487
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gll4680685[gb]AAD27732.1]AF13295 - (AF132957) CGI-23 protein [Homo sapiens]		ATPase-associated	52644507, 52645156, 52646842, 22278994, 22278998, 56994075, 264259, 60432049, 52645080, 35698052, 86712502, 52644045, 265008, 265009, 60432229, 60433356, 60433438, 52646317, 52644286, 265011, 87168559, 264448, 264288, 264369, 264688, 52644229, 264689, 21906765, 21906768, 265020, 60170615, 52644150, 33657023, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 83373044, 87168518, 264404, 22279002
1827	91847212 (3653, 3654)				264758

1828	85074017 (3655, 3656)	Novel Protein sim. GBank gll4503571[ref]NP_001419.1pEN01 - endolase 1. (alpha)	Contains protein domain (PF00113) - Enol-ase	oncogene	264488, 52646842, 56182575, 22278986, 35698288, 22278987, 22278989, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 86712502, 52644045, 56182435, 265008, 264511, 264512, 265007, 265008, 265009, 60170831, 60432228, 264593, 60433356, 60433438, 264758, 33108954, 21906754, 67168474, 265010, 265011, 87168558, 265017, 265018, 264761, 264762, 264448, 264764, 264683, 264288, 264388, 18108355, 264768, 18108357, 18108358, 264888, 264769, 264689, 21906768, 21906769, 356985917, 265021, 60170615, 33657023, 33657349, 263972, 55811576, 35698585, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22278002, 264563, 264482, 264585, 264484, 264567
1829	80107720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264910
1830	94312842 (3659, 3660)	Novel Protein sim. GBank gll246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278984, 22278985, 35698286, 22278988, 22278987, 22278989, 22278999, 29331822, 29331825, 35696052, 52646317, 52644298, 87168558, 265019, 21906769, 21906768, 21906767, 21906768, 21906769, 35695917, 265021, 33657023, 52645128, 33657109, 33657182, 27488261, 27488262, 35695763, 263974, 35698423, 35695855, 52644332
1831	84130863 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265019, 265022, 264693, 65274791
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gll1330345 (U58755) - coded for by C. elegans cDNA yk34p1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....			264602

1833	85314184 (3665, 3668)	Novel Protein sim. GBank gi 5174413 ref NP_006026.1 pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 22278997, 22278998, 22278999, 264259, 28331822, 28331824, 60432289, 29331827, 35686052, 29146499, 264508, 264509, 264908, 264907, 66712502, 264908, 52844045, 264909, 264512, 285008, 264591, 264593, 60433358, 21908754, 33857084, 265011, 265017, 264604, 265018, 285019, 264681, 18108351, 264683, 264288, 264685, 264766, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 285020, 285021, 264690, 264692, 33657023, 65274620, 33657182, 27486284, 33857349, 65274781, 264634, 264635, 284556, 264557, 264558, 264559, 18108385, 56526486, 87168518, 60432113, 22278000, 22278002, 264553
1834	80562780 (3667, 3668)				264259, 264907, 264689, 22279000, 22278002
1835	84135718 (3669, 3670)			UNCLASSIFIED	22278998, 28331822, 28331826, 87168474, 264603, 21908768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi 4759286 ref NP_004268.1 pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	28331825, 264908, 285019, 264784, 264686, 21908765, 264635
1837	84234297 (3673, 3674)	Novel Protein sim. GBank gi 3334400 sp Q24574 UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	22278995, 29146489, 265006, 265008, 265009, 265010, 264683, 21908765, 29148627, 29148628, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gi 1362569 p f A56154 - Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain		29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264601, 21908765, 21908768, 265021, 33657109, 264556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gi 127580 sp P23249 MOV10_MOUSE - PROTEIN MOV-10		UNCLASSIFIED	264683
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi 4572464 gb AAD23834.1 AF12365 - (AF123653) FEZ1 (Homo sapiens)			56182575, 28331824, 28331826, 60433356, 264764, 264288, 33857023, 263987, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	80992645 (3683, 3684)	Novel Protein sim. GBank gij1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 29331822, 29331824, 29331825, 66714117, 29331826, 29331827, 264907, 264909, 52844045, 56182435, 264510, 265008, 265007, 265009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264688, 264789, 33857023, 264693, 18108384, 33857109, 18108368, 264628, 55810764, 56182323, 18108384, 264593, 264766
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 264789, 29331826, 29331828, 264511, 265008, 265007, 264910, 264631, 264508, 264690, 264638, 264584, 264691, 60432229, 60432049, 264259, 264629, 33857023, 264488, 264909, 264587, 264595, 264766
1844	87444784 (3687, 3688)	Novel Protein sim. GBank gij2496887spIQ09232YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264908, 265022, 33857023, 87166518, 22279002
1845	85096673 (3689, 3690)	Novel Protein sim. GBank gij1175494spIQ09819YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	transcript factor	264259, 29331824, 264907, 264908, 66712502, 264510, 265007, 265008, 55812038, 265018, 21908765, 52644150, 33857109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 264584
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gij3881080[emb]CAA21739] - (AL032857) similar to EGF-like domain; cDNA EST yk298a12.3 comes from this gene; cDNA EST EMBL:D35388 comes from this gene; cDNA EST yk331n6.5 comes from this gene; cDNA EST yk298a12.5 comes from this gene; cDNA EST yk487g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87821487 (3693, 3694)	Novel Protein sim. GBank gij5059323[gb]AAD38967.1JAF15152 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcript factor	22278997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gij5701854[emb]CAB52191.1] - (AJ245417) Gdb protein [Homo sapiens]		lm7	29331825, 29331826, 29331827, 265017, 284683, 264288, 264786, 264788, 21908768, 264692, 22279002
1849	94287874 (3697, 3698)	Novel Protein sim. GBank gij4503665[ef]NP_001989.1pFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - ATPase-associated EGF-like domain		56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gij4589582[db]BAA76813.1] - (AB023186) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gij220637[db]BAA01471] - (D10827) zinc finger protein [Mus musculus]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_rna_bind	29331824, 35696052, 264910, 60433438, 264688, 35695917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi 5174829 ref NP_006080.1 pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278998, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52644045, 285007, 264810, 60432228, 60433356, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264886, 264887, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264693, 33857109, 18108370, 18108374, 55811578, 35695855, 56182323, 60432113, 22279002, 264583 264687, 264768, 52644507, 264789, 21906765, 21906767, 21906768, 22278995, 56984075, 22278998, 52644150, 264259, 264692, 29331822, 29331824, 52645129, 29331827, 33856970, 33857349, 35695763, 264508, 264908, 264628, 264907, 264629, 264909, 35698423, 35695855, 264510, 265008, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33857402, 18108385, 52646317, 52644288, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264567, 264288, 264369, 264766 264582
1853	91222267 (3705, 3706)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U98 [Human herpesvirus 6]		UNCLASSIFIED	
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gi 2072964 (U83568) - putative p150 [Homo sapiens]		nuclease	
1855	91221459 (3708, 3710)	Novel Protein sim. GBank gi 4539520 emb CAB39994.1 - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	nucd_recpt	18108392, 52646385, 65274572, 56182575, 22278994, 56984075, 22278998, 35698288, 22278998, 264259, 60432049, 264808, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264769, 18108359, 21906764, 21906768, 29148827, 265020, 265021, 265022, 52644150, 33857023, 33857109, 18108372, 18108374, 18108376, 35696423, 264631, 264636, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gi 3854978 emb CAA06945 - (AJ006278) acetylglucosaminyltransferase-like protein (Mus musculus)		UNCLASSIFIED	56984075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gi 4322670 gb AAD16120 - (AF094508) dentin phosphoryn [Homo sapiens]		ATPase-associated	22278999, 264259, 264808, 60170831, 264448, 264686, 265020, 265022, 33857109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gij4981903jgbAAD38415.1(AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	264757
1859	84407464 (3717, 3718)	Novel Protein sim. GBank gij4240317jdbjBAA74937.1j - (AB020721) KIAA0914 protein [Homo sapiens]		22278996, 29331824, 265007, 33109854, 265019, 264369, 21906768, 29148784, 27486261, 52644332, 22278002 265019
1860	17929308 (3719, 3720)	Novel Protein sim. GBank gij4009522 (AF089731) - connexin 31.1 [Homo sapiens]		
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gij2143637jpij184503 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase	284867, 284259, 29331822, 29331824, 29331825, 265007, 265009, 264591, 33109854, 265010, 265019, 264389, 264288, 264686, 264691, 264893, 27486264, 18108370, 18108374, 263977, 55811576, 56182323, 264639, 22278000, 22278002, 264482
1862	87372923 (3723, 3724)	Novel Protein sim. GBank gij125493jspjP07313jKMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35686286, 264259, 87188474, 264369, 21906768, 264558, 264563
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gij3820909jembjCAA08299j - (AJ010642) Dof protein [Drosophila melanogaster]		284601, 264766, 29148627, 29148629, 264692, 264628, 264635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gij4322263jgbjAAD15985j - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	22278989, 284259, 264907, 265018, 18108370, 264634, 264635, 264555, 264556, 264638, 18108387
1865	67740827 (3729, 3730)	Novel Protein sim. GBank gij2485727jspjQ83073jY256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256		22278989, 264490, 29331822, 66714117, 66712502, 265006, 265007, 265008, 265009, 264591, 60433438, 265010, 265018, 264760, 264448, 264768, 29148627, 28148629, 265020, 265022, 18108385, 60432113
1866	87286818 (3731, 3732)	Novel Protein sim. GBank gij5282617jembjCAB45748.1j - (AL080157) hypothetical protein [Homo sapiens]	kinase	18108374, 264769, 18108377, 21906765, 21906766, 35696423, 56182575, 21906769, 29148629, 35698286, 35695917, 265021, 264510, 264511, 264512, 264534, 264535, 60170831, 52844150, 264555, 264591, 264259, 264556, 264692, 264537, 33657023, 60433356, 28331822, 264559, 264595, 29331824, 18108385, 21906754, 33657182, 29331827, 35698052, 33658970, 87168518, 285017, 60431602, 22278000, 284508, 284509, 18108351, 264907, 264682, 284567, 18108372, 284765, 264486
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gij3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]	UNCLASSIFIED	264094

1868	87357459 (3735, 3736)	Novel Protein sim. GBank glj3881525[emb]CAA93884] - (Z70038) cDNA EST EMBL:D32578 comes from this gene; cDNA EST EMBL:D3254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357f10.5 comes from this gene [Caenorhabditis elegans]		nuclease	284489, 22278997, 22278999, 28331825, 28331828, 285008, 265009, 33657402, 87168474, 18108351, 21906785, 21906788, 21906789, 285020, 265021, 60170815, 27486284, 264628, 18108374, 264631, 18108385, 87168518, 22278000, 22278002, 284568, 264587
1869	86877292 (3737, 3738)	Novel Protein sim. GBank glj4826772[re]NP_004961.1[p]GFA - insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00550) - Leucine Rich Repeat	glycoprotein	284508, 284509, 264908, 264908, 284909, 264910, 284591, 264600, 18108351, 264683, 284788, 284789, 35895855, 284634, 264558, 284639, 18108385, 264563, 264486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank glj1868859[emb]CAB08722] - (Z86089) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	28331824, 60424269, 265007, 265008, 21908754, 265017, 265018, 265019, 264288, 264766, 284686, 264688, 21908788, 21908789, 35895917, 60170815, 264692, 18108388, 35895783, 35898423, 65274791, 264638, 284639, 56526486
1871	80234464 (3741, 3742)			UNCLASSIFIED	284509, 284905, 264595, 264768, 264635, 284636, 284583, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank glj2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	284510, 264594, 264585
1873	80213890 (3745, 3746)				284508, 264512, 265009, 265011, 18108351, 284687, 284681, 18108370, 18108374, 264635
1874	95351138 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	284488, 35895917, 284259, 284905, 264907, 264908, 264909, 263978, 264511, 264635, 284636, 284637, 284638, 33657402, 284558, 18108385, 264600, 264604, 264764, 264587, 284766
1876	87330516 (3749, 3750)	Novel Protein sim. GBank glj4589520[db]BAA76782.1] - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35898286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank glj263810[bs]122920 - collagen alpha chain [Riftia pachypila=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	284259, 28331822, 60432289, 264908, 284909, 284604, 264764, 284288, 284769, 18108378, 264556, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank glj3983356[gb]AAC83924.1] - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	284767, 264686, 284768, 263978, 264683, 284639, 265010, 264563, 284905, 284806, 284907

1878	95351058 (3755, 3756)	Novel Protein sim. GBank gij4510345jgbjAAD21434.11 - (AC006921) unknown protein (Arabidopsis thaliana)	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264569, 264488, 35696286, 56984075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 29146498, 264508, 264508, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33657402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264389, 264288, 264766, 264687, 264768, 264789, 21908768, 35695817, 265021, 60170815, 33657023, 264692, 264693, 33657109, 27486265, 264628, 18108370, 264629, 18108374, 35696423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264563, 264584, 264586, 264486, 264567, 264905, 264907, 264908, 265007, 264565, 264566
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gij4929843jgbjAAD34082.1jAF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gij1550785jembjCAA69283j - (Y08026) Immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264768, 264891, 264692, 83373044
1881	80214849 (3761, 3762)	Novel Protein sim. GBank gij93144jiprjIB40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhouser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1882	86562450 (3763, 3764)	Novel Protein sim. GBank gij2384956 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21906766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gij1351218jlpjP47226jTES2 MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	264908, 264910, 87168559, 21908766, 264636

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gij4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-97 protein [Homo sapiens]		UNCLASSIFIED	264486, 18108394, 58181686, 22278998, 80432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811388, 265010, 265011, 87168559, 264600, 265017, 264604, 265019, 264605, 264760, 55811150, 264761, 264882, 264763, 264683, 264764, 264288, 264369, 264768, 264686, 264768, 264769, 29148784, 35695917, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 80432113, 22279002, 264563, 264564, 264565, 264568, 264488, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gij2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	56182575, 264259, 264905, 264909, 265008, 264598, 264766, 265020, 264628, 60431528, 264634, 56526486, 264080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gij2854158 gb AAC02577.1 - (AF045641) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264910, 265018, 264766, 21906788, 29148629, 264690, 264693, 264628, 264555, 264488
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gij5174421 ref NP_006023.1 PCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - ATPase associated C2 domain		29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 264681, 264768, 29148627, 264693, 18108364, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264563
1888	87622804 (3775, 3776)	Novel Protein sim. GBank gij3319931 emb CAB10841 - (Z98046) dJ14O8.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gij1083308 pir A56559 - enhancer-trp-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helixcase	264908, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906765, 21908768, 21908769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gij4240185 dbj BAA74876.1 - (AB020660) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 28147620, 264807, 265009, 264600, 265018, 18108351, 264288, 264689, 21908765, 21908768, 21908769, 264691, 264692, 264693, 264628, 18108370, 264636, 264558, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	264666, 264768, 264687, 264692, 264693, 28331822, 29331824, 264508, 264905, 264808, 18108370, 264628, 264907, 264908, 264808, 18108378, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gl 56889535 dbj BAA03051.1 - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct	22278895, 264509, 87168559, 18108351, 264448, 264682, 265020, 264683, 18108374, 22279000
1893	88533926 (3785, 3786)			laminin	264569, 65274572, 22278987, 22278989, 264259, 29331822, 28331824, 68714117, 28331826, 264806, 265008, 265008, 265009, 264592, 265018, 264681, 264448, 264683, 18108354, 264389, 264684, 264685, 264766, 264687, 264688, 21908768, 265020, 265022, 60170615, 52644150, 264890, 264691, 264692, 33857023, 264693, 33857109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86888120 (3787, 3788)				264508, 264905, 264806, 264807, 264584, 264684, 264690, 264692, 264630, 264635, 264636, 264639, 264583
1895	87831891 (3789, 3790)	Novel Protein sim. GBank gl 5262574 emb CAB45729.1 - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264258, 60432289, 29331826, 264107, 264905, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33857109, 264628, 55810784, 18108379, 264634, 56182323, 56528486
1896	85873555 (3791, 3792)			UNCLASSIFIED	264807, 265008, 264682, 264686, 21908768, 264629, 264631, 264634, 264555, 264258
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gl 728636 sp P39193 ALU6 - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	UBA domain	cadherin	
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gl 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10			
1899	86673097 (3787, 3788)	Novel Protein sim. GBank gl 2909819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]		helicase	22278998, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35886052, 28331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21906765, 21906766, 21906768, 21908769, 60170615, 55810784, 22279000
1900	87641858 (3798, 3800)	Novel Protein sim. GBank gl 4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]	Contains protein domain (PF00908) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21908765, 21908769
				UNCLASSIFIED	264683

1801	95196647 (3801, 3802)	Novel Protein sim. GBank gl 585959 sp P38378 S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52844507, 52845158, 18108398, 52846365, 52846842, 18108397, 58182575, 22278994, 22278995, 56994075, 3588286, 22278997, 22278998, 264490, 60432049, 284259, 29331822, 52845080, 29331824, 29331825, 68714117, 29331828, 60432289, 29331827, 29331828, 35888052, 33658970, 29146498, 284908, 284907, 29331830, 284908, 52844045, 284909, 284112, 265008, 284512, 285008, 284910, 285009, 60170831, 60432228, 60433356, 33657402, 60433438, 55812038, 284758, 33108954, 21908754, 33657084, 52844286, 87168474, 265010, 285011, 87168559, 285017, 265018, 265019, 18108351, 264448, 284288, 264888, 52844228, 21908785, 21908786, 21908787, 21908789, 55811957, 35895917, 265020, 265021, 52844150, 18108382, 33657023, 264693, 283887, 33657109, 33657182, 27486264, 33657349, 35895763, 18108370, 18108378, 55811576, 35898423, 35895855, 60431850, 284636, 263981, 52844332, 60170394, 83373044, 18108385, 87168518, 60432113, 284584 264107, 263978
1802	80202013 (3803, 3804)	Novel Protein sim. GBank gl 4226613 gb AAD20451 - (AF098786) SLM-1 [Mus musculus]		dna_ma_bind	
1803	87778554 (3805, 3806)	Novel Protein sim. GBank gl 3747107 (AF085741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 29331825, 29331827, 264508, 264907, 285008, 60170831, 60433356, 60433438, 284759, 21908754, 284448, 264288, 285021, 285022, 33657023, 264693, 55811578, 284555, 284558, 22279000 264509, 264805, 264808, 264907, 264908, 285007, 284910, 264688, 264768, 264687, 264769, 264693, 264628, 18108374, 284634, 264636, 264637, 264585
1804	80434213 (3807, 3808)	Novel Protein sim. GBank gl 1352911 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struc1	
1805	95351140 (3809, 3810)	Novel Protein sim. GBank gl 3043714 dbj BAA25521 - (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial muT protein		284488, 284768, 284769, 284689, 29148829, 35695917, 35898288, 264259, 284692, 18108382, 33657023, 29331824, 33857109, 29146498, 264508, 264509, 284805, 284908, 284907, 68712502, 284908, 284909, 35698423, 35895855, 264510, 264511, 264512, 264910, 284634, 284635, 284637, 264638, 33657402, 284758, 85858542, 284602, 264760, 264761, 264482, 264563, 284762, 264483, 264764, 264586, 284288, 284768 264637
1806	12763822 (3811, 3812)			UNCLASSIFIED	

1907	95313641 (3813, 3814)	Novel Protein sim. GBank gi 4928585 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278998, 35696286, 22278998, 22278998, 264259, 60432048, 29331822, 29331825, 60424289, 29331828, 35696052, 264593, 60433356, 21806754, 55811386, 85658542, 87168559, 285018, 264681, 264682, 264684, 264288, 21806765, 21806766, 21806768, 265020, 265022, 264690, 52844150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313641 (3815, 3816)	Novel Protein sim. GBank gi 3986770 (AF109906) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181688, 22278995, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331828, 29331827, 29331828, 29146499, 264805, 264806, 264907, 264908, 66712502, 264909, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264596, 55812038, 33109954, 52846317, 265011, 265017, 264804, 265018, 265019, 264805, 55811150, 264681, 264448, 264288, 264886, 264688, 264789, 21806765, 21806766, 21806767, 21806768, 21806769, 55811957, 29146628, 35695917, 265020, 265022, 264691, 264692, 18108364, 65274820, 33657109, 33657349, 35695763, 18108374, 263978, 55810784, 55811578, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22279000, 22279002, 264566, 264489
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gi 2224653 dbj BAA20813 - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264805, 264806, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35696286, 22278998, 22278999, 35696052, 264509, 264905, 264808, 264907, 264908, 264909, 264511, 265007, 264512, 264810, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264786, 264768, 264687, 264769, 35695917, 265021, 52844150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1911	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 AC006530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33656970, 264908, 265007, 264591, 55812038, 87168559, 264448, 264369, 21906765, 21906768, 265022, 264691, 264693, 18108385, 55811576, 264556, 18108385, 18108388
1912	95413519 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1 - (AB028874) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181666, 22278994, 22278995, 56894075, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35686052, 264905, 264906, 264907, 264908, 52844045, 56182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 65274791, 264637, 56182323, 83373044, 56528486, 22278002, 264563, 264568
1913	95305548 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56894075, 22278996, 22278998, 22278999, 29331826, 29331827, 265008, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21906765, 21906768, 21906769, 21906769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423862 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1 - (AB023197) KIAA0880 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35686052, 264908, 264908, 264828, 264908, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	85340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82991.1 - (AB028882) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264688, 264628, 264635, 264637, 264639, 83373044, 264565
1916	79640761 (3831, 3832)				264693, 264639

1917	67821660 (3833, 3834)	Novel Protein sim. GBank gi 5688391 gb BAA82979.1 - (AB028850) KIAA1027 protein [Homo sapiens]		struct	264769, 264689, 21908765, 21908768, 22278996, 264259, 264691, 264693, 29331824, 29331825, 29331826, 29331828, 264805, 264908, 264628, 264907, 264908, 264909, 264510, 264630, 264910, 264634, 264635, 264636, 264637, 264638, 263981, 264639, 264758, 18108385, 21906754, 265011, 264604, 264583, 18108351, 264762, 264783, 264566, 264764, 264766
1918	95302705 (3835, 3836)	Novel Protein sim. GBank gi 5281517 gb AAD41524.1 AF154831 - (AF154831) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21906765, 21906767, 21906768, 56182575, 21906769, 22278994, 35698286, 35695917, 22278996, 22278997, 265021, 265022, 264534, 264690, 264691, 264692, 33657023, 264693, 29331824, 29331825, 33657109, 29331826, 52845129, 35696052, 29331828, 27486282, 27486284, 35695763, 264508, 264905, 264508, 264906, 264628, 264907, 18108370, 264908, 264829, 264909, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264596, 83373044, 264758, 52646317, 18108385, 52844286, 56528486, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264780, 264781, 264482, 264564, 18108351, 264762, 264692, 264585, 264448, 264784, 264586, 264489, 264587, 264369, 264288, 264766, 264487, 264685
1919	84143847 (3837, 3838)	Novel Protein sim. GBank gi 3878584 emb CA801237 - (Z77667) cDNA EST EMBL:CO8125 comes from this gene; cDNA EST EMBL:CO9753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 29331822, 265007, 60170831, 60432229, 60433438, 264448, 264682, 264288, 5581957, 33657023, 33657109, 65274791, 56182323, 22279002
1920	91228953 (3839, 3840)	Novel Protein sim. GBank gi 1809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12868 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	264510, 264511, 264512, 264586
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gi 4560997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693

1922	87641863 (3843, 3844)	Novel Protein sim. GBank gll138595[sp]P02845[VT2, CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) (CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGRP40)]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264809, 18108374, 265008, 264557, 264564, 18108351
1923	94323589 (3845, 3846)	Novel Protein sim. GBank gll119110[sp]P03211[EEN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 35880552, 264509, 264905, 264908, 264807, 264808, 66712502, 264809, 264511, 264512, 265007, 264910, 265008, 264591, 264592, 264593, 264594, 264595, 264758, 264598, 264759, 265011, 265017, 265018, 265019, 5581150, 264681, 264762, 264448, 264784, 264288, 264369, 264768, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21806768, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35696423, 264630, 264631, 264632, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87188518, 264583, 264584, 264585, 264586, 264587 29331826, 264806, 264808, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1924	87338825 (3847, 3848)	Novel Protein sim. GBank gll3877655[emb]CAA666571 - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:C1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gll4081903[gb]AAD36415.1(AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	22278995, 22278996, 22278997, 264259, 29331824, 88714117, 29148498, 264809, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 80170394
1926	88084739 (3851, 3852)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73. contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		struct	264805, 264906, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264692, 264693, 263978, 264631, 264634, 264637, 264563
1927	85654857 (3853, 3854)	Novel Protein sim. GBank gll3043632[dbj]BAA254801 - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87798054 (3855, 3856)	Novel Protein sim. GBank gll1665761[dbj]BAA133771 - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Inf	Inf	264488, 264259, 265017, 265021, 264692
1929	86987238 (3857, 3858)	Novel Protein sim. GBank gll5001993[gb]AAD37247.1(AF134321) chimeric A/GP/tryptsinogen-like serine protease precursor [Dissostichus mawsoni]	Extracellular link domain	UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1830	87889128 (3859, 3860)	Novel Protein sim. GBank gi 1708230 sp P52963 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35698286, 29331828, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264601, 265017, 265019, 264605, 264760, 264764, 264766, 264686, 264769, 265022, 35698423, 264638, 60432113
1831	87797279 (3861, 3862)	Novel Protein sim. GBank gi 404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264906, 264908, 60432229, 264758, 264764, 264288, 265020, 264692, 264634, 264637, 264684, 264691, 264635
1832	15030972 (3863, 3864)			UNCLASSIFIED	264595
1833	11613688 (3865, 3866)	Novel Protein sim. GBank gi 4115746 gb BAA36484 - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		strut	56182575, 56182435, 264510, 264757, 264758, 55812038, 55811366, 265018, 55811150, 21906765, 264691, 264631, 264635, 264637
1834	84426360 (3867, 3868)			UNCLASSIFIED	264686, 265011, 264511, 264905, 18108351, 264564, 264681, 264259, 18108370, 264566, 264764, 264359, 264595
1835	87752511 (3869, 3870)				60432289, 265007, 265010, 265011, 265018, 33657109, 18108374
1836	95414338 (3871, 3872)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			
1837	94847141 (3873, 3874)	Novel Protein sim. GBank gi 543187 pr S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85658542, 21906767, 35685917, 60170615, 264693, 33657109
1838	87403277 (3875, 3876)	Novel Protein sim. GBank gi 4544431 gb AAD22340.1 AC006855 - (AC006855) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00886) - Cullin family	collagen	264486, 28146488, 264905, 264559
1839	91004978 (3877, 3878)	Novel Protein sim. GBank gi 500856 gb BAA03210 - (D14168) 50kDa lectin [Bombyx mori]			
1840	87348810 (3879, 3880)	Novel Protein sim. GBank gi 1946300 emb CAA73132 - (Y12529) hypothetical protein [Silene latifolia]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 265017, 21906765, 21906766, 21908768, 55811957, 27488264, 35696423, 60432113, 264564
1841	94147177 (3881, 3882)	Novel Protein sim. GBank gi 4206386 (AF060570) - rig-1 protein [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	strut	264488, 29331822, 264448, 264683, 264288, 265020, 33657023, 264631
1842	87841670 (3883, 3894)	Novel Protein sim. GBank gi 4927204 gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 264259, 29331824, 29331827, 264905, 265008, 33657084, 265017, 265018, 264288, 264687, 21906765, 21906766, 21906767, 265020, 52644150, 27488264, 83373044, 18108387, 60432113, 22278902, 264565
1843	94325298 (3885, 3886)	Novel Protein sim. GBank gi 3122852 sp O15736 TIPO_DICDI - TIPO PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 264509, 18108370, 18108374, 264482
				kinase	22278998, 29331822, 29331827, 35696052, 284511, 265009, 264592, 60432228, 265017, 265018, 265019, 264684, 264692, 33657109, 65274791, 264636

1944	94232958 (3887, 3888)	Novel Protein sim. GBank gij1798570[dbj BAA13432] - (D87671) TIP120 [Rattus norvegicus]	UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 284259, 52845080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264810, 60170831, 60432228, 60433356, 33657402, 60433438, 264586, 33109954, 21908754, 87168474, 87168558, 265017, 265018, 265019, 18108351, 264369, 264686, 264768, 21908765, 21908766, 21908787, 21908769, 35695917, 265020, 265021, 60170615, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56528486, 87168518, 60432113, 22279000, 264563, 18108351, 264683, 264488, 264567
1945	87641872 (3889, 3890)	Novel Protein sim. GBank gij4927204[gb AAD33048.1]AF13391 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]	UNCLASSIFIED	60432289, 29331827, 35686052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21908767, 52644150, 264693, 27486264, 264637, 87168518, 264563
1946	87443880 (3891, 3892)	Novel Protein sim. GBank gij2498104[sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN	UNCLASSIFIED	224512, 284758, 284762, 264682, 264683, 284764, 264288, 264768, 264688, 21908768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gij3914801[sp O54888 RP2A2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)	mapolymerase	264909, 60170831, 284591, 284594, 235010, 285011, 264764, 264369, 264689, 264631, 264638
1948	85199174 (3895, 3896)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	struct	264389
1949	7640129 (3897, 3898)	Novel Protein sim. GBank gij3876768[emb CAA93466.1] - (Z69637) predicted using GeneFinder: Similarity to E. coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	UNCLASSIFIED	284488, 284768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1950	87788531 (3899, 3900)	Novel Protein sim. GBank gij2626753[dbj BAA23424] - (AB008782) sulfate transporter [Arabidopsis thaliana]	transport	56182576, 22278997, 52845080, 29331824, 29331825, 29331827, 55812038, 52846317, 265018, 265019, 264369, 21908765, 21908767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gij4929633[gb AAD34077.1]AF15184 - (AF151840) CGI-82 protein [Homo sapiens]	reductase	264581, 264593, 264594, 284595, 264555, 264556, 264557, 264558, 264565

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gll168715sp P31721 CTQB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	284259, 264558
1954	91226025 (3907, 3908)	Novel Protein sim. GBank gll4240271 dbj BAA74914.1 - (AB020689) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264488, 263994, 18108394, 35699286, 22278998, 29331822, 66714117, 29331828, 29331827, 284508, 264509, 264905, 264806, 264907, 264908, 264909, 264510, 265008, 265007, 265008, 264910, 265009, 60170831, 60432228, 265011, 265017, 264603, 264604, 265018, 18108351, 264685, 264768, 264769, 35695917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264558, 264638, 264557, 264638, 264558, 264559, 83373044, 18108385, 264563, 264564, 264586, 264486, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181886, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35696052, 264508, 29331830, 265008, 265009, 264591, 55812038, 67168474, 265017, 265018, 265019, 264448, 264766, 21906765, 21906768, 21906767, 55811857, 265020, 265021, 52645129, 33657109, 27486264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 80431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gll1665821 dbj BAA134071 - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264583, 264564

1857	84326510 (3913, 3914)	Novel Protein sim. GBank gij4589674[dbj BAA76558.1] - (AB023228) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52846842, 56182575, 22278987, 22278988, 22278989, 29331824, 68714117, 29331827, 28146488, 264593, 33657402, 33109954, 87188474, 265018, 264448, 264368, 264288, 264766, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 264892, 68274620, 27486264, 33857349, 27486265, 35695855, 22279002, 264482
1858	95313902 (3915, 3916)	Novel Protein sim. GBank gij4240227[dbj BAA74892.1] - (AB020678) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278988, 264092, 264094, 264259, 60432049, 29331824, 56182181, 68714117, 264107, 264109, 264909, 264511, 60170831, 60432228, 21908754, 265010, 21908769, 35695917, 265022, 65274620, 263987, 263976, 35686423, 264631, 264632, 264634, 264635, 18108385, 22279000, 22279002, 264593, 265019
1859	85701470 (3917, 3918)	Novel Protein sim. GBank gij2281983[embj CAB10860] - (Z98056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1860	80308608 (3919, 3920)	Novel Protein sim. GBank gij2274851[dbj BAA21515] - (D64159) 3-7 gene product [Homo sapiens]		struct	284905, 264806, 264907, 264808, 264909, 265006, 265007, 264910, 264595, 265017, 264604, 265018, 18108351, 264784, 264369, 264766, 264768, 21908765, 18108368, 264628, 18108379, 264635, 264636, 264637, 264638, 264486
1861	16292607 (3921, 3922)				264635
1862	91008365 (3923, 3924)			UNCLASSIFIED	65274572, 264592, 264593, 265019, 264891
1863	80938017 (3925, 3926)	Novel Protein sim. GBank gij3721653[dbj BAA33581] - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	85274572, 18108368, 35686286, 29331825, 60432289, 29331827, 264828, 265006, 265008, 60433356, 60433438, 21908754, 265020, 265021, 33657023, 33657109, 27486265, 35695855, 264555
1864	84317605 (3927, 3928)	Novel Protein sim. GBank gij5262638[embj CAB45757.1] - (AL080169) hypothetical protein [Homo sapiens]		cadherin	264488, 264092, 264259, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264805, 264760, 264762, 264448, 264764, 264288, 264685, 264766, 264768, 264769, 21908766, 264691, 264692, 264693, 18108370, 264628, 264629, 18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264484, 264565, 264566, 264486, 264567
1865	84317445 (3929, 3930)	Novel Protein sim. GBank gij4107017[dbj BAA36294] - (AB001773) PEM-6 [Clona savignyi]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264488, 264510, 264760, 264768, 264486

1866	84192058 (3931, 3932)	Novel Protein sim. GBank gi4929707[gb]AAD34114.1[AF15187] Cgl-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331826, 29331828, 29146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264488, 264567 29331824, 265010, 265017, 264288, 21906764, 263981, 56526486
1867	87396123 (3933, 3934)	Novel Protein sim. GBank gi2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	- esterase	
1868	88095641 (3935, 3936)	Novel Protein sim. GBank gi2584953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	- oncogene	35686286, 264905, 264509, 264908, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264683, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264584, 264585, 264586, 264587
1869	84328529 (3937, 3938)	Novel Protein sim. GBank gi2911274 (U20329) - spidrolin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264908, 264908, 18108351, 264482
1870	80596049 (3939, 3940)	Novel Protein sim. GBank gi4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1871	94843914 (3941, 3942)	Novel Protein sim. GBank gi134208[sp]P09593[SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264488, 264489, 22278998, 264259, 60432049, 68714117, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264509, 264906, 264807, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21908765, 33657023, 264692, 18108370, 264629, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22278000, 264563, 264564, 264565, 264566, 264486
1872	87845444 (3943, 3944)	Novel Protein sim. GBank gi4519623[dbj]BAA75671.1 - (AB017816) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265008, 264511, 265008, 52644296, 265018, 265019, 264761, 264688, 21908768, 21908769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86395533 (3945, 3946)			UNCLASSIFIED	29331826, 264692, 35696423, 264631, 264555, 264556, 264557, 264558, 264559
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gi3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264563

1884	85760889 (3867, 3868)	Novel Protein sim. GBank gij28866895[embjCAA17174.1] - (AL021887) fadD14 [Mycobacterium tuberculosis]		synthase	264688, 21808766, 55811957, 56984075, 265020, 265021, 22278999, 265022, 264259, 29331822, 33657182, 29148499, 264628, 18108370, 264808, 264629, 55811576, 35695855, 265008, 265007, 264591, 21808754, 33657084, 265010, 265017, 265019, 264288
1885	85636697 (3969, 3970)	Novel Protein sim. GBank gij5712131[gbjAAD47378.1]AF12049 (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263878, 55811576, 264637, 56182323, 18108385, 264584
1886	80200507 (3971, 3972)			UNCLASSIFIED	264488, 264629
1887	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443[gbjAAD31318.1]AF14457 - (AF144573) Mx-Interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		22278999, 29331830, 265007, 265018, 21806768, 33657023, 264892, 264693, 18108377, 264635, 60170394, 22279002
1888	94122108 (3975, 3976)			UNCLASSIFIED	264805, 264806, 264807, 264808, 264809, 264810, 264591, 264593, 264758, 264764, 264686, 264766, 265021, 264692, 264628, 264629, 35695855, 264630, 264635, 264638, 264637, 264638, 264639, 264483
1889	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spe87 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52844045, 56182435, 264112, 265007, 33657402, 52844229, 21806765, 21806768, 21806769, 55811957, 33657023, 263967, 33857109, 18108370, 22279000, 22279002
1890	65688888 (3979, 3980)	Novel Protein sim. GBank gij5701727[dbjBAA83074.1] - (AB024726) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1891	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287[dbjBAA74922.1] - (AB020706) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaplin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35688288, 56984075, 22278997, 22278998, 29331822, 29331824, 29331825, 60432288, 29331828, 264508, 264808, 264807, 264808, 56182435, 264510, 265007, 21808754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264368, 264288, 264685, 264766, 264687, 264769, 21806765, 21806768, 21806769, 55811957, 265020, 60431528, 263974, 18108378, 35688855, 264555, 264557, 264638, 83373044, 18108394, 87168518, 60432113, 22278000, 22278002, 264584, 264488
1892	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	struct	29331827, 264908, 264807, 264809, 265007, 264803, 264766, 264688, 264768, 21808768, 264628, 264635, 264636, 18108385, 56526488, 264568, 264587
1893	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264582, 35696423

1975	94316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 56182435, 265006, 264757, 55812038, 265010, 265017, 264369, 55811957, 65274791, 3589855, 58182323, 60432113, 264259, 35686052, 265018, 265020, 265021, 33657109, 56526486
1976	95358914 (3951, 3952)			UNCLASSIFIED	264908, 264596, 265021, 264566
1977	94852664 (3953, 3954)	Novel Protein sim. GBank gi 2499528 sp Q07782 NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gi 103421 p J1A33471 - transcription factor NTF-1 - fruit fly (Drosophila melanogaster) (fragment)		transcription factor	60170831, 264566
1979	87627709 (3957, 3958)	Novel Protein sim. GBank gi 2244815 emb CAB10238.1 - (Z97336) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	29331826, 29146498, 264905, 264807, 265007, 265009, 265010, 265018, 264686, 18108359, 21906768, 35695917, 265020, 60170615, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264585
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gi 4759290 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl- terminal hydrolase, X-linked (AF131849) Unknown [Homo sapiens]		ubiquitin	264489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gi 4406693 gb AAD20060 - (AF131849) Unknown [Homo sapiens]		UNCLASSIFIED	22278985, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264906, 264910, 264585, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21906767, 33657023, 27488264, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	80995367 (3963, 3964)	Novel Protein sim. GBank gi 5689523 dbj BAA83045.1 - (AB029016) KIAA1093 protein [Homo sapiens]			65274572, 29331825, 35686052, 33656970, 264909, 265008, 55811386, 264780, 264686, 264691, 27488264
1983	95096668 (3965, 3966)	Novel Protein sim. GBank gi 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	22278986, 35686286, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 264509, 264905, 264906, 264907, 66712502, 264908, 5264045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21906765, 55811957, 35695917, 264680, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35685855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1994	84329114 (3987, 3988)	Novel Protein sim. GBank gij5630077[gb]AAD45822.1AC00601 - (AC006017) similar to ALR; similar to AAC51735 (PID:g2359287) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	mapolymerase	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265008, 60432229, 33657402, 60433356, 264757, 80433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264368, 264685, 264686, 264768, 21908765, 21908767, 21908768, 21908769, 265020, 264690, 18108370, 264635, 264555, 65274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56528486, 22279000, 22279002, 264564 264488, 18108396, 22278994, 56994075, 22278996, 35689286, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331826, 29331827, 35696052, 29146499, 264905, 264907, 68712502, 56182435, 265006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85858542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21908765, 21908768, 21908767, 29148627, 21908768, 21908769, 29148628, 29148784, 265020, 265021, 264690, 18108361, 264683, 27468262, 27468264, 27468265, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87188518, 264404, 60432113, 264567 264564
1995	95414353 (3989, 3990)	Novel Protein sim. GBank gij4827040[ref]NP_005110.1pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit		UNCLASSIFIED	
1996	80254186 (3981, 3982)	Novel Protein sim. GBank gij791146[emb]CAA60020[- (X86028) extensin-like protein [Vigna unguiculata]		UNCLASSIFIED	
1997	87028423 (3983, 3994)	Novel Protein sim. GBank gij2642034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264808, 264809, 264592, 264593
1998	85262704 (3985, 3998)	Novel Protein sim. GBank gij4589634[dbj]BAA76839.1[- (AB023212) KIAA0995 protein [Homo sapiens]		UNCLASSIFIED	264113, 264685, 264555, 264567

1999	94324903 (3997, 3998)	Novel Protein sim. GBank g 5225312 gb AAD40846.1 AF07244 - (AF072441) cathepsin binding protein cabin 1 (Homo sapiens)	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424269, 29331827, 29331828, 35696052, 265006, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264783, 264682, 264369, 264685, 264686, 56181592, 265020, 264691, 33657023, 264693, 33657109, 27486264, 18108370, 18108378, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3999, 4000)	Novel Protein sim. GBank g 1723232 sp Q10155 YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME I		UNCLASSIFIED	52646365, 52646842, 22278984, 22278985, 22278986, 35696286, 22278987, 22278988, 22278989, 264258, 52645080, 29331822, 28331826, 28331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644286, 265017, 265018, 265019, 264761, 264369, 264288, 52644229, 21906765, 21906786, 21906787, 21906788, 21906789, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 65274620, 52645129, 27486281, 27486262, 27486264, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264566, 264587
2001	85072534 (4001, 4002)	Novel Protein sim. GBank g 107560 pir JB38637 - Ras inhibitor (clone JC285) - human (fragment)		UNCLASSIFIED	264789, 52644229, 65274572, 21906768, 22278986, 35696286, 35695917, 265020, 22278989, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264785
2002	80236368 (4003, 4004)	Novel Protein sim. GBank g 729433 sp P38657 ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264807, 265006, 264810, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074448 (4005, 4006)	Novel Protein sim. GBank g 86388 pir A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264805, 264806, 264808, 264810, 264596, 265017, 18108351, 264692, 264629, 264634, 264595

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4884249 emb CAB43230.1 - (AL049898) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	52645156, 52646842, 52646365, 56162575, 22278994, 22278995, 56994075, 22278996, 35696266, 22278997, 22278998, 22278999, 60432049, 284259, 52645080, 29331824, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264908, 264592, 60433356, 33657402, 52646317, 21906754, 33657084, 52644296, 87188474, 87168559, 265017, 265018, 265019, 264763, 264683, 264286, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33857108, 33657182, 27486261, 27486262, 33857349, 27486265, 35695763, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 284558, 18108385, 56526486, 87168518, 60432113, 284483, 284488, 264908
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gi 387950 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33985 comes from this gene; cDNA EST EMBL:D33922 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 410667 emb CAA22813 - (AL035064) queuine tma-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424269, 68714117, 35696052, 264906, 66712502, 264909, 264510, 60433356, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 29148627, 21906769, 29148784, 35695917, 60170615, 264681, 33657023, 65274620, 33657109, 55810764, 55811576, 35695855, 87168518, 60432113, 264563, 264482
2007	84325556 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BAA23712 - (AB007900) H0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	264488, 263984, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264760, 264762, 264764, 264766, 264685, 264767, 264768, 264769, 55811957, 35695917, 265020, 264691, 264693, 264628, 264629, 65274781, 35695855, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 264566
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550783 emb CAA69257 - (Y07960) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264909, 264768, 35695855

2009	85749240 (4017, 4018)	Novel Protein sim. GBank gj3882305[idbjBAA34512.1] - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278989, 264259, 264910, 264591, 265017, 264681, 264683, 21906768, 264681, 33657182, 33657349, 264631, 87166516, 264404, 22279002, 264563
2010	85422458 (4019, 4020)	Novel Protein sim. GBank gj5282629[embjCAB45753.1] - (AL080184) hypothetical protein [Homo sapiens]	Contains protein domain (PF000057) - Low-density lipoprotein receptor domain class A	eph	52844507, 52845156, 52846365, 52846842, 18108397, 65274572, 22278994, 56994075, 35698286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432228, 60433356, 21906754, 52646317, 33108954, 52844296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264685, 264687, 52844228, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52844150, 264681, 264692, 33657023, 263967, 52645129, 35695763, 18108376, 35696423, 65274791, 35695855, 264631, 264634, 60431850, 264637, 264638, 52644332, 60170394, 18108385, 87168516, 22279002, 264564, 264565, 264566, 264567
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gj3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	56182575, 56994075, 22278989, 264259, 29331824, 29331826, 29331827, 29331828, 35696052, 264906, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264369, 264288, 264685, 264766, 264687, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 65274620, 33657109, 264629, 264557, 264559, 83373044, 87168518, 60432113, 22279002
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gj1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264683, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108363, 18108384, 18108388, 22279000, 22279002, 264567
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gj4507985[re]NP_003427.1[pZNF1 - zinc finger protein 135 (clone pHZ-17)]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	dna_rna_bind	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21906767, 265020, 264692
2014	87347840 (4027, 4028)	Novel Protein sim. GBank gj1127720[sp]P20938[MYPO_HEIFR - MYELIN P0 PROTEIN PRECURSOR]		UNCLASSIFIED	264488, 29331826, 264907, 264636, 264555, 264639, 264558

2015	86094922 (4028, 4030)	Novel Protein sim. GBank gij1286 pir S22687 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56192575, 35696286, 264259, 35686052, 264508, 264906, 264907, 264510, 264512, 87168474, 265010, 264681, 264288, 264689, 264828, 35688423, 35685855, 264639, 264563, 264584
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gij285046 pir S26413 - t-complex protein Tc-10 - mouse		struct	264102, 264508, 264110, 285009, 33109954, 21806768, 265021, 33657109, 27488282, 263972, 18108374, 263978, 264555, 264564
2017	79464293 (4033, 4034)	Novel Protein sim. GBank gij124735 sp P18175 INVO_PIG - INVOLUCRIN		UNCLASSIFIED	264685, 264636
2018	78637067 (4035, 4036)	Novel Protein sim. GBank gij2143910 pir S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263978
2020	94674478 (4039, 4040)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	264259, 264508, 264591, 265018, 264682, 264288, 264688, 22279002
2021	88718818 (4041, 4042)	Novel Protein sim. GBank gij585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21806754, 21908768, 33657023, 33657109, 27486261, 87168518
2022	95285665 (4043, 4044)	Novel Protein sim. GBank gij4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabisopsis thaliana]			264757, 264767, 60170615, 18108385
2023	87722978 (4045, 4046)	Novel Protein sim. GBank gij5410230 gb AAD42892.1 AF07334 - (AF07334) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - ubiquitin Ubiquitin carboxyl-terminal hydrolases family 2		18108394, 22278999, 264259, 264905, 264908, 264908, 264595, 264762, 264769, 264634, 264636, 87168518, 80432113, 22279000, 264482, 264565
2024	87886443 (4047, 4048)	Novel Protein sim. GBank gij4755188 gb AAD29055.1 AC00701 - (AC00701) unknown protein [Arabisopsis thaliana]			60433438, 265017, 264688, 264692, 264693, 264636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gij4755188 gb AAD29055.1 AC00701 - (AC00701) unknown protein [Arabisopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 264509, 264906, 264909, 55812038, 265017, 265021, 265022, 80170615, 264558
2026	84122114 (4051, 4052)	Novel Protein sim. GBank gij1655699 emb CAA68032 - (Y07752) pterophorin-S [Volvox carteri]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 264112, 60170831, 87168559, 264288, 264688, 264689, 21906768, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264584, 264568, 264567
2027	80249001 (4053, 4054)			UNCLASSIFIED	263978, 264634, 264486

2028	94898884 (4055, 4056)	Novel Protein sim. GBank gij1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - HECT-domain (ubiquitin-transferase).	ubiquitin	52644507, 52645158, 52646842, 56182575, 56994075, 35989286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 284906, 264907, 264908, 29331830, 52644045, 58182435, 265006, 265009, 60432228, 33657402, 264595, 264757, 55812038, 21908754, 52646317, 52644286, 265010, 265011, 87168559, 265017, 265018, 265019, 284448, 18108354, 264288, 264389, 264766, 52644228, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 85274820, 33657109, 52645129, 18108368, 27486261, 27486282, 27486264, 27486285, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264558, 83373044, 58528486, 22279000, 22279002, 264563, 265009, 264595, 85658542, 264555, 264556, 284557, 264558, 264559, 83373044
2029	95382032 (4057, 4058)	Novel Protein sim. GBank gij3599940 (AF017368) - facicongenital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED	18108394, 56994075, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21908769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gij5630080(gbjAAD45825.1)AC00489 - (AC004890) similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264558, 18108382, 18108384, 65274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264686, 264769, 21908766, 21908767, 28148627, 264628, 35696423, 264634, 264556, 18108381, 80170394, 264558, 83373044, 18108385, 264482, 264484
2031	80245281 (4061, 4062)	Novel Protein sim. GBank gij5689491(dbjBAA83029.1) - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	56181562, 264628, 264632, 264555, 264556
2032	81232607 (4063, 4064)	Novel Protein sim. GBank gij5689491(dbjBAA83029.1) - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	264558, 18108382, 18108384, 65274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264686, 264769, 21908766, 21908767, 28148627, 264628, 35696423, 264634, 264556, 18108381, 80170394, 264558, 83373044, 18108385, 264482, 264484
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gij2484828(jspIQ64686)CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)		synthase	
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gij4828984(jref NP_005147.1)PROD1 - UNKNOWN	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278996, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21908767, 21908768, 21908769, 33657109, 83373044, 56528486

2035	83553451 (4089, 4070)				264389, 264686, 265022, 26526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gij2734081 (AF000195) - similar to oxysterol-binding proteins (Caenorhabditis elegans)		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35686286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331828, 29331828, 35686052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 80170831, 264594, 55612038, 33109954, 21806754, 87168559, 265017, 265018, 265018, 264762, 264369, 264288, 21806765, 21806767, 21806768, 21806769, 55811857, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4076, 4078)	Novel Protein sim. GBank gij380625[embjCAB07858] - (Z93765) predicted using GeneRinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823 comes from this gene; cDNA EST EMBL:D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264766, 264767, 264686, 18108358, 21806765, 21806769, 52644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35696423, 65274781, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264564, 264566
2039	95514628 (4077, 4078)	Novel Protein sim. GBank gij224653[dbjBAA20813] - (AB002394) KIAA0356 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21806766, 33657023, 264692, 264693, 33657109, 35696423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)				264592
2041	95071738 (4081, 4082)	Novel Protein sim. GBank gij2500825[ipjP70700]RPA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	mapolymerase	UNCLASSIFIED	264488, 22278998, 35696052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264768, 264769, 21806766, 265021, 265022, 264692, 33657109, 264628, 264628, 35696423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gij4408590gbjAAD20040] - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331826, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21906765, 35695917, 264535, 52644150, 264691, 264692, 18108365, 27486261, 27486262, 27486265, 18108374, 35696423, 65274781, 35695955, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gij5052554gbjAAD38607.1jAF14563] - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646365, 56994075, 22278997, 22278998, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 29148498, 264509, 264908, 52644045, 56182435, 265006, 33657402, 21906794, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264587
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264083, 29331827, 264905, 66712502, 264592, 264889, 21906765, 21908769, 265020, 264692, 264482, 264588, 264892
2045	79635532 (4089, 4090)	Novel Protein sim. GBank gij406698gbjAAD20062] - (AF131852) Unknown [Homo sapiens]			264258, 264806, 264683, 22279002
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gij4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29146498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2047	84576801 (4093, 4094)	Novel Protein sim. GBank gij4589656gbjBAA76850.1] - (AB023223) KIAA1005 protein [Homo sapiens]		UNCLASSIFIED	264909
2048	84606378 (4095, 4096)			UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264763, 21908767, 21908768, 264629, 264634, 264637, 22279002, 264584, 264565, 264566, 264567

2050	78633835 (4099, 4100)			UNCLASSIFIED	264683	264488, 264259, 264509, 264906, 264907, 264789, 18108374, 35686423, 264563, 264566, 264486
2051	87780768 (4101, 4102)			UNCLASSIFIED		
2052	88086393 (4103, 4104)	Novel Protein sim. GBank gl 4529889 gb AAD21812.1 - (AF134726) G9A [Homo sapiens]	Contains protein domain (PF00856) - SET domain	UNCLASSIFIED	kinase	264488, 263994, 35686052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 285008, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264389, 264766, 264686, 264768, 264769, 52644229, 264689, 35685917, 33657023, 33657109, 264628, 18108374, 35686423, 55811576, 35685855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gl 2995449 emb CAA75113 - (Y14848) mdline 1 protein [Mus musculus]		UNCLASSIFIED		22278986, 22278987, 264258, 28331822, 264102, 264508, 35685817, 263972, 264482, 60424179, 264094, 264259, 29331825, 60424259, 264906, 60432229, 60433356, 87168559, 265019, 264760, 264288, 264686, 21905768, 33657023, 264693, 55810764, 55811576, 264635, 56182323, 60432113
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gl 3876326 emb CAB02090 - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain			264488, 29331826, 60432289, 29331828, 60433356, 265019, 264683, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22279000, 264564
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gl 5353746 gb AAD42226.1 AF15913 - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED		

2056	88177396 (4111, 4112)	Novel Protein sim. GBank gij4826980/refINP_005042.1pQARS - glutamine-tRNA synthetase	Contains protein domain (PF00749) - tRNA synthetases class I (E and Q)	synthase	264488, 52845156, 56182575, 22278994, 35696286, 56994075, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 60432289, 29331827, 29331828, 33656970, 264104, 264908, 264908, 265008, 265008, 60170831, 264591, 60432229, 60433438, 18108348, 21908754, 33857084, 52644286, 87168474, 265010, 87168559, 265017, 265018, 264760, 18108351, 264681, 264682, 264448, 264683, 264368, 264288, 264685, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265022, 33657023, 18108362, 33657109, 18108368, 33657182, 27486281, 27486284, 27486285, 33657349, 264628, 18108370, 264629, 18108374, 18108377, 18108379, 35696423, 55811576, 20281152, 264636, 264952, 18108385, 18108388, 87168518, 264482, 264585, 264588, 264587, 52646842, 52646365, 56162575, 35696286, 22278996, 22278997, 22278998, 264093, 52845080, 35696032, 29331828, 33656970, 265009, 52846317, 55811386, 52844286, 52844229, 21906769, 35695917, 265021, 60170615, 52644150, 33657108, 33657182, 27486261, 27486262, 35695763, 35696423, 35695855, 52644332
2057	87877805 (4113, 4114)	Novel Protein sim. GBank gij728850spP08640JAMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	285007, 265008, 264591
2058	88276896 (4115, 4116)	Novel Protein sim. GBank gij119714spP13983JEXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	29331825, 264682, 264686, 264691, 264693, 22279002
2059	79866684 (4117, 4118)	Novel Protein sim. GBank gij2811122 (U87318) - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 29331824, 29331826, 264810, 55811957, 18108370, 55811576

2081	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2496947 sp Q09298 YQO9_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.8 IN CHROMOSOME II	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21906754, 85658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 58528486, 60432113
2082	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502081 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	struct	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264663, 18108351, 264762, 264585, 264764, 264487, 264766
2083	87801272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 dbj BAA78803.1 - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264564, 264484
2084	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 dbj BAA13413.1 - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35686286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264761, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108368, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264586, 264486
2085	95092238 (4128, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433358, 55811386, 85658542, 265018, 55811150, 264681, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264931, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002, 56182575, 264259, 264906, 264764, 264286, 56182323, 264567
2086	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	

2067	95303892 (4133, 4134)				35696286, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264369, 264286, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35695855, 264558, 264404, 264563, 264486
2068	84344754 (4135, 4136)				264687
2069	84319177 (4137, 4138)	Novel Protein sim. GBank gi 3152682 (AF084604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656870, 264509, 264905, 56182435, 265009, 60433356, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87168518, 60432113, 22278000, 22278002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gi 5712131 gb AAD47379.1 AF12049 - (AF12049) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264805, 264628, 264808, 264638
2071	86846116 (4141, 4142)	Novel Protein sim. GBank gi 3551531 dbj BAA33018 - (AB017437) avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265008, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	91718428 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophyseal hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264480, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264690, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27825664 (4145, 4146)	Novel Protein sim. GBank gi 1504026 dbj BAA13212 - (D86978) similar to C.elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	264556
2074	84324767 (4147, 4148)	Novel Protein sim. GBank gi 4240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 265008, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264567

2075	94314866 (4149, 4150)	Novel Protein sim. GBank gl 5138930 gb AAD40382.1 - (AF093680) transcription factor 11B [Homo sapiens]			18108394, 22278994, 22278996, 35698286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35698052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33857084, 264760, 264448, 264288, 264766, 264767, 264689, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27488262, 27486265, 35698423, 35695855, 264631, 264634, 264639, 87168518, 22278002, 264583, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385, 264592
2077	11369877 (4153, 4154)			UNCLASSIFIED	29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56526486
2078	87539364 (4155, 4156)	Novel Protein sim. GBank gl 4220590 db BAA74579 - (D87908) nuclear protein np85 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	ubiquitin	264768, 22278997, 265021, 264680, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264908, 264907, 264628, 20281069, 264908, 265007, 265009, 264632, 264636, 264591, 264592, 264638, 264758, 264759, 33109954, 264604, 265018, 265019, 22278002, 264563, 264564, 264448, 264684, 264567, 264685
2079	88095916 (4157, 4158)	Novel Protein sim. GBank gl 4240255 db BAA74906.1 - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gl 2408021 emb CAB16219.1 - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85858542, 265011, 265018, 265019, 21906767, 21906768, 264693, 18108385, 22278000, 22278002
2081	94847188 (4161, 4162)	Novel Protein sim. GBank gl 5524734 gb AAD4360.1 AF16635 - (AF166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - eph CUB domain	eph	284907, 265019
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gl 3880558 emb CAA94234 - (Z70271) predicted using GeneFinder: similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gl 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264508, 264112, 265009, 264593, 21906754, 265018, 265019, 264448, 264288, 264685, 21906768, 265020, 265022, 264691, 18108370, 85274781, 264631, 264555, 264563
2084	95189298 (4167, 4168)	Novel Protein sim. GBank gl 728836 p P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	94989476 (4169, 4170)	Novel Protein sim. GBank gij165569[emb]CAA69032] - (Y07752) pherophorin-S [Voivox carten]	UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264763, 264369, 264686, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gij3875032[emb]CAA88936] - (Z49125) similarity to Trichostromyolus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D38149 come...	UNCLASSIFIED	35696286, 264259, 35686052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263878, 35696423, 35695855, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264486
2087	21436337 (4173, 4174)			264489
2088	84111627 (4175, 4176)	Novel Protein sim. GBank gij3880530[emb]CAA16334, ij- (AL021481) similar to Phosphoglucosylase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70687 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...	UNCLASSIFIED	264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33108954, 87168474, 265017, 265018, 265019, 264448, 264683, 264389, 264685, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264682, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486285, 35696423, 35695855, 83373044, 87168518, 22278900, 264587, 18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264031, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656670, 29146498, 29146499, 264102, 264108, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264808, 66712502, 264828, 52644045, 264809, 56182435, 264110, 264112, 264510, 264511, 265008, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 60433438, 264595, 55812038, 264758, 21906754, 33657084, 55811386, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108358, 56181562, 264769, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 29148628, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264680,
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gij4758118[emb]NP_004623.1[pDAP3 - Death associated protein 3	cadherin	

2080	88222470 (4178, 4180)				22278995, 22278998, 22278999, 264259, 29331826, 35696052, 264910, 33657402, 60433438, 33109854, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21908765, 21908766, 21908767, 21908769, 35695917, 265022, 60170615, 33657023, 35696423, 35695855, 264952, 18108387, 22279000, 263984, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567, 22278997, 22278999, 66712502, 87168559, 264683, 265021, 264486
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gij4580997[gblAAD24571.1]AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	
2092	88223605 (4163, 4164)			homeobox	
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gij2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gij4829551[gblAAD34036.1]AF15179 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	35696286, 265017, 265018, 265019, 18108388
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gij1363238[pri]A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_rna_bind	35696286, 52644045, 265006, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486282, 18108374, 18108386
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gij3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182575, 22278996, 22278997, 22278999, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52644150, 264691, 264692, 33657023, 264693, 27486281, 35695763, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264638, 264639, 264563, 264483, 264565, 264566, 264486, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi1574501ref NP_006051.1 pLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170815, 264692, 33657108, 18108370, 264636, 264483
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi1758208ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	56984075, 264259, 264288, 265020, 264563
2099	95412927 (4197, 4198)	Novel Protein sim. GBank gi12685659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP1 (Bos taurus)		phosphatase	65274572, 264905, 65274444, 264681, 264636, 264555
2100	95332856 (4199, 4200)	Novel Protein sim. GBank gi13881189 emb CAB16514 - (Z98281) similar to ADP-ribosylation factor; cDNA EST EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337 comes from this gene; cDNA EST EMBL: C09829 comes from this gene; cDNA EST comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nuc_rept	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146488, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21908754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264782, 264448, 264369, 264288, 18108359, 264686, 21908765, 21908767, 21908768, 21908769, 265020, 265021, 33657023, 18108374, 35686423, 264558, 83373044, 87169518, 60432113, 22279000, 22279002
2101	87782604 (4201, 4202)	Novel Protein sim. GBank gi14589468 dbj BAA76781.1 - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	264091, 29331824, 264105, 265007, 265010, 18108380
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi13874149 emb CAA97423.1 - (Z73103) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	264468, 264489, 35686286, 264259, 35686052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264768, 21908769, 35685917, 18108374, 264634, 264555, 264558, 264563, 264482, 264486
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gi14240159 dbj BAA74858.1 - (AB020842) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	65274572, 56994075, 22278999, 264259, 29331824, 29331825, 35686052, 29331828, 68712502, 265009, 60170831, 264595, 33109954, 85658542, 67168558, 265017, 265019, 264448, 21908765, 21908768, 265022, 33657023, 27486282, 33657349, 35685763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264564
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22278000

2105	94848080 (4209, 4210)	Novel Protein sim. GBank gii1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....	UNCLASSIFIED	264488, 56182575, 22278994, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 5264045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432229, 33657402, 60433356, 264595, 60433438, 264758, 33657084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264782, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21906765, 21906766, 21908767, 21908768, 21908769, 35695917, 265020, 265022, 60170815, 52644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264584, 264566, 264567, 265006, 265019, 264906, 264639
2106	83365475 (4211, 4212)			
2107	79822862 (4213, 4214)	Novel Protein sim. GBank gii3881524[emb]CAA93883] - (Z70038) ZK1087.4 [Caenorhabditis elegans]		
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gii3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]	UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264756, 265011, 264600, 264801, 264764, 264768, 264767, 264768, 264769, 264693, 264629, 35695855, 264632, 264634, 264635, 264638, 264639, 83373044, 264486, 18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558, 264564
2109	80478719 (4217, 4218)		UNCLASSIFIED	
2110	87728075 (4219, 4220)	Novel Protein sim. GBank gii461043[pir]S37671 - bai2 protein - human	UNCLASSIFIED	
2111	87818419 (4221, 4222)			
2112	87293783 (4223, 4224)	Novel Protein sim. GBank gii2143639[pir]I56542 - calmodulin-binding protein - rat	UNCLASSIFIED	264768, 35695917, 264630, 264567, 264486, 264508, 264906, 264591, 264682, 22278002
2113	78841388 (4225, 4226)	Novel Protein sim. GBank gii4426629[gb]AAD20459] - (AF100860) protocadherin [Rattus norvegicus]	cadherin	265006
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gii3327184[db]BAA31660] - (AB014585) KIAA0685 protein [Homo sapiens]		66714117, 29331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21908769, 55811957, 265020, 265021, 33657109, 60170394, 264558, 65274572, 264689, 264691, 264692, 60432113
2115	90993785 (4229, 4230)	Novel Protein sim. GBank gii4757890[ref]NP_004328.1pC8OR - chromosome 8 open reading frame 1	UNCLASSIFIED	

2116	88259387 (4231, 4232)	Novel Protein sim. GBank glj2246532 (U83872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35886286, 22278999, 56182181, 29331824, 29331026, 29331827, 35896052, 264907, 56182435, 265008, 264591, 55812038, 5581386, 87168558, 264288, 264369, 21906769, 29148828, 33657023, 35895763, 5581576, 35896423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank glj2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	29331824, 264511, 265009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 56526486, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank glj1078307 (p1156573) - nuclear pore complex glycoprotein p62 - African clawed frog		glycoprotein	264259, 264803, 264807, 264908, 264510, 264511, 265009, 264910, 265010, 264802, 264288, 264788, 264693, 263987, 263972, 264638, 264559
2119	86999317 (4237, 4238)	Novel Protein sim. GBank glj4321407 (p1AAD15748) - (AF047890) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87788395 (4239, 4240)	Novel Protein sim. GBank glj4885527 (reflNP_005480.1) pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - eph Src homology domain 2		264091, 264259, 29331826, 29331828, 265017, 264604, 264288, 264685, 265020, 264691, 18108370, 55810764, 264555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank glj4757728 (reflNP_004886.1) pAGTA - angiotensin/vasopressin receptor AII(AVP)-like		UNCLASSIFIED	264601, 264766, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank glj4929551 (p1AAD34038.1) (AF151799) CGI-40 protein [Homo sapiens]			18108384, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811576, 264555, 264637, 18108382, 83373044, 18108383, 18108384, 56526486, 264585, 264567
2123	86787898 (4245, 4246)	Novel Protein sim. GBank glj2224551 (dbjBAA20764) - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	18108386, 264757, 265011, 18108351, 264691, 264634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank glj5689455 (dbjBAA83011.1) - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 264906, 264807, 264591, 264639, 264563
2125	85354041 (4249, 4250)	Novel Protein sim. GBank glj728831 (p1P39188) (ALU1_HUMAN - III) ALU SUBFAMILY J WARNING ENTRY III		UNCLASSIFIED	264259, 264509, 264807, 264511, 85658542, 264763, 21806765, 35895917, 264636, 264486
2126	95084231 (4251, 4252)	Novel Protein sim. GBank glj4539264 (embjCAB39853.1) - (AL049485) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264488, 264489, 29331827, 35896052, 264905, 264509, 264908, 264809, 264510, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264596, 264758, 264801, 264803, 265018, 264804, 264605, 264760, 264881, 264762, 264683, 264764, 264684, 264288, 264685, 264689, 60170815, 33657023, 33657109, 55810764, 264635, 264636, 264637, 264638, 264639, 83373044, 264554, 264566

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gll4868435[gb]AAD31315.1(AF143236) apoptosis related protein APR-2 [Homo sapiens]			35696286, 28331826, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 265008, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264782, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264567, 56182575, 35696286, 56182181, 28331824, 60432289, 35696052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264784, 264288, 264368, 264687, 264768, 55811957, 264692, 18108368, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)				66714117, 264828, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22279000 263981
2129	95102089 (4257, 4258)			UNCLASSIFIED	
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gll2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gll1088886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	potassium_channel	35696052, 264909, 264768, 35695917
2132	95381096 (4263, 4264)	Novel Protein sim. GBank gll5689373[db]BAA82973.1 - (AB028944) KIAA1021 protein [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	264488, 22278998, 264259, 28331827, 28331828, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 265008, 264511, 265007, 264910, 264591, 264592, 264595, 264756, 21906754, 33108954, 87168474, 265011, 264600, 264601, 264605, 265018, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21908769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gij4220489 (AC006069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52646365, 52646842, 56984075, 35986286, 22278997, 22278998, 60432049, 56182181, 86714117, 60424289, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 58182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 55812038, 33109854, 21908754, 55811386, 265010, 264603, 265017, 285018, 265019, 55811150, 18108351, 264682, 264368, 264288, 52644229, 56181562, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 60170815, 33657023, 33657109, 60431528, 18108374, 35696423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264553, 264566
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gij3875351[emb]CAB09415] - (Z96047) DY3.6 [Caenorhabditis elegans]			56181686, 35696286, 21908754, 55811386, 265011, 265017, 18108351, 264765, 264768, 264688, 21908768, 35695917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	88078813 (4269, 4270)	Novel Protein sim. GBank gij568955[dbj]BAA83063.1] - (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278999, 29331828, 35696052, 264908, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87188559, 264601, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35695763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264584
2136	84346478 (4271, 4272)	Novel Protein sim. GBank gij2662167[dbj]BAA23715] - (AB07903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gij4884110[emb]CAB43262.1] - (AL030090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264559, 264909, 33109854, 264763, 21908768, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gij5174778[gb]AAD40696.1] - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase_associated	264259, 29331828, 35696052, 264909, 285008, 265017, 265018, 18108351, 264288, 21908768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264558, 264557, 264558, 264559
2139	84843882 (4277, 4278)	Novel Protein sim. GBank gij3850821[emb]CAA77135] - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]			264905, 264810, 264581, 55812038, 55811386, 85658542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18108364, 55811576, 83373044, 18108385, 56526486, 264482

2140	87645655 (4278, 4280)	Novel Protein sim. GBank glij417293jgbjAAD20418j - (AC007019) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264508, 265008, 264759, 265018, 264448, 264288, 21806768, 55811957, 265021, 33857023, 27488265, 35696423, 264636, 264558, 264557, 264559, 264566
2141	78023988 (4281, 4282)			UNCLASSIFIED	265020, 264683
2142	80041222 (4283, 4284)			UNCLASSIFIED	263978
2143	84140051 (4285, 4286)	Novel Protein sim. GBank glij2135766jpijS53362 - nucin 5AC (clone JER47) - human (fragment)		UNCLASSIFIED	22278987, 28331827, 264807, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank glij2078483 (U43200) - anilfreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	65274572, 264259, 28331824, 28331827, 264808, 264808, 264581, 265011, 87168559, 264600, 265019, 264288, 264768, 21806768, 21906767, 55811576, 35696423, 65274791, 22278902
2145	20564305 (4289, 4290)			UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank glij255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR-S28503) [Caenorhabditis elegans]		UNCLASSIFIED	264809, 60433356, 264686
2147	80432811 (4293, 4294)	Novel Protein sim. GBank glij3080398jembjCAA18718.1j - (AL022603) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank glij728637spjP39184jALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY IIII		UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank glij1198633spjP20693jFCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	Contains protein domain (PF00059) - glycoprotein Lectin C-type domain	UNCLASSIFIED	28331824, 28331826, 35698052, 264758, 87168474, 265018, 52644150, 33857109
2150	84140059 (4299, 4300)	Novel Protein sim. GBank glij5420387jembjCAB46679.1j - (AJ243459) proteophosphoglycan [Lishmania major]		UNCLASSIFIED	22278988, 28331822, 28331824, 28331828, 284764, 264769, 21906768, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank glij5689407jdbjBAA82887.1j - (AB028958) KIAA1035 protein [Homo sapiens]			22278988, 56894075, 22278989, 60432048, 264259, 28331822, 28331824, 28331826, 35698052, 28331828, 264508, 264511, 60433356, 264758, 264598, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21806765, 21806766, 21806768, 265020, 60170615, 33857109, 33857182, 33857349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000
2152	78321840 (4303, 4304)	Novel Protein sim. GBank glij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase		18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388

2153	88313371 (4305, 4308)	Novel Protein sim. GBank gi 4758704 ref NP_004216.1 pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278996, 22278998, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87188474, 87188559, 265017, 265019, 264760, 264288, 264368, 264766, 264687, 264769, 52644228, 21806768, 21806768, 35695917, 33657023, 33657108, 35695855, 264631, 264632, 264635, 264638, 264639, 18108385, 264483, 264564, 264486
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gi 225150 pr j1209265U - chorion protein B11 [Bombyx mori]		UNCLASSIFIED	56994075, 264094, 265008, 265019, 264288, 21908767, 35695917
2155	87424072 (4308, 4310)			UNCLASSIFIED	18108392, 18108398, 22278996, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 56182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gi 3970966 (AC004974) - spa-1- like; similar to AF026504 (PID:g2555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)	Novel Protein sim. GBank gi 1076211 pr jS50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gi 4650844 db BAA77027.1 - (AB026190) Kelch motif containing protein [Homo sapiens]			264586
2159	80083728 (4317, 4318)	Novel Protein sim. GBank gi 2878925 db BAA24826 - (AB007897) KIAA0437 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4319, 4320)				264634
2161	87739131 (4321, 4322)	Novel Protein sim. GBank gi 1504006 db BAA13202 - (D88966) similiar to human ZFY protein. [Homo sapiens]		UNCLASSIFIED	265008
2162	94318526 (4323, 4324)			UNCLASSIFIED	65274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264596, 264758, 265011, 264600, 264762, 264763, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264681, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264566, 264567
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gi 3876537 emb CAA98270 - (Z73974) cDNA EST yk29115.3 comes from this gene; cDNA EST yk28115.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	58182575, 22278996, 264093, 264683, 33657023, 65274620, 60432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	94329169 (4328, 4330)	Novel Protein sim. GBank gi 1086794 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56894075, 22278986, 22278987, 22278989, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284806, 29331830, 56182435, 265008, 21908754, 33657084, 265011, 265018, 264448, 264288, 264369, 21908765, 21908768, 21908769, 265020, 265021, 264691, 264692, 33657023, 65274620, 35685855, 264556, 60170394, 83373044, 60432113, 22278982, 284567, 52845156, 22278984, 22278986, 66714117, 29331828, 52844045, 265018, 265019, 284369, 21908765, 21908767, 21908768, 21908769, 265021, 265022, 264693, 27486262, 35685763, 18108376, 56528486, 87188518, 264587
2166	97618934 (4331, 4332)	Novel Protein sim. GBank gi 2706522[emb]CAA75816] - (Y15885) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin		56182575, 35686286, 29331824, 29331826, 29146498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 285017, 265018, 18108351, 264369, 21908764, 21908765, 21908768, 29148627, 21908769, 52844150, 33657109, 35686423, 18108381, 18108384, 18108385, 60432113, 264567
2167	87718984 (4333, 4334)	Novel Protein sim. GBank gi 2224713[db]BAA20840] - (AB002384) KIAA0386 [Homo sapiens]	UNCLASSIFIED		66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264663, 264768, 264768, 264568
2168	86898334 (4335, 4336)	Novel Protein sim. GBank gi 4321407[gb]AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00664) - ABC transporter transmembrane region.	transport	264829, 264555, 264559
2169	87886937 (4337, 4338)	Novel Protein sim. GBank gi 5106521[gb]AAD39741.1[AF10536] - (AF105365) K-CI cotransporter KCC4 [Homo sapiens]	UNCLASSIFIED		65274572, 56182575, 22278987, 22278988, 264259, 29331825, 264509, 264906, 56182435, 60433438, 55812038, 264596, 55811386, 265019, 264762, 264763, 264448, 264764, 264684, 264286, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35686423, 55811576, 65274791, 264634, 264639, 264558, 87168518, 60432113, 264564
2170	84141033 (4339, 4340)	Novel Protein sim. GBank gi 4309681[gb]AAD15478] - (AC006930) R33423.1 [Homo sapiens]	UNCLASSIFIED		264369, 265020, 264558
2171	80194050 (4341, 4342)	Novel Protein sim. GBank gi 2493778[sp]Q09458[Q35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5]	UNCLASSIFIED		264259, 264558
2172	85452460 (4343, 4344)		UNCLASSIFIED		264369
2173	87036740 (4345, 4346)		UNCLASSIFIED		
2174	95003288 (4347, 4348)				264806, 35695855, 264555, 264557

2175	94325850 (4349, 4350)	Novel Protein sim. GBank gi 1263287 (U47855) - fibroin-3 [Araneus diadematus]	UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35696052, 264109, 264508, 264509, 264805, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264598, 264758, 55812038, 265011, 264800, 264603, 264780, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21808768, 55811957, 35695917, 265020, 265022, 264691, 264692, 33657023, 264693, 264628, 264629, 55811578, 35696423, 65274781, 35695855, 264631, 264632, 264634, 264635, 264638, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	oncogene 52644507, 52646842, 22278984, 35696286, 22278986, 22278989, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264910, 33657402, 264758, 52644296, 87168559, 265018, 264688, 21908765, 21906767, 21806769, 35695917, 52644150, 264690, 33657023, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264486
2177	84128842 (4353, 4354)	Novel Protein sim. GBank gi 5454072 ref NP_006416.1 pSLU7 - step II splicing factor SLU7	kinase	18108392, 22278987, 22278989, 264093, 33657402, 265019, 264448, 264766, 264689, 21906767, 21806768, 21806769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gi 473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - eph Hsp70 protein	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87168474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)		UNCLASSIFIED	60424289, 264760, 264628, 264632

2180	95351397 (4358, 4360)	Novel Protein sim. GBank gi 3122317 sp P90848 KMH8_DICD1 - MYOSIN HEAVY CHAIN KINASE B (MICK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52844507, 22278994, 35696286, 22278997, 22278999, 284259, 52845080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 284508, 284509, 284908, 29331830, 284909, 284510, 285006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265018, 284763, 284882, 284883, 284884, 284288, 264886, 21906765, 21906766, 21906769, 285020, 265021, 265022, 52844150, 33657023, 33657108, 27486265, 33657348, 18108374, 35696423, 35695855, 263981, 60170394, 18108385, 56528486, 87168518, 60432113, 22278000, 264482, 264568, 264567, 264486 28331827, 264389, 18108378, 284584
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gi 3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gi 5420387 emb CAB46878.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264764, 264288, 21906787, 21906788, 21908769, 33657109, 18108378, 80170394, 22278000, 22278002 264760
2183	85460849 (4365, 4366)	Novel Protein sim. GBank gi 3873408 gb AAC77482.1 - (U17129) unknown [Rhodococcus erythropolis]			
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gi 3114713 (AF061346) - Edp1 protein [Mus musculus]		Inf	29331822, 29331825, 29331826, 56182435, 265011, 284685, 264688, 21908768, 18108370, 264629, 264631, 284636, 264557
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gi 5106956 gb AAD39906.1 AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens] (AL021811) putative protein [Arabidopsis thaliana]			29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526488
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gi 2864625 emb CAA16972 - (AL021811) putative protein [Arabidopsis thaliana]		ATPase-associated	284259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264780, 284788, 55811957, 33657023, 55811576, 56182323, 264563
2187	87388173 (4373, 4374)			UNCLASSIFIED	35696052, 284905, 284906, 284907, 264908, 264510, 284511, 265008, 264910, 264758, 265018, 264762, 264681, 264766, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264588, 264488 18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264908, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gi 5107816 gb AAD40129.1 AF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gi 3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278998, 284259, 29331826, 21906754, 264389, 264288, 263987

2190	87639197 (4378, 4380)	Novel Protein sim. GBank gij132575 sp P29315 RINI_RAT - RIBONUCLEASE INHIBITOR		nucleaseinhib	22278996, 22278999, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52844298, 265010, 265018, 264685, 264688, 56181562, 21908789, 35695917, 265022, 60170394, 22279000, 29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559, 264558
2191	95198928 (4381, 4392)	Novel Protein sim. GBank gij5327002 emb CAB46272.1 - (Y18503) XAP-5-like protein [Homo sapiens]			
2192	11126316 (4383, 4394)	Novel Protein sim. GBank gij482600 sp P34400 MI10_CAEEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain		
2193	94140073 (4385, 4396)	Novel Protein sim. GBank gij5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264809, 265008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810764, 55811576, 65274781, 35695855, 60431850, 56182323, 60432113, 264592
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			
2195	88063023 (4389, 4390)	Novel Protein sim. GBank gij2832763 emb CAA15685.1 - (AL009191) /prediction=(method); /prediction=(method); /match=(desc); /match=(desc); /motif=(desc: [Drosophila melanogaster])		UNCLASSIFIED	22278996, 22278999, 35696052, 265006, 21908754, 265017, 35695917, 265021, 265022, 35695855
2196	95091831 (4391, 4392)	Novel Protein sim. GBank gij5262487 emb CAB45699.1 - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 60432289, 29331827, 35696052, 29331828, 264508, 52844045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52644228, 21908765, 21908766, 21908767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 264636, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gij4928567 gb AAD34044.1 AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			264768, 264769, 21908765, 21908766, 21908767, 29148627, 55811957, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432228, 56182323, 33657402, 264758, 83373044, 21908754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264389
2198	88060814 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953_1 [Homo sapiens]		UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank gij2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]				264105, 264110, 264112, 264688, 55811857, 33657023, 264682, 263967, 20281071, 56526486
2200	87405385 (4398, 4400)	Novel Protein sim. GBank gij3043634[dbj BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct			29331824, 264763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gij3913470[sp O57314 DHBX, ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2]	Contains protein domain (PF00106) - short chain dehydrogenase			29331824, 35696052, 264905, 264907, 33657402, 55811386, 265017, 265018, 264288, 21906768, 35695917, 265020, 265022, 33657023, 33657108, 27486281, 18108370, 35696423, 35696855, 264555, 264556, 83373044, 87168518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gij5262665[emb CAB45767.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED			264489, 264259, 29331824, 60432289, 35696052, 264905, 264909, 264592, 265017, 265018, 265019, 18108351, 264762, 264448, 264368, 264288, 264766, 21908765, 21908768, 264690, 264691, 264692, 33657109, 264634, 264636, 264555, 264639, 264558, 264559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gij1172845[sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25]	Contains protein domain (PF00071) - Ras family	glycoprotein		52646385, 56894075, 264259, 28331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87168559, 265018, 265019, 264605, 264288, 21906769, 35695917, 33657023, 264682, 33657109, 35695763, 18108376, 264638, 22279000, 264568, 264567
2204	88088671 (4407, 4408)	Novel Protein sim. GBank gij121036[sp P29348 G8T3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT (GUSTOUCIN ALPHA-3 CHAIN)]	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED		
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gij4589480[dbj BAA76768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_rna_bind		18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264806, 265007, 265008, 265009, 60432228, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21906768, 21908769, 264690, 264691, 264683, 18108368, 55811578, 65274791, 264634, 18108381, 18108384, 60432113, 22279002, 264563, 264568
2206	20620008 (4411, 4412)		UNCLASSIFIED			264581
2207	87787870 (4413, 4414)	Novel Protein sim. GBank gij455753[ref NP_000372.1 pMID1 - midline 1 protein]	Contains protein domain (PF00622) - SPRY domain			29331822, 56182181, 29331827, 35696052, 52644045, 265006, 265019, 56181562, 55811957, 265021, 33657023, 35695763, 35695855, 60170394, 60432113, 264568
2208	86100830 (4415, 4416)					264908, 265019, 18108351, 21906769
2209	87800420 (4417, 4418)	Novel Protein sim. GBank gij3986748 (AF105228) - tuftelin [Bos taurus]	struct			264112, 265009, 264691, 18108365, 18108374, 264634, 20281168

2210	57152407 (4418, 4420)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	264685, 264686, 18108365, 22278002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA09214 - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278998, 264082, 264094, 26331822, 66714117, 29331826, 29331828, 264907, 52644045, 265009, 60170831, 21906754, 87188558, 265017, 265019, 18108351, 264683, 18108354, 264369, 264766, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 33657109, 18108370, 18108374, 264638, 56182323, 18108384, 18108387, 87168518, 264555
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CAB48878.1 - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278996, 22278997, 35696052, 264905, 66712502, 264908, 264828, 56182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906768, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108379, 55811576, 264556, 264637, 264558, 83373044, 22278002, 264482, 264483

2214	95361453 (4427, 4428)	Novel Protein sim. GBank gll4504325[ref]NP_000173.1 pHADH - hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	264488, 52644507, 18108394, 56182575, 22278894, 22278895, 35696286, 58994075, 22278897, 22278898, 22278899, 264490, 60432049, 264259, 52645080, 26331822, 29147820, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35698052, 29331828, 20281100, 264508, 264907, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433356, 60433436, 33109954, 33657084, 52644286, 87168474, 265010, 265011, 87168558, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644229, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 35895917, 265020, 265021, 265022, 264532, 60170615, 264690, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 33657182, 27486262, 27486264, 27486265, 35895763, 18108370, 264629, 60431528, 18108374, 18108378, 55810764, 35896423, 35895855, 264634, 264636, 52644332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526466, 87168518, 60432113, 22278002, 264482, 264564, 264565, 264566, 264809, 265006, 264555, 264558, 87168518
2215	95419208 (4428, 4430)	Novel Protein sim. GBank gll1847160 (AF000288) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		
2216	87614048 (4431, 4432)	Novel Protein sim. GBank gll1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]		
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gll5031707[ref]NP_005503.1 pGARP - glycoprotein A repetitions predominant	UNCLASSIFIED	264693
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gll3878636[emb]CAA8953] - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL:700719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00560) - Leucine Rich Repeat	264288, 33657109, 264556
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gll1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696423, 264563
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gll1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family	264682, 264683, 264688, 264689, 264693, 18108370, 18108378

2220	95354165 (4439, 4440)	Novel Protein sim. GBank gi 4507261 ref NP_003145.1 pSTAT - statherin			264488, 18108394, 18108395, 35686286, 264259, 264097, 60432289, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 264593, 264594, 60433356, 264595, 55812038, 264756, 85858542, 265010, 264601, 264603, 265019, 264605, 264760, 264762, 264448, 264768, 264369, 264768, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264691, 33857023, 264692, 18108362, 18108368, 264628, 264628, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264566, 264486, 264567
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)				
2223	85091649 (4445, 4446)				
2224	87386515 (4447, 4448)	Novel Protein sim. GBank gi 3876005 emb CAA84789 - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES...	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED UNCLASSIFIED	264908, 265020, 35695855 265010, 264685, 264690, 264693, 264628, 263974, 263976, 55811576, 264555, 264638, 83373044, 264483
2225	85749484 (4449, 4450)	Novel Protein sim. GBank gi 1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]		transport	22278994, 22278995, 22278999, 52644045, 264600, 265018, 21908785, 21908789 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265007, 264691, 264634, 264486
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gi 4826524 emb CAB42852.1 - (AL049848) hypothetical protein [Homo sapiens]			22278999, 265006, 265008, 18108354, 28148629, 28148784, 27486261, 18108374, 264637, 18108384
2227	87721135 (4453, 4454)			UNCLASSIFIED	264091, 264092, 264094, 29331822, 29331825, 86714117, 264693, 263972, 264639, 83373044, 264563
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi 606976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gi 3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342915 (4459, 4460)	Novel Protein sim. GBank gij226154[prfj]1412350A - DNA polymerase [Human adenovirus type 2]	UNCLASSIFIED	264488, 264788, 52844507, 264789, 21908765, 21908768, 21908767, 21908769, 22278995, 35695917, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21908754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328_1 [Homo sapiens]	UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gij5281316[gb]AAD41476.1[AF133124] transcription factor IIC63 [Homo sapiens]	transcription factor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265008, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264682, 264764, 264683, 264368, 264288, 264688, 264687, 264689, 21908765, 21908768, 21908767, 21908769, 29148629, 35695917, 264690, 52644150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264564, 264906, 33657402, 265018, 264288, 264688, 265020, 264635, 18108385
2233	87755282 (4465, 4466)	Novel Protein sim. GBank gij4249733[gb]AAD13780] - (AF109377) [dBp [Mus musculus]		
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij1706559[sp]P54352[EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)]	kinase	56182435, 264369, 264688, 21908765, 265020, 264693, 264556, 56528486
2235	91012318 (4469, 4470)	Novel Protein sim. GBank gij4972734[gb]AAD34762.1] - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675[prfj]B53814 - p20 protein - human	Contains protein domain (PF00011) - Hsp20/alpha crystallin family	264568, 264687, 264789, 265022, 264259, 60432049, 264691, 29331826, 60432289, 20281149, 264908, 264807, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734[gb]AAD34762.1] - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	264488, 264769, 21908765, 21908766, 21908767, 21908768, 21908769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432228, 33657402, 60433356, 60433438, 83373044, 18108385, 21908754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	94998857 (4475, 4476)			(Contains protein domain (PF00286) - Viral coat protein)	284509, 284907, 284629, 284634, 284564
2239	87798688 (4477, 4478)				29331825, 285008, 264369, 33637109, 18108370, 18108374, 284557, 284559
2240	94121471 (4479, 4480)	Novel Protein sim. GBank gij2982311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]		Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	264488, 65274572, 56182575, 35698266, 22278997, 284508, 284259, 28331827, 35698052, 264508, 52644045, 56182435, 284511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 18108351, 284683, 264288, 264768, 284687, 284688, 284769, 21908765, 21908768, 21908769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35696423, 35695859, 87168518, 22279000
2241	80091951 (4481, 4482)	Novel Protein sim. GBank			264893, 264629
2242	81228075 (4483, 4484)	gij284312spj70541jE2BG_RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)	UNCLASSIFIED synthase		22278995, 22278996, 22278997, 22278998, 284259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264596, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 284288, 52644229, 21906765, 21906768, 21908767, 21908768, 21908769, 265020, 265021, 33657109, 27486282, 27486284, 18108374, 35695855, 284634, 284637, 56182323, 83373044, 56526466, 87168518, 264564
2243	78902026 (4485, 4486)	Novel Protein sim. GBank gij2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]		UNCLASSIFIED	265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gij470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]		UNCLASSIFIED	264604
2245	85318545 (4489, 4490)		Contains protein domain (PF00534) - Glycosyl transferases group 1		52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21908754, 265011, 264603, 264764, 264687, 21908767, 21908768, 21908769, 55811957, 265022, 284681, 284629, 35696423, 264638, 18108387, 60432113, 22278990, 22279002, 264566

2246	94848710 (4491, 4492)	Novel Protein sim. GBank gl 4986086 dbj BAA78326.1 - (AB028069) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278985, 35696286, 22278986, 22278987, 22278989, 264259, 35698052, 264106, 264905, 264907, 265008, 265007, 265008, 60433438, 33108954, 87168559, 265018, 265019, 264288, 21908765, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265022, 27486264, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gl 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	52645156, 52646365, 52645080, 35696052, 33656870, 52646317, 33657084, 265017, 21908768, 21908769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486262, 33657348, 27486285, 18108387
2248	95412986 (4495, 4496)	Novel Protein sim. GBank gl 4758502 ref NP_004123.1 pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	calhepsin	264488, 264259, 264907, 29331830, 264909, 265007, 265009, 264595, 21908754, 65274444, 264603, 265019, 264762, 264448, 264288, 264688, 21908768, 55811957, 265021, 284691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264486
2249	94685662 (4497, 4498)	Novel Protein sim. GBank gl 4038461 (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	264768, 264628, 264636, 264637
2250	79827508 (4498, 4500)	Novel Protein sim. GBank gl 3738140 emb CAA21241 - (AL031852) valyl-Hma synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gl 3218467 emb CAA07090.1 - (AJ006529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264884, 264288, 264690, 264628, 55811576, 264555, 264556, 264557, 264558, 264559, 264568
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gl 4929325 gb AAD33953.1 AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 29331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433356, 285010, 18108351, 21908767, 21908768, 264691, 263974, 263977, 264486, 264567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gl 4502847 ref NP_001271.1 pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF000076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	284569, 18108394, 18108398, 56182575, 58994075, 35696286, 22278999, 264084, 60432049, 264258, 28331822, 29331824, 29331825, 29331826, 60432286, 29331827, 29331828, 35696052, 264108, 264508, 264509, 264906, 264907, 29331830, 66712502, 264908, 264909, 264510, 265006, 264511, 265007, 265008, 265009, 60170831, 60432228, 60433358, 60433436, 264758, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264764, 264288, 264388, 264768, 264686, 264768, 264769, 21908765, 21908767, 55811957, 264691, 33657023, 264692, 18108362, 85274620, 263969, 264628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108378, 55811576, 35698423, 35698555, 264630, 264634, 264635, 264636, 264558, 263981, 264638, 56182323, 60170394, 264558, 18108381, 18108382, 83373044, 18108385, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264486, 264587, 18108391
2255	91010546 (4509, 4510)	Novel Protein sim. GBank gl 5541865 emb CAB51072.1 - (AL096858) hypothetical protein [Homo sapiens]	Contains protein domain (PF000076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 56182575, 22278997, 22278998, 264258, 29331822, 29331825, 29331826, 29331827, 29331828, 264508, 264905, 264906, 264907, 66712502, 264908, 56182435, 264510, 264511, 265008, 264593, 264595, 21806754, 33109954, 87168474, 265011, 265017, 265018, 264682, 264784, 264369, 264288, 264768, 264685, 264688, 264768, 21908765, 21908766, 21908768, 21908769, 265020, 60170815, 52644150, 264690, 264692, 264693, 33657109, 33657349, 264632, 264636, 52644332, 56182323, 22279000, 22279002 264768, 264689, 18108374
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gl 3327174 db BAA31655 - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	
2257	80088235 (4513, 4514)			UNCLASSIFIED	
2258	86090516 (4515, 4516)	Novel Protein sim. GBank gl 3025446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF000060) - Ligand-gated ion channel	misc_channel	22278996, 22278998, 264681, 21908765, 21908768, 264587 264908, 264592, 264764

2259	85384155 (4517, 4518)	Novel Protein sim. GBank gij4884140[emb]CAB43278.1]- (AL050110) hypothetical protein (Homo sapiens)		UNCLASSIFIED	18108386, 65274572, 56182575, 22278997, 22278998, 284259, 28331822, 28331827, 264805, 68712502, 264808, 264809, 56182435, 265007, 265008, 60432229, 33657084, 87168559, 18108351, 264448, 264883, 264288, 264369, 56181582, 265021, 60170615, 264680, 33657109, 60431628, 18108374, 52644332, 56182323, 18108385, 22279000, 22278002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gij3080663 (AC004614) - similar to I-spondin proteins AB008086 (PID:g2529225) (Homo sapiens)	Contains protein domain (PF00080) - Thrombospondin type 1 domain	oxidase	56182575, 265020, 264805, 264905, 264808, 33696423, 264511, 264635, 55812038, 264758, 265018, 265019, 264805, 264760, 264583
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gij3334528[emb]CAA1613[em] (AL021308) predicted using FGENEH (Homo sapiens)		UNCLASSIFIED	
2262	91639282 (4523, 4524)	Novel Protein sim. GBank gij487759[gb]AAD31421.1[AF12444 - (AF124440) MAGE tumor antigen D1 (Homo sapiens)]			56182575, 22278998, 28331822, 28331825, 60432288, 28331827, 35898052, 264508, 66712502, 52844045, 56182435, 265008, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21908765, 21908767, 55811957, 35695917, 52644150, 33657023, 33657109, 55811578, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gij3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264828, 52844150, 18108381, 264693, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gij1657601 (U66220) - unknown (Nannocystis exedens)		UNCLASSIFIED	264886, 264488, 264768, 264769, 264681, 264508, 264905, 264509, 264808, 264907, 264908, 264809, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264584, 264585, 264784, 264568, 264486, 264766
2265	86918663 (4529, 4530)	Novel Protein sim. GBank gij477072[pir]JA48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	264688, 264810, 264764
2266	87773458 (4531, 4532)	Novel Protein sim. GBank gij3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomalprot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21908754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21908765, 21908768, 35695917, 265021, 18108374, 264638, 22278000, 22279002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gij3580229[emb]CAA20687.1] - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 35696052, 29331828, 264905, 264509, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264762, 264448, 264288, 264368, 264768, 52644229, 35695917, 264691, 33657023, 18108382, 33657109, 35698423, 264634, 18108381, 87168518, 264598
2268	85693887 (4535, 4536)	Novel Protein sim. GBank gij728832[sp]P39189/ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III	cadherin		264488, 264259, 264509, 264595, 265010, 265017, 264766, 18108385, 264488
2269	86177977 (4537, 4538)	Novel Protein sim. GBank gij103418[pi]J517885 - Tcd37 protein - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	58182575, 60432049, 265007, 265009, 264591, 87168559, 264605, 18108351, 21906764, 265020, 264629, 60431528, 264638, 18108385, 18108387, 60432113
2270	80410327 (4539, 4540)				264763
2271	91010392 (4541, 4542)				264809, 56182435, 265008, 56812038, 55811957, 33657023, 264693, 33657109, 55810764, 55811576, 56182323
2272	84208220 (4543, 4544)				264905, 264908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gij4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin	UNCLASSIFIED	52645156, 22276996, 22276999, 60432049, 264259, 29331822, 29331824, 29331825, 29331828, 29331827, 35696052, 264909, 265008, 264593, 60433438, 21906754, 265018, 264688, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27488264, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 58182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gij1480112[emb]CAA67981] - (X99642) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 28331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264591, 21906754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264766, 21906765, 21906766, 21906767, 21906768, 52644150, 264693, 18108384, 35695763, 18108374, 35698423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gij3165406 (AC004755) - (fos37502.2 [Homo sapiens])	Contains protein domain (PF00122) - E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)			UNCLASSIFIED	264555, 264556

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gij2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1389906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278899, 35696052, 265008, 265019, 264389, 265020, 265022, 55810764, 264404, 22279002
2278	84133079 (4555, 4556)	Novel Protein sim. GBank gij2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 29331826, 60433356, 60433438, 21908754, 265018, 33657023, 264639, 83373044, 264585
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gij119714 (spIP13883) EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264585
2280	94239723 (4559, 4560)				265008, 33108954, 265010, 265019, 265020
2281	95283048 (4561, 4562)	Novel Protein sim. GBank gij4240299 (dbj BAA74928.1) - (AB020712) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264908, 264808, 52644045, 265008, 33657402, 60433356, 264758, 265011, 265019, 264681, 264683, 264684, 264886, 21908765, 21906767, 21906788, 21906789, 60170615, 264690, 52644150, 18108362, 264692, 18108368, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56526486, 22279000, 264566, 264587
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gij1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21908787, 21908769, 55811957, 33657023, 52645129, 33657109, 33657182, 27486282, 263972, 55811576, 87168518, 20281169
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gij2495729 (spIQ82556) Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35696052, 29146499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33108954, 33657084, 55811386, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264288, 264688, 21906765, 21908767, 21908768, 29146627, 21906769, 55811957, 265020, 265022, 33657182, 27486261, 18108370, 264628, 18108374, 55810784, 18108379, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264587

2284	95414955 (4567, 4568)	Novel Protein sim. GBank gi 2498797 sp Q6431.1 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNA)			60424179, 52644507, 18108394, 52646842, 22278994, 35698286, 22278998, 22278997, 28331824, 28331825, 60432289, 29331826, 28331827, 35696052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85658542, 87188559, 265018, 265019, 55811150, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 33657023, 33657182, 27486262, 27486264, 27486265, 18108376, 55810764, 35698423, 35698555, 60431850, 87188516, 60432113, 284482, 264584 collagen
2285	87781484 (4568, 4570)	Novel Protein sim. GBank gi 3342234 (U93809) - nuclear antigen EBNA-1 [Cercopithecine herpesvirus 15]			
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi 3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]			
2287	82986696 (4573, 4574)	Novel Protein sim. GBank gi 630805 pf S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)			
2288	84133083 (4575, 4576)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	UNCLASSIFIED	22278995, 56994075, 22278997, 22278999, 264259, 60432288, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21906765, 21906766, 21906767, 21906768, 33657023, 264557, 22279000, 22279002 264582
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gi 3253120 (AC005175) - R31449_3 [Homo sapiens]		struc	18108394, 264907, 265008, 265009, 33109954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2282	84328834 (4583, 4584)	Novel Protein sim. GBank gi 4803672 emb CAB42643.1 - (AJ133789) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	56182575, 35686286, 56894075, 29331824, 29331825, 35686052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168558, 265018, 18108351, 264763, 264448, 264389, 264288, 56181582, 264768, 21908765, 21908766, 21908767, 21908769, 265021, 265022, 33657023, 264683, 65274620, 33657108, 27486264, 264628, 55810764, 55811578, 35685855, 56182323, 56528486, 87188518, 22278000, 264567
2283	87759213 (4585, 4586)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - struct Leucine Rich Repeat	struct	264488, 18108397, 35686286, 264092, 264259, 29331822, 29331828, 264908, 264908, 264511, 264512, 265009, 264810, 18108351, 264764, 264389, 264288, 264685, 264768, 265020, 265022, 264534, 35686423, 264631, 264637, 18108381, 56182323, 264639, 18108385, 264404, 264563, 264565
2284	86693580 (4587, 4588)	Novel Protein sim. GBank gi 2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - nuclease Exonuclease	nuclease	22278997, 22278998, 22278999, 264259, 26331822, 60432289, 29331828, 35686052, 265018, 264684, 264288, 264686, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 264682, 33657109, 18108376, 35686423, 35685855, 264634, 22279000, 22279002, 264563, 264486
2285	95312200 (4589, 4590)			UNCLASSIFIED	22278996, 60432289, 264682, 264683, 264688, 18108374
2286	80030781 (4591, 4592)				263974, 263978
2287	94321251 (4593, 4594)	Novel Protein sim. GBank gi 5689501 dbj BAA83034.1 - (AB028005) KIAA1082 protein [Homo sapiens]		transcriptfactor	264488, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331828, 35686052, 264807, 264908, 52644045, 56182435, 264112, 265008, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21908754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21908765, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 264680, 264681, 33657023, 264692, 264693, 33657108, 55811578, 56182323, 60170394, 83373044, 18108385, 56528486, 264564, 264486

2298	95312207 (4595, 4598)	Novel Protein sim. GBank gij3875051[emb CA802849] - (Z81050) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65564 comes from this gene; cDNA EST EMBL:D69046 comes from this gene; cDNA EST yk366b12.3 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...		collagen	60424178, 56181686, 22278995, 35696286, 22278998, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 60424289, 35696052, 28331828, 68712502, 56182435, 264510, 265006, 60433438, 21908754, 33109954, 55811386, 285010, 285018, 55811150, 264762, 18108351, 264882, 284683, 264286, 264684, 264686, 264688, 56181562, 264689, 21906768, 21906767, 29148629, 55811857, 29148784, 35695917, 265020, 18108362, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35698423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22278000, 264482, 264587, 264486
2299	80193720 (4587, 4588)				264369
2300	94124346 (4599, 4600)	Novel Protein sim. GBank gij2443886 (AC002284) - Unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 22278998, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 265009, 264758, 265010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264768, 264769, 21908768, 21908767, 35695917, 285021, 264691, 33657023, 35695763, 18108370, 18108374, 35696423, 35695855, 264631, 264636, 264638, 18108385, 22278002, 264563
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gij2143637[pir j84505] - calcium-dependent actin-binding protein - rat		struct	264908, 264758, 265017, 21908765, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gij2887497 (AC004144) - R34001_1 [Homo sapiens]		UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gij4884194[emb CA843220.1] - (AL049948) hypothetical protein [Homo sapiens]		Contains protein domain (PF00047) - struct immunoglobulin domain	264259, 60432049, 264907, 264909, 264910, 60432229, 33657402, 265011, 265018, 264762, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gij2494162[sp Q10005]YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	264259, 29331824, 21906767, 33657182, 33657348
2305	90935911 (4609, 4610)	Novel Protein sim. GBank gij4972666[gb AAD34738.1] - (AF132150) unknown [Drosophila melanogaster]			65274572, 22278986, 264908, 265006, 21908769, 264691, 264486

2308	85334940 (4611, 4612)	Novel Protein sim. GBank gl 4829585 gb AAD34043.1 AF15180 - (AF151806) CGI-48 protein (Homo sapiens)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278995, 22278998, 35698288, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35698052, 264508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 85658542, 265010, 265011, 264601, 265017, 265018, 264604, 265019, 18108351, 264448, 264288, 264766, 264769, 21908765, 21906766, 21906767, 21906768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35698423, 35698555, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264568, 264488 264828
2307	79415283 (4613, 4614)	Novel Protein sim. GBank gl 4758732 ref NP_004522.1 pMOCs - molybdenum cofactor synthesis 2		UNCLASSIFIED	
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gl 4758732 ref NP_004522.1 pMOCs - molybdenum cofactor synthesis 2		synthase	35698288, 264259, 29331822, 29331824, 264112, 264512, 264757, 21906754, 264288, 264690, 27486264, 264631, 264634, 264404 18108397, 22278998, 22278997, 22278998, 22278999, 60432049, 29331822, 29331828, 60432289, 66712502, 60432228, 60433356, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21906766, 21906768, 265020, 264691, 264692, 264693, 65274620, 65274791 264508
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gl 3878059 emb CAB17070 - (Z89842) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72944 comes from this gene; cDN...		glycoprotein	
2310	79601668 (4619, 4620)	Novel Protein sim. GBank gl 2137337 pir j 46281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	18108397, 56182575, 22278998, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265008, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264688, 33657023, 20281149, 20281069, 264628, 263972, 55811576, 35698423, 20281071, 264632, 264636, 18108385, 18108387, 87168518, 22279000, 264563, 264488
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gl 2137337 pir j 46281 - gene mCBP protein - mouse		transcriptfactor	

2312	87549881 (4623, 4624)	Novel Protein sim. GBank gi 2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56894075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331828, 29331827, 52844045, 60432228, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 284288, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170815, 33657023, 27486261, 27489264, 35696423, 35695855, 18108385, 22279000, 22279002, 263981
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gi 3043626 dbj BAA25477 - (AB011123) KIAA0551 protein [Homo sapiens]			52844507, 52846365, 52846842, 22278996, 22278997, 22278999, 264259, 52845080, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 52844045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 284288, 264369, 21906765, 21906766, 21906768, 35695917, 52844150, 33657023, 33657109, 52845129, 33657349, 35695763, 18108374, 35696423, 35695855, 52844332, 22279000, 22279002, 264563, 264567
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gi 5596714 emb CA851401.1 - (AL035398) dJ796117.2 (CGI-51) [Homo sapiens]		UNCLASSIFIED	52844507, 52846365, 52846842, 22278996, 22278997, 22278999, 264259, 52845080, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 52844045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 284288, 264369, 21906765, 21906766, 21906768, 35695917, 52844150, 33657023, 33657109, 52845129, 33657349, 35695763, 18108374, 35696423, 35695855, 52844332, 22279000, 22279002, 264563, 264567
2315	80430118 (4629, 4630)			UNCLASSIFIED	264805, 264906, 264767, 264768, 264693, 55811578, 264635, 56182323, 18108385, 52844507, 52845156, 52846365, 22278994, 22278995, 22278996, 56894075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52845080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264908, 264907, 29331830, 52844045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52846317, 33109954, 33657084, 52844286, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264369, 52844229, 21906764, 284689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52844150, 33657023, 18108362, 52845129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264631, 264556, 52844332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264568, 264567
2316	94312181 (4631, 4632)	Novel Protein sim. GBank gi 5531827 gb AAD44488.1 - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - glycoprotein UBX domain		52844507, 52846365, 52846842, 22278996, 22278997, 22278999, 264259, 52845080, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 52844045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 284288, 264369, 21906765, 21906766, 21906768, 35695917, 52844150, 33657023, 33657109, 52845129, 33657349, 35695763, 18108374, 35696423, 35695855, 52844332, 22279000, 22279002, 264563, 264567

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)			UNCLASSIFIED	265008, 264910
2319	95101781 (4637, 4638)	Novel Protein sim. GBank glj5262613[embjCAB45746.1] - (AL080155) hypothetical protein [Homo sapiens]			264486, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 56994075, 35686286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21908754, 52644288, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644229, 21908764, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486284, 33657349, 35685763, 18108370, 18108376, 18108379, 35686423, 264558, 83373044, 18108385, 56526486, 87168518, 264564, 264565, 264566
2320	91622426 (4639, 4640)	Novel Protein sim. GBank glj728837[spP39184]ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265019, 21908765, 18108372, 18108387, 22279002
2321	94320377 (4641, 4642)	Novel Protein sim. GBank glj3873837[embjCAB02700] - (Z81029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com...		UNCLASSIFIED	264486, 264687, 18108394, 264689, 21908765, 18108397, 18108398, 21908767, 21908768, 65274791, 22278995, 35685855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170815, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433436, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87803165 (4643, 4644)	Novel Protein sim. GBank glj5678957[embjCAB51685.1] - (AL108630) BACRTA4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	- dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264769, 264638

2323	94840445 (4845, 4846)	Novel Protein sim. GBank gi 2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00226) - eph DnaJ domain	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 56182435, 264511, 265008, 60433358, 60433438, 55812038, 33109954, 21908754, 85658542, 87168474, 265011, 87168559, 265017, 265019, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21908765, 21908767, 21908768, 55811957, 35695917, 265021, 33657023, 18108362, 27468262, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22279002 264592, 264593, 265020 265020
2324	86633607 (4647, 4648)	Novel Protein sim. GBank gi 5419865 emb CAB46377.1 - (AL098732) hypothetical protein [Homo sapiens]	ATPase, associated	
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi 231885 sp P29981 CP4C_BLAD1 - CYTOCHROME P450 4C1 (CY1VC1)	Contains protein domain (PF00067) - cyto450 Cytochrome P450	265006, 264759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi 231885 sp P29981 CP4C_BLAD1 - CYTOCHROME P450 4C1 (CY1VC1)	UNCLASSIFIED	
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi 4240227 dbj BAAT4892.1 - (AB020676) KIAA0869 protein [Homo sapiens]	UNCLASSIFIED	
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi 1245105 (U46463) - glutamine repeat protein-1 [Mus musculus]	UNCLASSIFIED	264259, 264508, 264903, 264908, 264907, 264908, 265007, 264512, 264910, 264758, 265010, 264766, 264768, 264769, 33657023, 264693, 264628, 264631, 264634, 264638, 264639, 264486
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi 169343 sp P42208 DIF6_MOUSE - DIFF6 PROTEIN	Contains protein domain (PF00735) - Cell division protein	60433438, 264595, 265017, 264766, 264692, 264629, 264635, 264636, 264638, 56182323, 60432113, 264566
2330	87335396 (4659, 4660)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	UNCLASSIFIED	265017, 264685, 60432113, 264088 265009
2331	86980463 (4661, 4662)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	transport	
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi 2104452 emb CAB08778 - (Z85397) unknown [Schizosaccharomyces pombe]	ATPase, associated	35696286, 22278998, 29331824, 60424269, 265008, 265008, 265018, 264448, 264764, 21908765, 35695917, 35695855, 264636, 22279000, 264568
2333	88209958 (4665, 4666)	Novel Protein sim. GBank gi 3879885 emb CAA92691.1 - (Z68318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07830 comes from this gene; cDNA EST EMBL:C08493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST ...	UNCLASSIFIED	56182575, 56994075, 28331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263978
2334	84319788 (4667, 4668)	Novel Protein sim. GBank gi 4966270 gb AAB52261.2 - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA, dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...]	Contains protein domain (PF00441) - dehydrogenase Acyl-CoA dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80046103 (4668, 4670)	Novel Protein sim. GBank gi 3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - IQ calmodulin-binding motif	struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gi 1929056 emb CAA72805 (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	264907, 35695917, 18108378
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gi 4495083 emb CAB39181.1 (Z85986) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 66182181, 29331825, 60424259, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 285019, 21906768, 35695917, 264891, 33657023, 33657109, 263972, 35696423, 35695859, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gi 2224689 dbj BAA20829 (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 264908, 56182435, 265009, 60433438, 264596, 265010, 265019, 18108354, 264288, 264369, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gi 3873550 emb CAA22127 (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264592, 264369, 264691, 264558
2340	80937716 (4679, 4680)				
2341	87775281 (4681, 4682)	Novel Protein sim. GBank gi 3874563 emb CAB02797 (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...			65274572, 22278994, 35696286, 22278997, 22278999, 264259, 20331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264786, 264685, 21906769, 35695917, 264891, 264892, 35696423, 87168518, 22279000
2342	95334988 (4683, 4684)	Novel Protein sim. GBank gi 3874563 emb CAB02797 (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 264908, 264809, 264682, 22279000, 264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265009, 60170831, 60432229, 60433356, 87168474, 265017, 265018, 265019, 264448, 264389, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810764, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264593, 264564, 264965, 264586, 264567, 264907, 264512, 265011, 264683
2343	87775448 (4685, 4686)	Novel Protein sim. GBank gi 4929741 gb AAD34131.1 AF151894 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	
2344	79953198 (4687, 4688)	Novel Protein sim. GBank gi 2506307 sp P13944 CA1C - CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	UNCLASSIFIED	264758
2345	94319789 (4689, 4690)	Novel Protein sim. GBank gi 2506307 sp P13944 CA1C - CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	UNCLASSIFIED	264498, 264259, 66712502, 264759, 83373044, 264568

2348	94131820 (4691, 4692)	Novel Protein sim. GBank gl 1255411 (U53153) - one short region of weak similarity to <i>S. cerevisiae</i> protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to <i>S. cerevisiae</i> glucose repression mediator protein (SP:P14922) [<i>Caenorhabditis elegans</i>]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35696052, 28331828, 33857402, 60433356, 33108954, 87168559, 264603, 265018, 18108351, 264681, 264685, 21906766, 265021, 33657109, 55811576, 35695855, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264663, 264684, 264768, 264687, 264688, 264691, 264692, 55811576, 18108394, 35696286, 264259, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265008, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264288, 264768, 264768, 264889, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35696423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264587, 264486
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gl 4884106[emb]CAB43254.1] - (AL050082) hypothetical protein [Homo sapiens]			35696052, 28146498, 264909, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 28331822, 28331824, 29331825, 29331827, 29331828, 33109954, 21906754, 265010, 87168559, 265018, 265019, 264761, 264681, 264288, 18108357, 21906766, 21908767, 264691, 264692, 35695855, 87168518, 22279000, 22279002, 264482
2351	88980042 (4701, 4702)	Novel Protein sim. GBank gl 728832[sp]P39189[ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII]		kinase	56182575, 264909, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gl 731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gl 1346955[sp]P48809[RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337199 (4707, 4708)	Novel Protein sim. GBank gl 731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	91636788 (4709, 4710)	Novel Protein sim. GBank gij4938503[emb]CAB43881.1] - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56994075, 22278986, 35696286, 22278989, 264259, 29331825, 29331826, 29331828, 29148498, 264905, 264908, 265005, 264758, 87168474, 265010, 265017, 264687, 21808765, 21908767, 21908769, 264691, 264692, 263887, 18108370, 87168518, 22279000
2356	85327688 (4711, 4712)	Novel Protein sim. GBank gij5138920[g]AAD40377.1] - (AF092135) PTD014 [Homo sapiens]			52644507, 22278985, 35696286, 22278986, 22278987, 22278988, 264259, 29331824, 86714117, 29331825, 60432289, 35696052, 29331828, 264908, 86712502, 264512, 265007, 265008, 60170831, 60432229, 60433358, 60433438, 264758, 52646317, 33108954, 21908764, 55811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 60170815, 33657109, 27486284, 35695763, 55810764, 18108379, 35686423, 55811578, 35695855, 60170394, 56182323, 83373044, 18108385, 56526486, 264404, 60432113, 22279000, 264482, 264583, 264586, 264486, 264587
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gij4929741[g]AAD34131.1]AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	284498, 264789, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264566, 264369, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gij4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278987, 22278989, 264509, 264905, 264592, 18108351, 264681, 264682, 264768, 32833986, 18108374, 264556, 18108385, 264482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank gij1086830 (U41264) - coded for by C. elegans cDNA yk20f8.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk39g6.5; coded for by C. elegans cDNA yk20f8.5; coded for by C. elegans cDNA yk16g12....		UNCLASSIFIED	35696286, 22278988, 264905, 264511, 285007, 265008, 60433438, 264288, 264686, 21908769, 265020, 264692, 35695855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gij3881545[emb]CAA93779] - (Z68904) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	94232191 (4721, 4722)	Novel Protein sim. GBank gij746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278985, 22278989, 264512, 265009, 264757, 21908765, 65274820, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	01721193 (4723, 4724)	Novel Protein sim. GBank gll1171093[sp]P19706[MYSB.ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)]		UNCLASSIFIED	22278998, 264259, 28331822, 29331824, 60432289, 284509, 264512, 60432229, 60433356, 264448, 264682, 264683, 264369, 21906785, 21906788, 21906789, 60432113, 22279000, 22279002 264907, 264628, 264635
2363	95006635 (4725, 4728)	Novel Protein sim. GBank gll854065[emb][CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gll5639830[gb]AAD45886.1[AF14601] - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278998, 56994075, 3569288, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21906754, 87168474, 265010, 87168559, 264603, 265017, 265018, 265019, 264760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264766, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35698423, 35698585, 264635, 264558, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56528486, 264482, 264564, 264486, 22278998, 22278998, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264687, 264689, 21906785, 21906787, 21906788, 21906789, 265021, 33657023, 33657109, 83373044, 264568
2365	94140746 (4728, 4730)	Novel Protein sim. GBank gll1840045 (U49082) - transporter protein [Homo sapiens]		transport	
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264568
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gll1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35698286, 21906788, 55810764, 65274791, 284587 264628
2368	94322190 (4735, 4736)				

2369	94314334 (4737, 4738)	Novel Protein sim. GBank gij5360901[dbj]BAA82158.1] - (AB029343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52644507, 52646842, 35698286, 264092, 264094, 52645080, 35698052, 264107, 29331830, 52644045, 265008, 265007, 265009, 52644298, 52644229, 264689, 21906765, 21906766, 35695917, 265020, 52644150, 263987, 33657108, 27486285, 35695763, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385, 264508, 264809, 264596, 264369
2370	79804120 (4739, 4740)			UNCLASSIFIED	
2371	57280408 (4741, 4742)			UNCLASSIFIED	
2372	87642413 (4743, 4744)			UNCLASSIFIED	
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gij4589592[dbj]BAA76813.1] - (AB023186) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	263967, 263981
2374	94123885 (4747, 4748)	Novel Protein sim. GBank gij5105131[dbj]BAA80445.1] - (AP000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exonuclease family	UNCLASSIFIED	264634, 60432113 265008, 265007, 265008, 265009, 265011, 264766, 35695917, 35695855, 263981, 264557, 264585
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gij1351115[sp]P47759[SRPB MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)]		UNCLASSIFIED	60432048, 29331824, 264907, 52644045, 264512, 60433356, 21908754, 52644288, 87188559, 264448, 21908765, 21908768, 21908769, 33657023, 18108368, 55811576, 52644332
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gij2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	ATPase-associated	264259, 29331830, 264909, 264910, 285009, 60433438, 21908754, 265017, 265018, 265019, 264682, 264288, 264685, 21908767, 263972, 35695855, 87168518, 60432113
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gij5257005[gb]AAD41239.1] - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	18108394, 65274572, 22278987, 22278989, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29146499, 284509, 265006, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 264764, 264288, 21908767, 21908768, 29148627, 29148628, 265021, 33657023, 33657108, 18108370, 18108374, 18108378, 35698423, 264556, 83373044, 18108385, 18108388, 55526466, 22278000, 22278002, 264583
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gij1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35698286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433358, 87168474, 265011, 265018, 264288, 21908765, 33657023, 264557, 56182323, 83373044, 18108385, 22278002, 264482
2378	65444324 (4757, 4758)	Novel Protein sim. GBank gij3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	265017, 264288, 21908768

2380	86923062 (4759, 4760)	Novel Protein sim. GBank gi 4502899 ref NP_001845.1 pCOL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87600241 (4761, 4762)	Novel Protein sim. GBank gi 4455609 emb CAB36555 - (AL031846) dJ742C18.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR)romatin Organization Modifier domain	helicase	56182575, 264091, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264683, 264288, 264685, 264686, 264687, 264691, 264692, 264693, 55811578, 264636, 264567
2382	91225982 (4763, 4764)	Novel Protein sim. GBank gi 4325130 gb AAD17276 - (AF119716) dML-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	26331824, 60432289, 264895, 264596, 21906754, 264789, 265022, 264693, 263867, 33657109, 264629, 264631, 264558, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi 1902982 db BAA19005 - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	265009, 21906765, 21906766
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gi 2462851 (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	struct	264488, 52644507, 52645156, 52646365, 35696286, 22278999, 52645080, 29331824, 29331826, 35696052, 29331828, 264906, 264928, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264558, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95418485 (4769, 4770)			UNCLASSIFIED	264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	64742848 (4771, 4772)	Novel Protein sim. GBank gi 4029899 gb AAD34110.1 AF151873 CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 26146488, 264112, 264511, 60170831, 60432229, 264595, 60433438, 87168474, 87168559, 264682, 21906765, 21906766, 21906767, 21906768, 26146629, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14987890 (4773, 4774)			UNCLASSIFIED	284634
2388	11424604 (4776, 4778)			UNCLASSIFIED	284595
2389	95310850 (4777, 4778)	Novel Protein sim. GBank gij4758059jrefjNP_004372.1pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED dna_rna_bind	284488, 22278998, 22278999, 284508, 284905, 284908, 284907, 284908, 284909, 285008, 284511, 284512, 284910, 284591, 21908754, 284601, 284604, 284761, 18108351, 284764, 284288, 284766, 284768, 284769, 21906765, 21908768, 284892, 284693, 35698423, 284635, 284638, 284555, 8337304, 22278000, 284488
2390	94320912 (4778, 4780)	Novel Protein sim. GBank gij1644239jdbjBAA122231 - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	52644507, 56182576, 22278995, 35698286, 22278998, 22278997, 22278999, 29331822, 29331825, 29331826, 35696052, 284905, 52844045, 285009, 284758, 284759, 33109954, 52644296, 85656542, 285011, 265017, 265018, 284605, 52844229, 21906765, 21906767, 21906768, 21906769, 35695917, 52844150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35698423, 35695855, 284555, 52644332, 56182323, 60170394, 83373044, 56526488
2391	80036184 (4781, 4782)			UNCLASSIFIED	263976
2392	84245016 (4783, 4784)	Novel Protein sim. GBank gij4240159jdbjBAA74863.11 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	35698286, 35698052, 284508, 284905, 284509, 284908, 284907, 284908, 284909, 284510, 284511, 284512, 284910, 285009, 284591, 284758, 284600, 284604, 284762, 284448, 284764, 284369, 284766, 284786, 284769, 284689, 35695917, 264629, 18108374, 263978, 35698423, 35695855, 284631, 284634, 284635, 284638, 284637, 284638, 60170394, 284639, 284565, 284486

2393	95302833 (4785, 4786)	Novel Protein sim. GBank gij4508667[je]NP_000993.1[prPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - ribosomal prot Ribosomal protein L10	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 35698286, 22278996, 22278997, 22278998, 264093, 60432049, 264259, 29331822, 29147620, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146499, 264508, 264509, 264905, 264907, 264908, 66712502, 52644045, 264828, 264909, 58182435, 264112, 264113, 264510, 265008, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52846317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264369, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21906785, 21908766, 21808767, 21908768, 21908769, 55811957, 26148629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108368, 27486261, 27486282, 33657349, 35695763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35698423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265008, 264592, 55811386, 265010, 265011, 265017, 265018, 264448, 264683, 264288, 21908765, 21908768, 21908769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264564, 264568, 264567
2394	94323266 (4787, 4788)	Novel Protein sim. GBank gij4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q98676 (PID:g3025333) [Homo sapiens]	Contains protein domain (PF00086) - zinc finger, C2H2 type	264259, 29331824, 264910, 264288, 265021, 93373044, 18108387, 264563, 264568
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gij5712756[gib]AAD47636.1[AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]	dna_ma_bind	

2398	195086700 (4791, 4792)	Novel Protein sim. GBank gij106322[pri]B34087 - hypothetical protein (L1H 3' region) - human	(Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	52846365, 18108397, 56182575, 35698286, 22278997, 22278999, 60432049, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284110, 60170831, 29331830, 68712502, 284110, 60170831, 284591, 33857402, 60433438, 55812038, 33109954, 21806754, 33857084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 284768, 52844228, 21808768, 21908767, 265020, 285021, 60170615, 284692, 33857023, 65274620, 52845129, 33657182, 27488262, 27488264, 27488265, 284629, 18108374, 35698423, 35698555, 284631, 284558, 52844332, 284558, 83373044, 18108388, 87168518, 22279002, 284482
2397	87280854 (4793, 4794)				52844507, 52645156, 56182575, 264259, 28147620, 284905, 284907, 284908, 284909, 284910, 284758, 52644286, 284603, 284604, 284762, 284681, 284764, 18108357, 284769, 21808768, 264693, 264628, 264635, 264638, 284639, 284564
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gij3258609 (AC005178) - H53_GS1 [Homo sapiens]		UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gij786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 68714117, 60432289, 284906, 29331830, 58182435, 284112, 284910, 33109954, 21806764, 87168474, 284600, 285017, 285018, 265019, 264764, 264765, 21806765, 21806766, 21806767, 21806769, 35895917, 285020, 265022, 60170815, 33657023, 18108370, 18108374, 284558, 60170394, 284558, 87168518, 22279000, 22279002, 284564, 284566, 284487
2400	91214118 (4799, 4800)	Novel Protein sim. GBank gij2352822[gbi]AAB69285.1] - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	21808768, 52846842, 56994075, 33657182, 27488262, 52844298, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gij2352822[gijAAB6285.1] - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	52644507, 52645156, 52644228, 264688, 21908764, 21908765, 52646385, 52646842, 21908766, 21908767, 21908768, 22278995, 35695917, 56894075, 35696286, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33657109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486261, 27486262, 33656970, 33657349, 27486265, 35695763, 264108, 264905, 35696423, 35695855, 265006, 265007, 265008, 265009, 264637, 52644332, 55612038, 52646317, 18108385, 52644298, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264583, 264288, 264807, 264908, 264809, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gij4689258[gijAAD27832.1]AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]		
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gij4929575[gijAAD34048.1]AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00002) - C-type lysozyme/alpha-lactalbumin family	22278999, 35696052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gij2315798 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	35696286, 29331826, 35696052, 265008, 265018, 21908769, 264564
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gij464178[dbj]BAA03581 - (D14853) polyprotein [Hepatitis C virus]	UNCLASSIFIED	35696286, 29331822, 265007, 21908754, 265017, 265018, 265019, 264763, 264369, 21908765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88084501 (4811, 4812)	Novel Protein sim. GBank gij2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264108, 264908, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264369, 264685, 264686, 21908768, 21908769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563
2407	79465005 (4813, 4814)			264686, 264688
2408	87391503 (4815, 4816)	Novel Protein sim. GBank gij423442[pri]S33513 - gene F1f protein - mouse	UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gij1176001spIP45988 YNZ6, CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29146488, 52644045, 60433436, 33657084, 87168474, 264760, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281069, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518, 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gij4966262 gb AAC48052.2 - (UBA849) Contains similarity to Plam domain: PF00646 (F-box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gij3114713 (AF061346) - Edp1 protein [Mus musculus]		Inf	29331824, 29331827, 29331828, 264764, 264369, 33657109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gij5410336 gb AAD43038.1 - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_na_bind	22278998, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21906766, 265020, 33657109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gij5262705 emb CAB45778.1 - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264488, 264259, 29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264682, 264764, 264766, 264686, 264768, 264688, 265021, 33657023, 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264564, 264565, 264566, 264567, 264488, 52645156, 52646842, 52646385, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433356, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22279002
2414	94312590 (4827, 4828)	Novel Protein sim. GBank gij1082340 ptr S52863 - DNA-binding protein R kappa B - human		ubiquitin	

2415	88089002 (4828, 4830)	Novel Protein sim. GBank gij423915 pir jA45439 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	264259, 264908, 60433356, 33557402, 21906754, 265018, 264687, 264689, 21906769, 55811857, 265021, 264690, 264691, 33657023, 264693, 35698423, 58182323, 56526486
2416	94118358 (4831, 4832)	Novel Protein sim. GBank gij3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gij1084944 pir jS54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gij1176572 pir j45895 YNA4 CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR.2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60432289, 29331828, 264905, 264907, 264511, 265009, 60432229, 21906754, 87168558, 265019, 264682, 21906768, 21906769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264566
2419	82374248 (4837, 4838)	Novel Protein sim. GBank gij284006 pir jS18732 - autoantigen, 64K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264558, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gij107621 pir jS50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	57805345 (4841, 4842)	Novel Protein sim. GBank gij2224567 dbj BAA20772] - (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gij4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	transport	18108392, 18108394, 18108398, 264806, 265006, 265010, 18108351, 18108374, 18108385
2423	88058380 (4845, 4846)	Novel Protein sim. GBank gij4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 60432049, 29331822, 29331826, 60432289, 29331828, 265008, 265009, 60433356, 21906754, 265017, 265018, 265019, 21906766, 21906768, 21906769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gij2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278997, 60432049, 264259, 29331828, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265018, 264766, 21906768, 55811857, 264692, 33657023, 33657109, 55811576, 56182323, 63373044, 18108385, 18108388, 60432113, 22278000
2425	87415901 (4849, 4850)	Novel Protein sim. GBank gij2077932 dbj BAA19878] - (D85556) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gij2039368 gb AA853003.1] - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21906767, 18108370, 18108374, 263976

2427	87622893 (4853, 4854)	Novel Protein sim. GBank gij4680895jgbjAAD27737.1 AF13296 - (AF132862) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	264259, 20281098, 35686052, 265008, 264584, 285011, 264760, 18108351, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21900766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gij1537070 (U63840) - nucleoprotein p54 [Rattus norvegicus]		22276896, 22278999, 35686052, 21906754, 264288, 21908765, 21908768, 21908769, 35695917, 265020, 263972, 22279002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gij601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	22278999, 29331824, 264606, 264809, 264511, 265009, 21906754, 265017, 265018, 265019, 264448, 264683, 264288, 21908765, 21908768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)		UNCLASSIFIED	264112, 264681
2431	87648884 (4861, 4862)	Novel Protein sim. GBank gij3860729jembjCAA14630j - (AJ235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein	29331826, 29331827, 35696052, 29146499, 264905, 264806, 264681, 264288, 264689, 21908765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gij3878387jembjCAA93287j - (Z69360) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89268 comes from this gene; cDNA EST yk295b8.5 comes from this gene [Caenorhabditis elegans]	protease	264634, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gij2224593jdbjBAA20784j - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264569, 264805, 265018, 264762, 264683, 264681, 264558, 264557, 264639, 264558 264563
2434	19520148 (4867, 4868)		UNCLASSIFIED	264555
2435	20759044 (4869, 4870)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]	UNCLASSIFIED	265008, 264758, 265010, 264689, 27486281, 263972, 18108374, 18108381
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gij3641352 (AF091234) - putative transcription factor [Mus musculus]	UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264585
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gij3860014 (AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	29331826, 264508, 264805, 264509, 264806, 264907, 264908, 264809, 264511, 265008, 264512, 264910, 265009, 264591, 33857402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35695917, 33857023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264584, 264585, 264566, 264567

2439	94850950 (4877, 4878)	Novel Protein sim. GBank gi4263519 gb A015345 - (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182575, 56181686, 56994075, 22278996, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 68714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 264509, 264906, 264908, 52644045, 60431735, 33109954, 21906754, 33657084, 55811386, 52644296, 87169474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644228, 56181582, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 33657109, 33657182, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 60431528, 263977, 55810764, 35696423, 65274791, 35695855, 60431850, 56182323, 60432113, 22278900, 22279002, 264567
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264639, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gi3024889 sp P56524 Y288 HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (H46116)	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278986, 22278989, 29331822, 264768, 264693
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gi4508013 ref NP_002703.1 pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264906
2443	84305948 (4885, 4886)	Novel Protein sim. GBank gi1170658 sp Q02975 KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)		UNCLASSIFIED	
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gi4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264259, 18108382, 18108383, 18108385, 22279000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gi2135950 pri S58222 - PQ-rich protein - human			264259, 35696052, 264369, 18108381
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gi4753887 emb CAA05409.2 - (AJ002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845148 (4893, 4894)	Novel Protein sim. GBank gi4885613 ref NP_005409.1 pST5 - suppression of tumorigenicity 5	cadherin		56182575, 264259, 29331824, 29331826, 29331827, 60433356, 60433438, 284758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4896)			UNCLASSIFIED	22278986, 22278987, 22278989, 28331828, 3586052, 264107, 264110, 87168474, 87168559, 18108351, 21908767, 21908769, 27488262, 263978
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gij1728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		cadherin	264259, 264628, 265007, 264595, 265021, 56526486
2450	86597784 (4899, 4900)			UNCLASSIFIED	264906
2451	91014563 (4901, 4902)	Novel Protein sim. GBank gij1710021 sp P35280 RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	glycoprotein	264083, 28331822, 28331824, 28331825, 66714117, 28331826, 28331828, 3588052, 284907, 66712502, 28331830, 264810, 285009, 264758, 285017, 265018, 264762, 264448, 264288, 21908767, 265021, 33857023, 264693, 33857109, 263959, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gij1504034 dbj BAA13216 - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264583
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gij2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369908) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nglrecep	264509, 264512, 18108385
2454	95310891 (4907, 4908)	Novel Protein sim. GBank gij1076802 pir S49915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263894, 66714117, 28331827, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264686, 264768, 264769, 264534, 264691, 264692, 33857023, 264693, 33857109, 264628, 263978, 35895855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264488
2455	85288301 (4909, 4910)	Novel Protein sim. GBank gij543817 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278986, 264259, 3588052, 264905, 264908, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264688, 21908766, 21908767, 21908769, 29148829, 35895917, 265020, 265022, 33857023, 33857109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264566, 264567
2459	88168700 (4911, 4912)	Novel Protein sim. GBank gij2588630 (AC003079) - Ankyrin-like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank glj3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	56181686, 264905, 264907, 264511, 264596, 55811386, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526486, 264563
2458	85875304 (4915, 4916)	Novel Protein sim. GBank glj2384942 (AF022885) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264693, 264634, 264559
2459	87551813 (4917, 4918)	Novel Protein sim. GBank glj5441942gbjAAD43187.1 (AC004997) supported by mouse EST AA538043 (NID: g2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank glj4929701gbjAAD34111.1 (AF15187) - (AF151874) CGI-116 protein [Homo sapiens]		kinase	65274572, 35696286, 22278996, 22278987, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 29148499, 264102, 264109, 60433438, 265017, 265018, 265019, 264288, 21908765, 21908766, 21908769, 35695917, 265020, 264691, 33657023, 27486261, 18108374, 35695855, 87168518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank glj4426962gbjAAD20633] - (AF128062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86988002 (4923, 4924)	Novel Protein sim. GBank glj5420387embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			264809, 264758, 264684, 18108374, 264637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank glj5052516gbjAAD38588.1 (AF14561) - (AF145613) BcdNA.GH03108 [Drosophila melanogaster]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91218957 (4927, 4928)	Novel Protein sim. GBank glj5410300gbjAAD43021.1] - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	protease	264489, 52846842, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35698052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52648317, 33109954, 33657084, 265017, 265018, 265019, 264782, 264448, 264764, 264288, 264766, 21906765, 21906766, 21908767, 21908768, 21908769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22279002, 264486

2465	85357483 (4928, 4930)	Novel Protein sim. GBank gij4508401refjNP_002871.1 pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00068) - Eukaryotic protein kinase domain	oncogene	18108392, 52644507, 52645156, 52846365, 22278994, 22278995, 35696288, 22278996, 22278998, 264259, 29331822, 29331824, 29331825, 60424269, 60432289, 29331827, 35696052, 29331828, 284907, 29331830, 52844045, 264809, 56182435, 264511, 265007, 265008, 265009, 264910, 33857402, 60433438, 55812038, 21906754, 33109854, 265010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264389, 264288, 264685, 264767, 21908765, 21908767, 21908768, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 52645129, 33657109, 27486261, 27486284, 35695763, 264628, 263972, 18108374, 35695855, 264636, 264637, 60170394, 56526486, 87168518, 60432113, 264563, 264564, 264566, 264487 264389
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gij4321619 gb AAD15788.1 - (AF051098) seven transmembrane domain orphan receptor (Mus musculus)			
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gij3513300 (AC005595) - F16601.1, partial CDS [Homo sapiens]		UNCLASSIFIED	56894075, 2644908, 21908768, 33657023
2468	87614898 (4935, 4936)	Novel Protein sim. GBank gij2143455 gij 56106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	29331824, 52644045, 265008, 264910, 265019, 21908765, 21908769, 265021 264288, 264628
2469	88294397 (4937, 4938)	Novel Protein sim. GBank gij5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gij5419882 emb CAB46424.1 - (AL086749) DKFZp434G153 [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811578, 56182323
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gij4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]		UNCLASSIFIED	264092, 60432048, 29331825, 60433356, 265010, 265011, 18108351, 264764, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gij4538009 emb CAB39630.1 - (AL040481) putative protein [Arabidopsis thaliana]			60424179, 65274572, 22278998, 60424269, 29331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gij3252827 (AC004382) - Unknown gene product [Homo sapiens]			65274572, 56894075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264693, 264369, 265020, 264693, 264563, 264564

2475	94321683 (4949, 4950)	Novel Protein sim. GBank gi1216468 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain (PF00008) - tgf EGF-like domain	264259, 29331822, 265008, 265007, 265010, 265011, 264448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108362, 264693, 18108370, 18108374, 18108379, 35696423, 83373044, 18108383, 18108385, 264564, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gi13252827 (AC004382) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	264259, 60424269, 66714117, 264905, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21906767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)		UNCLASSIFIED	263978
2478	17659165 (4955, 4956)		UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gi1644232 [dbj BAA11082] - (D67066) N-WASP [Bos taurus]	Im7	56994075, 22278999, 21906754, 264682, 21906785
2480	95295605 (4959, 4960)		UNCLASSIFIED	264905, 264807, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gi15689459 [dbj BAA83018.1] - (AB028989) KIAA1068 protein [Homo sapiens]	collagen	55274572, 56182575, 22278997, 264084, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264508, 264905, 264908, 264907, 264908, 52644045, 264909, 56182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 264288, 264766, 264686, 264768, 21906768, 55811957, 265020, 264691, 264692, 264693, 264629, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gi1321249 [pir J28407] - guanine nucleotide-exchange activator CDC25 homolog - mouse	UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264693, 264631, 264632, 264636, 264638, 264639, 264583
2483	87731583 (4965, 4966)		UNCLASSIFIED	264488, 22278995, 264083, 264085, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108386, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gi1728831 [sp P39188] ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	kinase	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gi1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 264769, 264689, 35695917, 265022, 264692, 264693, 56182323

2486	87748878 (4871, 4872)	Novel Protein sim. GBank gi 2662167 dbj BAA23715 - (AB007803) KIAA0443 [Homo sapiens]			265017, 264555
2487	95343105 (4873, 4874)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264106, 264905, 264907, 29331830, 264908, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109954, 87168559, 265018, 264681, 264288, 264687, 21906765, 21908766, 21906767, 21908768, 21908769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35696423, 35696855, 60170394, 18108385, 56526486, 22278000, 22279002, 264563, 264482, 264565, 20281169, 18108391, 264910, 264448, 264288, 264684, 264691, 264634
2488	87652451 (4875, 4876)			UNCLASSIFIED	264886, 264693, 55811576, 22278002
2489	82890585 (4877, 4878)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1 - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complement receptor	264907, 265008, 22278002
2490	88068609 (4879, 4880)	Novel Protein sim. GBank gi 2586624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2491	91242116 (4881, 4882)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		Im7	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21906764, 21906768, 264692, 60431528, 87168518, 60432113, 22278000
2492	95308202 (4883, 4884)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcript factor	

2483	95422415 (4885, 4988)	Novel Protein sim. GBank gij4240307[dj]BAA74932.1] - (AB020718) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - struct R3H domain	18108394, 264807, 65274572, 56182575, 22278995, 56994075, 60432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29148488, 264508, 264805, 264805, 264509, 264906, 264907, 29331830, 264909, 264510, 265008, 264511, 265007, 264512, 265008, 265009, 264910, 21908754, 265011, 264600, 265017, 265018, 264604, 264805, 265019, 55811150, 264762, 18108351, 264881, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 264691, 264892, 33657023, 33657349, 18108370, 18108374, 18108376, 55810764, 18108379, 55274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22278000, 22279002, 264482, 264566, 264486
2484	30793118 (4887, 4988)	Novel Protein sim. GBank gij5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED collagen	263894, 22278997, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264766, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811576, 264636, 264637, 18108385, 22279000, 264584, 264567, 264486
2485	94234551 (4889, 4990)	Novel Protein sim. GBank gij4808220[emb]CAB42832.1] - (AL022316) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]	struct	29147620, 264905, 265008, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2486	80018765 (4991, 4992)	Novel Protein sim. GBank gij1200503 (U47824) - B [Homo sapiens]	UNCLASSIFIED	52644507, 22278996, 22278999, 29331824, 29331828, 33657402, 21908754, 87168474, 265019, 264369, 264689, 21908765, 21908766, 21908767, 21908768, 265020, 33657023, 18108376, 18108387
2487	61723554 (4993, 4994)	Novel Protein sim. GBank gij3510234 (AC005581) - R31237_1, partial CDS [Homo sapiens]	UNCLASSIFIED	29331827, 264512, 264910, 264288, 18108374, 35695855
2488	67724033 (4995, 4996)	Novel Protein sim. GBank gij3510234 (AC005581) - R31237_1, partial CDS [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	264909, 55812038, 264631, 264637, 264558

2500	94640324 (4999, 5000)	Novel Protein sim. GBank gij3881275[emb]CAA21725] - (A032655) predicted using GeneFinder; similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52844507, 52845156, 22278995, 56994075, 35698286, 22278998, 264259, 52845080, 29331824, 29331825, 66714117, 60432289, 29331828, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644298, 87168474, 87168559, 264603, 264681, 264448, 264683, 264288, 264369, 52644229, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 33657182, 35695763, 35698423, 35698585, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303898 (5001, 5002)	Novel Protein sim. GBank gij4928615[gb]AAD34068.1[AF15183] CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	65274572, 56182575, 35698286, 22278998, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35698052, 264905, 264808, 264907, 264808, 264809, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264598, 87168474, 87168559, 264600, 264601, 264802, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264369, 264288, 264768, 18108357, 21906765, 21906766, 21906767, 21906769, 29148628, 35695917, 264692, 33657023, 264829, 35698423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264566
2502	90893716 (5003, 5004)	Novel Protein sim. GBank gij3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like, similar to P22059 (PID:g129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxyesterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264892, 33657109, 263873, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gij2196674[emb]CAA72638] - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868708 (5007, 5008)	Novel Protein sim. GBank gij550420[emb][CAA48220] - (XG8101) trg [Rattus norvegicus]			264488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331826, 29331826, 29331827, 35696052, 264808, 264808, 52644045, 265009, 60433356, 33657402, 60433348, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264766, 52644228, 21906765, 21906766, 21906767, 21906768, 52644150, 264682, 27486261, 27486282, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)				
2506	81232326 (5011, 5012)	Novel Protein sim. GBank gij2137562[pir][49835 - mouse Dhm1 protein - mouse		UNCLASSIFIED	264605
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gij5174489[ref][NP_006035.1]pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	nuclease	264488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278998, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331826, 29331828, 264509, 56182435, 264112, 264593, 60433356, 55812038, 21906764, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170815, 33657023, 27486264, 18108378, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gij4826433[emb][CAB42889.1] - (AL031447) dJ126A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		histone	264488, 263994, 264592, 264595, 264369, 264688, 264768, 35695917, 35696423, 264583
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264583, 264565
				UNCLASSIFIED	265007, 265008, 18108357, 264556, 264567

2510	95421378 (5018, 5020)	Novel Protein sim. GBank gl 3293537 gb AAC25762.1 - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_rna_bind	65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432228, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21906767, 21906768, 21906769, 55811857, 35695917, 265020, 265022, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27488262, 33657348, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 222789002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gl 4323152 gb AAD16228.1 - (AF098863) Ets-protein Sp1-C [Mus musculus]			
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gl 4502075 ref NP_001135.1 pAMFR - autocrine motility factor receptor	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264259, 29331825, 29331826, 29146499, 264907, 264909, 265008, 264591, 60432229, 21906754, 264763, 264683, 264768, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gl 3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424178, 52845156, 18108394, 22278994, 35696286, 56984075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108368, 33657109, 27486261, 27486262, 33657349, 18108374, 55810764, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gl 2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87894508 (5029, 5030)	Novel Protein sim. GBank gl 375772 emb CAA18783 - (AL022727) dJ80119.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	Contains protein domain (PF000001) - 7 transmembrane receptor (rhodopsin family)	-tm7	
2516	87786808 (5031, 5032)			UNCLASSIFIED	264259, 28146498, 264905, 264288, 29146829, 35695917, 27486261, 264634
2517	87784866 (5033, 5034)	Novel Protein sim. GBank gl 4220527 emb CAA23000 - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264805, 264908, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5038)	Novel Protein sim. GBank gi 4928591 gb AAD34058.1 AF151818 - (AF151818) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 264909, 284511, 265007, 60432229, 60433356, 60433438, 55812038, 265010, 265017, 264448, 264288, 264889, 21906768, 21906769, 265022, 52644150, 264893, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 264088, 264259, 66714117, 29331826, 29331827, 29331828, 264907, 66712502, 265008, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22279002, 264584, 264259, 264908, 264910, 264682, 21906769, 265020, 264583
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gi 4263748 gb AAD15420 - (AC004883) similar to KIA0766; similar to PID:g3882253 [Homo sapiens]	kinase		
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	transport		
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gi 5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	histone		264488, 264489, 263994, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265008, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264595, 264566, 264567
2522	87764052 (5043, 5044)	Novel Protein sim. GBank gi 4580011 gb AAD24201.1 U81002 - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		264489, 22278997, 20281171, 21806754, 35695917, 263987, 263978, 263981, 20281169
2523	95340487 (5045, 5046)	Novel Protein sim. GBank gi 1609327 (U76374) - skm-BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		263969
2524	95340489 (5047, 5048)				56994075, 22278986, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87188559, 265019, 264288, 21906765, 21906769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486261, 35696423, 65274791, 264559, 83373044, 56526486, 87188518, 264567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gij2073564 (U80223) - eukaryotic initiation factor eif-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278987, 22278988, 60432049, 60432289, 29331828, 264905, 265008, 55812038, 21908764, 265018, 284369, 21908765, 21908766, 21908767, 21908769, 35695917, 265020, 265021, 33857109, 60431528, 83373044, 60432113, 22279000, 22279002, 284565
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gij4589828[dijBAA76836.1] - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	60424179, 264768, 264687, 264769, 264689, 65274572, 21906767, 58182575, 21908768, 21908769, 55811857, 22278994, 22278995, 35696286, 35695917, 22278996, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33657023, 29331822, 29331824, 60432289, 29331828, 29331827, 29331828, 27486262, 264508, 264509, 264905, 284907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35696423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264598, 264758, 83373044, 52846317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264568, 264289, 264488, 264587, 264769
2527	88084580 (5053, 5054)	Novel Protein sim. GBank gij2258437 (AF008197) - synocollin [Rattus norvegicus]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gij2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2529	86870926 (5057, 5058)	Novel Protein sim. GBank gij3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	264908, 264769, 265020, 265021, 18108383
2530	80259878 (5059, 5060)				264359, 264556
2531	87768931 (5061, 5062)			UNCLASSIFIED	29331822, 29331824, 60432289, 264508, 264509, 264908, 265011, 264769, 21908768, 33657023, 87168518, 22279000
2532	87419778 (5083, 5084)	Novel Protein sim. GBank gij2864625[embjCAA18972] - (AL021811) putative protein [Arabidopsis thaliana]			264593
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gij437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264555

2534	87332322 (5087, 5088)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21908769, 265020, 265022, 33657109, 22279000
2535	91225056 (5069, 5070)	Novel Protein sim. GBank gi 4488311 (emb CAB37992) - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696286, 60432289, 29331828, 66712502, 265006, 60432229, 265017, 265018, 265019, 264288, 264369, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gi 728836 P39193 ALU8_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	Kinase		18108398, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264769, 264689, 21906765, 21906766, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gi 4557026 ref NP_003913.1 pHERC - guanine nucleotide exchange factor p532	ubiquitin		65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265011, 264760, 264288, 264685, 35695917, 60170815, 264691, 33657023, 65274620, 33657109, 18108374, 35696423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)			UNCLASSIFIED	
2539	94144916 (5077, 5078)			UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264885, 264768, 87168518, 22279000, 264565, 264568
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gi 1362647 pir J53876 - sex-regulated protein Janus A - fruit fly (Drosophila pseudoobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gi 1711658 P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264681, 264639, 29331824, 264603, 264604, 264805, 264907, 264908, 264768

2542	95288162 (5083, 5084)	Novel Protein sim. GBank gi 5225320 gb AAD40850.1 AF08310 - (AF083107) siritin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophysial hormones, N- terminal Domain	UNCLASSIFIED	284488, 18108394, 52846385, 52846842, 65274572, 22278994, 35898286, 22278998, 284259, 52845080, 29331822, 29331824, 29331827, 35898052, 33656870, 264907, 284909, 52844045, 284510, 265008, 284512, 285007, 265008, 265009, 264810, 60431735, 52846317, 52844288, 285010, 265011, 265018, 265019, 18108351, 264683, 264288, 284685, 264687, 52844229, 264769, 21908766, 21908767, 21908769, 52844150, 33657023, 33657109, 52845129, 33657182, 27486261, 27486264, 33657349, 35695763, 18108374, 35696423, 35695855, 264631, 284634, 284635, 284558, 83373044, 18108385, 18108387, 87168518, 264563, 284584
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gi 5419857 emb CAB46374.1 - (AL086723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	65274572, 56182575, 22278999, 264259, 29331826, 264907, 264510, 264511, 264592, 264595, 264784, 264389, 264288, 264684, 264766, 264689, 21908765, 21908767, 21908769, 60170815, 264692, 264693, 55811576, 65274791, 264636, 264558, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim. GBank gi 2488110 sp Q63191 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52846385, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 284905, 264808, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264686, 264687, 264689, 21806765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 284482, 264563, 264567
2545	87742845 (5089, 5090)	Novel Protein sim. GBank gi 3327046 dbj BAA31591 - (AB014516) KIAA0616 protein [Homo sapiens]			28331825, 264806, 265009, 60170831, 265017, 264369, 21906767, 60170815, 264692, 33657109
2546	88093861 (5091, 5092)	Novel Protein sim. GBank gi 2896032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143868 (5093, 5094)	Novel Protein sim. GBank gi 4929607 gb AAD34084.1 AF151827 CGI-68 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 56182575, 22278985, 56994075, 22278986, 22278987, 22278988, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35696052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265008, 265007, 264512, 265008, 265009, 60170831, 60432228, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906765, 21906766, 21908767, 21906768, 29148627, 21906769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27486261, 18108370, 18108374, 55810764, 55811576, 35696423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87168518, 22278002, 264564, 264566, 264488
2548	88179079 (5095, 5096)			UNCLASSIFIED	264488, 18108384, 52646365, 22278994, 35696286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433358, 87188559, 264684, 264369, 52644229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264563, 264567
2549	94196083 (5097, 5098)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278986, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21908764, 21908765, 21906766, 21908767, 21908769, 265020, 265021, 52644150, 264691, 18108368, 60431602, 18108376, 35696423, 56182323, 18108387, 264567, 56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638
2550	87778584 (5099, 5100)	Novel Protein sim. GBank gi 2143886 pir J52523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gll4337103 gb AAD18079 - (AF129756) NG26 [Homo sapiens]		Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21806754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 264693, 33657109, 35698423, 264638, 56182323, 83373044, 22279000
2552	95332820 (5103, 5104)				UNCLASSIFIED	56182375, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35698423, 35695955, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gll171858 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION			UNCLASSIFIED	264686, 264488, 263976, 264768, 29331826, 35696052, 35698423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264762, 264906, 264592, 264891, 264586, 264908, 264684, 264567, 264909, 264768
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gll728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII			cadherin	22278997, 29331822, 264508, 21906769, 33657023, 33657109, 56182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gll4894319 emb CAB43280.1 - (AL050084) hypothetical protein [Homo sapiens]			nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gll4106984 (AC003038) - R30923_1 [Homo sapiens]		Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695955, 264558, 264567
2557	79437803 (5113, 5114)					264595
2558	87617581 (5115, 5116)	Novel Protein sim. GBank gll119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN			UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2559	88086382 (5117, 5118)	Novel Protein sim. GBank gll4538998 emb CAB39619.1 - (AL049481) AIG1-like protein [Arabidopsis thaliana]			UNCLASSIFIED	22278997, 29331822, 29331826, 60433358, 265011, 264288, 264765, 264766, 264769, 21808765, 21906766, 60432113, 264482
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gll5051399 emb CAB44995.1 - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE protein)) [Mus musculus]		Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gll5326825 gb AAD42050.1 AF044953 - (AF044953) NADH:ubiquinone oxidoreductase PCIV subunit [Homo sapiens]			UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432228, 87168558, 265017, 265018, 265019, 264689, 21906766, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264559, 18108385, 87168518, 22279002

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gij4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278998, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21906765, 55811957, 60170815, 33657023, 264693, 35695855, 87188518, 264488, 35686286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264586, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gij4886447[emb]CAB43371.1) - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264488, 35686286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264586, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gij1352944[sp]P47179YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR		sulfotransferase	264488, 35686286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21908767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264586, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2565	85530908 (5129, 5130)	Novel Protein sim. GBank gij628012[pr]A53933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - struct	UNCLASSIFIED	66714117, 264909, 263978, 264632, 18108370, 35695855, 264556, 264558, 18108383
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gij628012[pr]A53933 - myosin I myr 4 - rat	Myosin head (motor domain)		265020, 60170615
2567	86143590 (5133, 5134)	Novel Protein sim. GBank gij466009[sp]P34548YJN4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	60424179, 18108394, 56181888, 56894075, 22278999, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21908766, 21908767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810764, 18108378, 83373044, 18108385, 60432113, 264482
2568	91233099 (5135, 5136)	Novel Protein sim. GBank gij466009[sp]P34548YJN4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III			

2569	95313784 (5137, 5138)	Novel Protein sim. GBank gij2599560 gijAABB4166.1 - (AF029874) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP Transcription factor	transcription factor	18108394, 56182575, 56181886, 22278995, 22278986, 56994075, 35696286, 22278997, 22278998, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264805, 264808, 56182435, 265008, 265009, 264910, 60432228, 264592, 60433356, 60433438, 21808754, 87168558, 265017, 265018, 265019, 264682, 264448, 264288, 21808765, 21808768, 21808767, 21808768, 29148627, 21808769, 35695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263987, 35695763, 20281089, 263974, 18108374, 55810784, 35698423, 35698555, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56528488, 87168518, 22279000, 22279002, 264568
2570	94136784 (5139, 5140)	Novel Protein sim. GBank gij4758954 ref NP_004567.1 pPPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278996, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264688, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264638, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gij732218 pIP34609 YO60_CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III		struct	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gij4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21808754, 29148627, 29148628, 263972, 263974, 18108374, 263978, 35695855, 60170394, 264559, 18108385

2573	95313928 (5145, 5146)	Novel Protein sim. GBank gi 399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 60424179, 65274572, 56182575, 56181686, 22278895, 56994075, 22278987, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21908754, 87188474, 265010, 265011, 87168558, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 58181562, 264689, 21908765, 21908766, 21908767, 29148627, 21908768, 21908769, 265020, 265021, 265022, 60170615, 264690, 52844150, 264691, 264692, 33657023, 65274820, 18108365, 18108368, 27488265, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 58182323, 60170394, 83373044, 18108384, 87188518, 60432113, 264482, 264564, 264565, 264566, 264567, 22278895, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 285008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21908765, 21908766, 21908768, 55811857, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 63373044, 18108385, 284482
2574	94746814 (5147, 5148)	Novel Protein sim. GBank gi 3334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	264482, 264564, 264565, 264566, 264567, 22278895, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 285008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21908765, 21908766, 21908768, 55811857, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 63373044, 18108385, 284482
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi 4928728 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	264482, 264564, 264565, 264566, 264567, 22278895, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 285008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21908765, 21908766, 21908768, 55811857, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 63373044, 18108385, 284482
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi 4880881 gb AAD27730.1 AF132955 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264908, 60433438, 264681, 18108351, 264288, 52844150, 264628, 35698423
2577	86996821 (5153, 5154)	Novel Protein sim. GBank gi 4337103 gb AAD18079 - (AF129756) NG26 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87786941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264586, 264603, 264604, 264605, 264766, 21908769, 264628, 264630, 264634, 264639, 264583, 29331822, 29331824, 264767
2579	87282879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	88168788 (5159, 5160)	Novel Protein sim. GBank gij2588628 (AC003080) - Similar to KIAA0299; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	87898048 (5161, 5182)	Novel Protein sim. GBank gij4406642(gb)AAD20049] - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00395) - collagen PDZ domain (Also known as DHR or GLGF).		56994075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264756, 87188559, 21908769, 265022, 35695655, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gij2739367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]	eph		264488, 264907, 264908, 264910, 264764, 264684, 264768, 264636, 264555, 264565
2583	91220950 (5165, 5166)	Novel Protein sim. GBank gij4378112(emb)CAA16521.1] - (AL021578) dJ453C12.2 (similar to transcription factor RBP. L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcript factor	56181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)		UNCLASSIFIED		264908, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436128 (5169, 5170)	Novel Protein sim. GBank gij2736151 (AF021835) - mylonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]	kinase		264768
2586	91226136 (5171, 5172)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433356, 33657402, 265018, 264782, 264288, 21908766, 21908767, 21908769, 265022, 264691, 83373044, 56528486, 22278002
2587	80430943 (5173, 5174)				264908, 265019, 264768, 264683, 55811576, 56182323
2588	80074385 (5175, 5176)		UNCLASSIFIED		264564
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gij302159(emb)CAA71415] - (Y10389) nuclear protein [Xenopus laevis]	UNCLASSIFIED		35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264789, 35698423, 264636
2590	87054528 (5179, 5180)	Novel Protein sim. GBank gij2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	glucoamylase		22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192187 (5181, 5182)	Novel Protein sim. GBank gij5702202(gb)AAD47199.1(AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]	eph		264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33108954, 264448, 55811957, 265020, 18108370, 55811576, 22278002

2592	95332648 (5183, 5184)	Novel Protein sim. GBank gi 302498 sp Q60936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264906, 264909, 265007, 265008, 264910, 60432229, 264594, 60433356, 60433438, 55812038, 18108348, 21906754, 265011, 87168559, 265017, 265019, 264764, 264369, 264288, 264766, 265021, 60170615, 33657023, 33657109, 264629, 35896423, 35695855, 264557, 264638, 60170394, 56182323, 83373044, 56526486, 87168518, 264563, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]	tm7		22278999, 29331825, 264758, 21908754, 52646317, 265010, 18108351, 264288, 264389, 21906768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4929587 gb AAD34054.1 AF15181 - (AF15181) CGI-59 protein [Homo sapiens]	UNCLASSIFIED		264488, 18108398, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21908754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21908768, 33657109, 263875, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264563, 264564, 264566, 264567
2595	79561976 (5189, 5190)	Novel Protein sim. GBank gi 4309681 gb AAD15478 - (AC006830) R33423_1 [Homo sapiens]	UNCLASSIFIED		264692
2596	87536637 (5191, 5192)		UNCLASSIFIED		22278998, 264259, 265018, 264448, 265021, 60431528
2597	94784089 (5193, 5194)		UNCLASSIFIED		264905, 264509, 264908, 264762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264486
2598	88084948 (5195, 5196)	Novel Protein sim. GBank gi 1001351 dbj BAA10838 - (D64006) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED		22278998, 264259, 29331824, 87168474, 264683, 21906766, 35695917, 264691, 33657023, 33657109, 18108370, 18108374, 264564, 264565
2599	87642889 (5197, 5198)	Novel Protein sim. GBank gi 3941737 (AF109719) - BAT2 [Mus musculus]	MHC		264766, 264769, 21906766, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526488, 22279000, 264566
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gi 4263521 gb AAD15347 - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	kinasereceptor		35696286, 264093, 264288, 21906769, 35696423, 35695855

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gi728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264908, 265007, 265008, 264591, 60433356, 33657402, 60433438, 21908754, 265011, 265018, 265019, 18108351, 264448, 264369, 21908769, 265020, 60170615, 264693, 33657109, 18108370, 18108376, 56182323, 18108381, 18108385, 22278002, 264563, 60433438, 21908754, 87168559, 264601, 264359, 264288, 21908767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gi4406632 gb AAD200471 - (AF131801) Unknown (Homo sapiens)		UNCLASSIFIED	264488, 65274572, 22278995, 22278998, 56994075, 22278987, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264787, 264689, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486262, 18108374, 35698423, 65274791, 35695855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22278000
2604	94676801 (5207, 5208)	Novel Protein sim. GBank gi5454030 ref NP_006488.1 pRRP2 - RAS-related on Chromosome 22		oncogene	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35698423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gi3628745 gb BAA33366 - (AB013721) mitsugumin 23 (Oryctolagus cuniculus)		UNCLASSIFIED	22278998, 264480, 60432049, 264259, 60432289, 264909, 265008, 60433358, 60433438, 264758, 21908764, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21908765, 21908768, 21908768, 21908769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636, 22278998, 264510, 264512, 265009, 264766, 22279002, 264568
2608	87746408 (5211, 5212)				

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gij4826626igbjAAD30202.1] - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264808, 264807, 264808, 56712502, 264828, 56182435, 55912038, 265010, 265017, 265018, 265019, 264768, 264689, 21906765, 55811957, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264639, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gij2226005 (U49873) - ORF2: function unknown [Homo sapiens]			
2609	94843781 (5217, 5218)	Novel Protein sim. GBank gij3024889ispjP56524Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)	Contains protein domain (PF00850) - Histone deacetylase family	histone	284488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55912038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21906765, 21906767, 21906769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274781, 264636, 264556, 55182323, 18108385, 56526486
2610	88177654 (5219, 5220)	Novel Protein sim. GBank gij4336855igbjAAD17989] - (AF106473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]		transcriptfactor	18108394, 22278994, 56894075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 55182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263967, 33657182, 27486261, 18108374, 263976, 55811576, 264638, 87168518, 60432113
2611	97428890 (5221, 5222)	Novel Protein sim. GBank gij3876761embjCAA92994] - (Z68760) predicted using Genefinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278999, 265017, 264684, 21906768, 22278000
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gij5879136igbjAAD46874.1jAF160934) BcDNA.LD14188 [Drosophila melanogaster]		transport	265009, 264910, 264759, 265017, 21906767, 18108365, 18108386, 60432113
2613	79481496 (5225, 5226)				
2614	87643948 (5227, 5228)	Novel Protein sim. GBank gij5533081igbjAAD45009.1jAF18118 - (AF181181) P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase	UNCLASSIFIED	264685
2615	87381898 (5229, 5230)			UNCLASSIFIED	22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264766, 264769, 52844229, 21906765, 33657109, 27486264, 18108370, 263972, 264555, 60432113, 264768, 18108394, 264692, 264693, 264508, 264509, 264807, 264828, 264808, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264766

2616	87428895 (5231, 5232)	Novel Protein sim. GBank gij3876761[emb]CAA92994) - (Z68760) predicted using Genefinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 60432049, 80432289, 264828, 60433358, 264594, 80433438, 33109954, 87188474, 265011, 265017, 265019, 264288, 264766, 21906765, 21906767, 265020, 265021, 18108376, 18108377, 18108387, 87188518, 264482, 264567
2617	88976888 (5233, 5234)	Novel Protein sim. GBank gij728831[sp]P39188/ALU1 - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265019, 264369, 264683, 55811576, 22279002
2618	81231682 (5235, 5236)	Novel Protein sim. GBank gij3319282 (AF049103) - Huntinglin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264908, 264907, 68712502, 29331830, 265008, 264910, 265009, 60433356, 80433438, 264758, 21908754, 265011, 87188559, 265017, 265018, 264389, 264288, 264766, 264768, 264688, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 33657023, 264692, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56526486, 264583
2619	87684000 (5237, 5238)	Novel Protein sim. GBank gij2431772 (U66411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	284239, 60432289, 60433438, 21908754, 264369, 60432113, 264566
2620	95314841 (5239, 5240)	Novel Protein sim. GBank gij4322567[gb]AAD16097] - (AF090436) dactishund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52644507, 52645158, 52646842, 65274572, 22278995, 56994075, 35698286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644228, 264688, 264689, 21908765, 21908768, 35695917, 52644150, 264692, 33657109, 35695783, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002
2621	80253495 (5241, 5242)				264594, 264638
2622	81780390 (5243, 5244)	Novel Protein sim. GBank gij4557341[ref]NP_001174.1pATP6 - ATPase, H ⁺ transporting, lysosomal subunit 1; vacuolar proton pump: H-ATPase subunit			264488, 264908, 264907, 264908, 264512, 265007, 264758, 35695917, 264634, 264638, 264563, 264482
2623	91639306 (5245, 5246)	Novel Protein sim. GBank gij3880355[emb]CA805299] - (Z82285) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148829

2624	81639308 (5247, 5248)	Novel Protein sim. GBank gij3860355[embjCAB05289] - (Z82285) predicted using GeneFinder (Caenorhabditis elegans)	UNCLASSIFIED	56181686, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35698052, 29146499, 66712502, 52644045, 265007, 265008, 60433356, 33109854, 21906754, 265010, 265011, 265018, 264448, 264288, 21906765, 21906766, 21906767, 29146629, 35695917, 265021, 265022, 27486285, 18108370, 60431528, 55811576, 35695855, 56182323, 18108385, 87168518, 22278002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gij2887429[dbjBAA24857] - (AB007887) KIAA0427 [Homo sapiens]	UNCLASSIFIED	264091, 264511, 263981
2626	18533787 (5251, 5252)	Novel Protein sim. GBank gij487416 (L20302) - actin filament protein [Gallus gallus]	struct	265008
2627	87638823 (5253, 5254)	Novel Protein sim. GBank gij88462[pirjA27307] - proline-rich phosphoprotein (gene PRH1, Db allele) - human	UNCLASSIFIED	22278996, 265007, 265009, 264448, 21906767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gij3123552[embjCAA18609] - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]	UNCLASSIFIED	22278997, 22278998, 264259, 60432048, 29331822, 29331824, 29331825, 29331827, 35698052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264389, 264288, 18108357, 21906765, 21906768, 265022, 65274781, 264638, 18108387, 87168518, 22278002
2629	87376490 (5257, 5258)	Novel Protein sim. GBank gij4928595[gbjAAD34058.1]AF15182 - (AF151821) CGI-63 protein [Homo sapiens]	synthase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	79188364 (5259, 5260)	Novel Protein sim. GBank gij321605[pirjJQ1161] - Gag protein - Visna virus (strain EV1)	UNCLASSIFIED	264636, 18108385
2631	94845908 (5261, 5262)		dna_mn_bind	52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35698286, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35698052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33637084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264389, 264766, 264768, 52644229, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35698423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264566, 264486, 264685
2632	36730414 (5263, 5264)			

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gii1139548[db][BAA10889] - (D84009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265008, 265007, 265008, 265009, 55812038, 33657084, 55811388, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264686, 29148628, 33657023, 264693, 33657182, 35695763, 55811576, 264639, 56182323, 83373044, 18108385, 56526486, 87168516, 22278000, 22278002, 264585
2634	87330821 (5267, 5268)	Novel Protein sim. GBank gii544161[emb][CAB46854.1] - (AJ988555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gii4680863[gb]/AAD27721.1[AF13294] - (AF13294) CGI-12 protein [Homo sapiens]		22278997, 264259, 29331824, 68714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264446, 264288, 21906766, 21908767, 21906768, 29148829, 18108378, 55811576, 35695855, 87168518, 22278000, 264589, 29331822, 29331828, 265008, 60170831, 264681, 264765, 264685, 29148627, 21908769, 29148784, 265022, 60170815, 264635, 18108385, 56526486, 22278002, 264567
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gii3879146[emb][CAB07646] - (Z93386) Similarity to Yeast hypothetical 52.8 KO protein (SW:P43618); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D80025 comes ...	Contains protein domain (PF01646) - Peptidase family M20/M25/M40	264488, 264489, 52844507, 264887, 52646365, 52846842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52645080, 68714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29148488, 264508, 264805, 264908, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52846317, 21908754, 52844286, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264687, 264769, 21908765, 21908766, 21906767, 21906768, 21906769, 35695917, 265021, 60170815, 264691, 33657023, 264692, 264693, 65274620, 27486284, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264564, 264565, 264566, 264488, 264567
2637	95011298 (5273, 5274)	Novel Protein sim. GBank gii4768208[ref][NP_004081.1]pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	

2638	94326733 (5275, 5278)	Novel Protein sim. GBank gij4929889[gib]AAD34105.1[AF15186] - (AF15186) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52844507, 52646842, 18108398, 58182375, 22278895, 22278896, 35698286, 22278897, 22278899, 284259, 60432049, 28331822, 60424269, 28331826, 35698052, 29146498, 284905, 52844045, 56182435, 60433358, 33657402, 55812038, 55811386, 265018, 284288, 284768, 52844229, 56181562, 28148627, 28148629, 55811957, 28148784, 35695917, 265021, 52844150, 33657023, 65274620, 33657109, 35695763, 18108374, 55810784, 35698423, 55811576, 35698855, 60431850, 56182323, 60432113, 264404
2639	95361346 (5277, 5278)	Novel Protein sim. GBank gij2190007[dij]BAA20355] - (AB004109) phosphatidylserine synthase II [Cricetus griseus]		synthase	264488, 28331825, 35696052, 284508, 264509, 284909, 264512, 33657402, 60433438, 284758, 85658542, 284600, 265020, 265021, 33657109, 264628, 35698423, 264555, 284639, 284583, 284584, 284565, 264598, 284486
2640	87761330 (5279, 5280)	Novel Protein sim. GBank gij3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm, score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 87.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	28331822, 28331826, 264906, 33108954, 265017, 265018, 21806768, 35695763, 264636, 264637, 18108387
2641	11689634 (5281, 5282)	Novel Protein sim. GBank gij2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264828
2642	87412575 (5283, 5284)			UNCLASSIFIED	264259, 28331822, 33657402, 265019, 264359, 284691, 284634, 56526488, 22279002
2643	87643961 (5285, 5286)	Novel Protein sim. GBank gij4480304[emb]CAB36785.1] - (AL035678) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278897, 264259, 28146489, 56182435, 264910, 265010, 18108351, 264682, 284683, 284369, 284684, 264685, 264686, 28148627, 264690, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gij3789797[gib]AAC67502.1] - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nudl_rept	264107, 264687
2645	17277228 (5289, 5290)	Novel Protein sim. GBank		UNCLASSIFIED	265007
2646	84148542 (5291, 5292)	gij1708722[sp]P49749[EVX2] MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264909, 264687, 284632, 83373044

2647	91212678 (5293, 5294)			UNCLASSIFIED	56182575, 22278986, 35696286, 22278988, 264259, 29331822, 56182181, 29331825, 60424269, 60432289, 35696052, 68712502, 264908, 265007, 55812038, 33109854, 21906754, 33657084, 265019, 264448, 264286, 56181562, 21906765, 21906768, 21906768, 21906768, 35695917, 285020, 265021, 52844150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264584
2648	87600587 (5295, 5296)				29146498, 56182435, 33109854, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2649	94128783 (5297, 5298)	Novel Protein sim. GBank gij3041852 (AC004539) - unknown function; similar to Y09105 (PID:g1666171) [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278988, 29331824, 29331826, 60432289, 66712502, 56182435, 60170831, 60432229, 33657402, 33109854, 21906754, 265017, 264686, 264688, 21906765, 21906768, 60170815, 264693, 263987, 18108370, 263976, 60170394, 60432113, 22279002, 264563
2650	87287533 (5299, 5300)	Novel Protein sim. GBank gij5360271 [dbj BAA81808.1] - (AB028335) HrPET-3 [Halocynthia roretzi]			264685
2651	88088745 (5301, 5302)	Novel Protein sim. GBank gij4240225 [dbj BAA74891.1] - (AB020675) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF00054) - Laminin G domain	synthase	29331824, 29331826, 28331827, 265007, 55812038, 21906754, 18108366, 18108384, 22279002, 264567
2652	10343125 (5303, 5304)	Novel Protein sim. GBank gij4493856 [emb CAB11123.2] - (Z98651) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....		UNCLASSIFIED	264692
2653	87798735 (5305, 5306)	Novel Protein sim. GBank gij4493856 [emb CAB11123.2] - (Z98651) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....		UNCLASSIFIED	265018, 18108370, 18108387, 264568
2654	95103240 (5307, 5308)				60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 85274727
2655	91228018 (5309, 5310)	Novel Protein sim. GBank gij3875272 [emb CAB02861] - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transcript factor	56182575, 56181686, 264092, 264259, 56182181, 60432289, 264907, 33657402, 55812038, 21906754, 87168559, 265017, 264448, 264369, 264286, 21906765, 21906768, 21906767, 21906768, 33657109, 18108370, 264628, 55811576, 264558, 264639, 83373044, 56526488, 264404, 60432113
2656	84582601 (5311, 5312)	Novel Protein sim. GBank gij3043718 [dbj BAA25523] - (AB011189) KIAA0597 protein [Homo sapiens]			264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank glj5689503[dbj BAA63038.1] - (AB029009) KIAA1088 protein [Homo sapiens]		dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank glj3688089 (AC005757) - R32611_1 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331826, 29331828, 285019, 264683, 21906768, 35695917, 264693, 35695855, 264637, 87188518, 264486, 264567
2659	87600755 (5317, 5318)	Novel Protein sim. GBank glj5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265016, 284369, 264789, 21908769, 284693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank glj728837[sp P39194 ALU7 - HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF000036) - EF hand	kinase	264486, 65274572, 35696286, 22278988, 22278990, 264259, 29331822, 29331824, 60432289, 29331826, 35698052, 264908, 56182435, 265008, 265009, 60433358, 284594, 285010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 28148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35698423, 35695855, 284556, 60170394, 18108385, 22278000, 22278002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank glj4758048[ref NP_004739.1 pCPR8 - cell cycle progression 8 protein		glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 284760, 264448, 284369, 264288, 21906765, 21906768, 265022, 284691, 33657023, 27488282, 60431528, 18108374, 35695855, 18108388, 284482
2662	80228739 (5323, 5324)	Novel Protein sim. GBank glj3874714[emb CAA91263] - (Z68494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]		dehydrogenase	264555, 264556, 264558, 264486
2663	87780623 (5325, 5326)	Novel Protein sim. GBank glj1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]	Contains protein domain (PF000008) - EGF-like domain		264906, 264909, 264757, 284758, 264767, 284691, 33657023, 284638
2664	85518328 (5327, 5328)	Novel Protein sim. GBank glj4884406[emb CAB43311.1] - (AL050190) hypothetical protein [Homo sapiens]		oncogene	35696286, 264509, 264595, 264288, 264685, 264686
2665	87770662 (5329, 5330)	Novel Protein sim. GBank glj2500570[sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1		UNCLASSIFIED	35696286, 22278999, 29331822, 35696052, 264906, 264907, 264909, 284510, 284511, 284512, 284593, 60433438, 265019, 264681, 21906765, 21906768, 21906767, 21908769, 265020, 265022, 35696423, 35695855, 22278002, 264482, 264488
2666	87826472 (5331, 5332)	Novel Protein sim. GBank glj5106956[gb AAD39806.1 AF113615] - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]		UNCLASSIFIED	29331825, 285007, 264910, 60432228, 265019, 264288, 21906767, 264558, 22278002
2667	87422720 (5333, 5334)	Novel Protein sim. GBank glj2500570[sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1	Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	284907, 29331830, 264681, 264683, 264288, 35695855, 264632, 284556, 264557, 264558, 264559, 264563, 284565, 264567

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi 5454186 ref NP_006327.1 pZYG - ZYG homolog	UNCLASSIFIED	56181686, 35695286, 22278998, 22278998, 22278998, 56182181, 29331824, 60424269, 29331825, 3569052, 29331828, 66712502, 56182435, 60433356, 264758, 21906754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 264448, 264369, 264288, 21906765, 21906768, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264682, 33657109, 35695763, 60431528, 18108374, 35696423, 55811576, 264634, 60431850, 83373044, 18108385, 87168518, 22278000, 264583, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi 2147012 pir JC4899 - proline rich protein - rat		264489, 264689, 21906767, 65274572, 56182575, 21906788, 29148827, 21906769, 29148629, 35696286, 35695917, 22278996, 22278998, 265021, 265022, 60170615, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331826, 29331827, 35696052, 29331828, 29148488, 29148499, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274791, 35695955, 265006, 264910, 264635, 60432228, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi 1723523 sp Q10362 YD8B_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME 1	Contains protein domain (PF00628) - PHD-finger	18108370, 263974
2671	91214936 (5341, 5342)	Novel Protein sim. GBank gi 4768277 gb AAD28444.1 AF06425 - (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21906754, 264682, 264288, 265021, 33657023, 33657109, 33657162, 27486261, 27486262, 27486265, 18108376, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi 4966346 gb AAD34677.1 AC00634 - (AC006341) Contains two PF01344 Kelch motif domains. [Arabidopsis thaliana]	Contains protein domain (PF01344) - Kelch motif	264767

2873	87430748 (5345, 5346)	Novel Protein sim. GBank gij5457337[embl CAB41505.2] - (AJ238876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00644) - Poly(ADP-ribose) polymerase catalytic region.	polymerase	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 285018, 265019, 264448, 21906768, 21906769, 265020, 265021, 33657109, 27486282, 35695763, 60431850, 60170394, 87168518, 284563
2874	94847121 (5347, 5348)	Novel Protein sim. GBank gij4756824[ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcriptiador	264488, 22278996, 35696286, 284091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 85658542, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2875	70563835 (5349, 5350)			UNCLASSIFIED	264691
2876	79628393 (5351, 5352)			UNCLASSIFIED	264906, 265008
2877	84328600 (5353, 5354)	Novel Protein sim. GBank gij1078042[pri S2154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - AMP-binding enzyme	UNCLASSIFIED	18108394, 65274572, 56182575, 22278994, 22278995, 56984075, 22278996, 35696286, 22278997, 22278998, 264480, 264259, 52845080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146499, 29331830, 284908, 52844045, 265008, 265007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264882, 284448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33657109, 27486284, 27486265, 33657349, 35695763, 18108370, 18108374, 18108387, 55811576, 35696423, 35695855, 83373044, 18108387, 22279000, 22279002, 264584

2678	95001694 (5355, 5356)	Novel Protein sim. GBank gl 88760 p j A40465 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263994, 264489, 18108394, 52646842, 35698288, 22278998, 264259, 29331825, 35698052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109954, 52646317, 21906754, 265010, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52844150, 264691, 33657023, 264693, 18108384, 18108385, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264488, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gl 709233 p P07514 NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	UNCLASSIFIED	264498, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264808, 56182435, 264113, 264511, 265008, 60433438, 264758, 85656542, 87168474, 265011, 265017, 265019, 264288, 21908766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264568, 264259, 264102, 264905, 264908, 285007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263872, 264630, 264635, 264638
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gl 4589504 p j BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	UNCLASSIFIED	264488, 22278995, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264764, 264887, 264768, 264769, 21908769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264488
2681	80933844 (5361, 5362)	Novel Protein sim. GBank gl 728637 p P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Kinase	UNCLASSIFIED	35696286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 56526486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gl 423468 p j JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264909, 264769, 264635, 264638
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gl 5114351 p j AAD40286.1 - (AF158271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	

2684	85787151 (5367, 5368)	Novel Protein sim. GBank gl 4868469 emb CAB43385.1 - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	86054289 (5369, 5370)	Novel Protein sim. GBank gl 3342729 (AC005331) - R31341_2 [Homo sapiens]		UNCLASSIFIED	
2686	87628690 (5371, 5372)	Novel Protein sim. GBank gl 4650844 db BAA77027.1 - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - struct Kelch motif		264259, 29331822, 60432289, 29331827, 29331830, 284909, 284512, 264598, 264789, 264534, 264555, 264556, 264557, 264558, 60170394, 264559, 264486
2687	87898183 (5373, 5374)	Novel Protein sim. GBank gl 5281314 gb AAD41475.1 AF13312 - (AF133123) transcription factor IIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108394, 18108396, 22278996, 35696286, 22278997, 29331826, 29331828, 68712502, 21908754, 265011, 264760, 264761, 264763, 264689, 21806765, 35696423, 264559, 18108385, 264563
2688	79959584 (5375, 5376)				264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gl 3880023 emb CAA97339 - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q09695); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		22278997, 22278998, 22278999, 29331824, 35696052, 264906, 264908, 56182435, 264512, 264910, 265009, 60433438, 21906754, 18108351, 264682, 264683, 264767, 21908765, 21906766, 21906768, 33657023, 33657182, 27466262, 27466284, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gl 2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gl 4107276 emb CAA67130 - (X98508) acetyl-CoA synthetase [Solanum tuberosum]		synthase	55274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264598, 33109954, 265017, 264448, 264288, 264369, 264684, 21906768, 60170615, 60431528, 55810784, 284634, 264636, 264556, 264637, 22279002, 264564, 264568
2692	84111914 (5383, 5384)	Novel Protein sim. GBank gl 3513303 (AC005594) - R26984_1 [Homo sapiens]	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	
2693	20438807 (5385, 5386)			UNCLASSIFIED	264592
2694	84111918 (5387, 5388)	Novel Protein sim. GBank gl 3122400 sp O35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN			264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gl 4972740 gb AAD34765.1 - (AF132177) unknown [Drosophila melanogaster]		collagen	35696286, 56994075, 22278999, 284259, 35696052, 29331830, 265011, 264288, 56181562, 264690, 264692, 33657023, 27486262, 263976, 18108376, 35696423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264568
2696	87874040 (5391, 5392)	Novel Protein sim. GBank gl 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		synthase	264594, 21806768, 18108370, 18108372

2697	91638472 (5393, 5394)	Novel Protein sim. GBank gl 5689473 dbj BAA83020.1 - (AB028881) KIAA1088 protein [Homo sapiens]		UNCLASSIFIED	3508286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87188474, 265010, 265011, 87188559, 264601, 265017, 265018, 265019, 264761, 18108351, 264448, 264288, 264768, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170819, 33657109, 18108378, 35698423, 35685855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87188518, 22278002, 264563, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank gl 841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	22278985, 35696286, 22278986, 22278987, 22278988, 22278989, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35658970, 264908, 29331830, 264909, 52644045, 264910, 60433356, 33657402, 33109854, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906767, 21906768, 29148829, 35695917, 265021, 265022, 52644150, 33657023, 33657182, 27486281, 35698423, 65274781, 264638, 60432113, 22279000
2699	87780650 (5397, 5398)			UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139838 (5399, 5400)	Novel Protein sim. GBank gl 5174385 ref NP_006006.1 p8120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432228, 60433438, 55811386, 265017, 55811150, 264448, 56181562, 55811957, 264693, 33657109, 60431528, 264628, 55810764, 55811576, 65274781, 60431850, 60432113
2701	94148594 (5401, 5402)	Novel Protein sim. GBank gl 1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108384, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29148499, 265006, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486281, 18108374, 18108378, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295368 (5403, 5404)	Novel Protein sim. GBank gl 2605987 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87649514 (5405, 5406)	Novel Protein sim. GBank gl 5689399 dbj BAA82883.1 - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar).		60432288, 265007, 21906765, 21906768, 265021, 264563

2704	87649515 (5407, 5408)	Novel Protein sim. GBank gl 4335684 gb AA063294 - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29148499, 264905, 264908, 264907, 52644045, 264511, 33657402, 264600, 264602, 265017, 264605, 264761, 18108351, 264764, 264687, 264769, 265021, 264691, 264692, 18108382, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5409, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264768, 264638, 264566, 264486
2706	94326788 (5411, 5412)	Novel Protein sim. GBank gl 3255952 emb CAA16821.1 - (AL021728) /prediction=(method:; /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 85274572, 22278994, 56894075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33658970, 264907, 264908, 264909, 52644045, 56182435, 265006, 265007, 80433438, 55812038, 21906754, 52644298, 265010, 264601, 265017, 265018, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 264690, 264691, 33657023, 264692, 264693, 65274620, 27468264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22278900
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gl 3417294 (AC004381) - Unknown gene product [Homo sapiens]			22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gl 545790 pbs 147178 - DARPP-32-dopamine and cAMP-regulated phosphoprotein (human, brain, Peptide, 204 aa)	UNCLASSIFIED		65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433436, 33109954, 265010, 265011, 264369, 264288, 264785, 264693, 264565
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gl 3169705 (AC004780) - F17127.1 [Homo sapiens]			29331822, 18108370, 18108374, 63373044
2710	87627979 (5419, 5420)	Novel Protein sim. GBank gl 446831 emb CAB37992 - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]	UNCLASSIFIED		29331824, 264759, 264683, 18108382, 18108388

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gij3122400 spj035682 JUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	284488, 284687, 52645156, 264769, 21908764, 21908765, 21908767, 21908768, 21908769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 60424289, 29331828, 33657182, 29331827, 27486282, 33857349, 264508, 264805, 264907, 60431528, 264908, 264909, 55810764, 35698423, 65274791, 35695855, 265007, 264910, 60431850, 60432228, 264557, 264558, 55812038, 33108954, 18108385, 21906754, 33657084, 87168518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264555, 264764, 264566, 264288, 264766 264488, 35698286, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 264906, 66712502, 52844045, 265008, 60432229, 33657402, 60433356, 265010, 265019, 18108351, 264881, 264288, 264685, 21908765, 21908766, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 60170615, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35698423, 35695855, 264559, 52644332, 56182323, 87168518, 60432113 66714117, 264906, 264563
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gij5081315 gijAAD39343.1 AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	
2713	88003064 (5425, 5426)	Novel Protein sim. GBank F25965_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gij4321968 gijAAD158971 - (AF067430) Smarcat1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gij2477513 (AC002398) - F25965_3 [Homo sapiens]		glycoprotein	264091, 264259, 29331822, 66714117, 264908, 264389, 264693, 264556, 264563
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gij3327046 gijBAA315911 - (AB014516) KIAA0818 protein [Homo sapiens]			264593, 264558
2718	79604062 (5435, 5436)				264693
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gij746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5438, 5440)	Novel Protein sim. GBank gij1335873 (U46690) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108374, 60424179, 264489, 56182435, 21908765, 21908766, 35698423, 22278997, 265020, 265022, 265008, 265008, 264092, 264638, 60432229, 264691, 264892, 33657023, 264693, 33657402, 83373044, 29331824, 18108366, 60424269, 29331826, 18108365, 52645129, 21908754, 35698052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22279002, 264905, 264482, 264563, 264908, 18108351, 264881, 18108370, 29331830, 264908, 66712502, 52644045, 264909, 264928, 18108354, 22278995, 35698286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21908768, 265021, 33657109, 263969, 60431528, 264629, 55811576, 65274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000, 35698286, 22278999, 21908754, 265017, 264762, 264288, 21908765, 21908767, 21908768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gij4929663 [gb]AAD34092.1 [AF15185] CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023		264508, 264509, 264906, 264908, 264910, 55812038, 264766, 264687, 264628, 264636, 264488
2722	81638007 (5443, 5444)	Novel Protein sim. GBank gij3212997 [gb]AAC23434.1 - (AC004997) match to ESTs AA687999 (NID:g2626700), AA185465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g12314); similar to various tre-like proteins including: AF040854 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - TBC domain	oncogene	18108396, 22278999, 20281099, 29331824, 29331826, 60432289, 29331828, 60170831, 60432228, 60433438, 18108351, 264682, 21908766, 21908767, 21908769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2723	87387732 (5445, 5446)			UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21908754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35698423, 18108385, 22279000
2724	87639553 (5447, 5448)	Novel Protein sim. GBank gij4680681 [gb]AAD27730.1 [AF13295] CGI-21 protein [Homo sapiens]		ubiquitin	264488, 264628, 264685
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21908754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35698423, 18108385, 22279000
2726	86880599 (5451, 5452)	Novel Protein sim. GBank gij3342738 (AC005328) - R26680_1, partial CDS [Homo sapiens]		MHC	264488, 264628, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gij731267isp139218RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - RNA pseudouridylylate synthase	synthase	65274572, 56182575, 22278994, 56984075, 22278998, 22278997, 22278999, 60432049, 29331822, 29331824, 68714117, 29331826, 29331827, 35686052, 29331828, 33656870, 264509, 66712502, 284910, 33657402, 60433436, 264758, 55812038, 21908754, 33657084, 55811388, 265018, 265019, 264767, 21908765, 21908767, 21908769, 55811857, 35685917, 52644150, 33657023, 33657108, 33657182, 27486281, 27486282, 27486265, 33657349, 55811576, 35686423, 35695855, 264630, 60431850, 264636, 56182323, 87168518, 60432113, 22278000, 264564, 264589
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gij3880433jemb[CAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	16108394, 56182435, 21908767, 55811857, 35685855, 265021, 264680, 264556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gij2408095jemb[CAB16300] - (Z66521) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 264259, 60432288, 66712502, 56182435, 264448, 264288, 264389, 55811857, 265021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gij3880433jemb[CAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264687, 29331824, 29331826, 35686052, 264107, 56182435, 265008, 265009, 264582, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148827, 55811857, 265021, 264680, 18108368, 18108374, 264557, 264558, 264559, 18108387, 56526486, 264566, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gij1723239isp10166jYAUJ_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35686052, 265008, 264758, 264762, 264448, 264288, 29148827, 21908769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gij3880433jemb[CAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	264687, 264489, 18108358, 56182435, 264689, 35686423, 55811857, 265021, 265006, 265008, 264910, 265009, 264680, 264555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 264389, 264587
2733	87363080 (5465, 5466)			UNCLASSIFIED	29331825, 264509, 264809
2734	94140286 (5467, 5468)	Novel Protein sim. GBank gij4519621jdbjBAA75670.1] - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	60424178, 52644507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433356, 265019, 55811150, 264881, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712336 (5469, 5470)	Novel Protein sim. GBank gij3850569 (AC005278) - ESTs gbj721276, gbj745403, and gbjAA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278998, 60432289, 29331827, 28146498, 284108, 284909, 284112, 33657402, 87168474, 285017, 264762, 264448, 264764, 264684, 21908765, 264693, 33857109, 263976, 264636, 264638, 264557, 22279000, 22279002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604528 (5473, 5474)				284690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gij2558501[dbjBAA22886] - [D63850] hepatoma-derived growth factor [Mus musculus]			264488, 265008, 264768, 264691
2739	94318834 (5477, 5478)	Novel Protein sim. GBank gij5420387[embjCAB46678.1] - [AJ243459] proleophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gij3417386[embjCAA75495] - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265008, 265007, 265008, 80432229, 33657402, 55812038, 87168474, 285010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657109, 18108370, 18108374, 55810764, 35696555, 264634, 60431850, 264639, 56182323, 18108362, 18108385, 65274727, 22279002, 264564
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gij3242764 (AC005154) - similar to protein U28928 (PID:9861308) [Homo sapiens]		UNCLASSIFIED	22278996, 52644045, 52644229, 21906768, 21906769, 265020, 60170815, 264691
2742	87848644 (5483, 5484)	Novel Protein sim. GBank gij4758412[reijNP_004472.1]pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2 (GalNAc-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264803, 264758, 55812038, 264369, 29148627
2743	87627091 (5485, 5486)	Novel Protein sim. GBank gij4468311[embjCAB37892] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264908, 264908, 265008, 60433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264680, 264691, 264693, 263969, 263971, 35696555, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gij3880433[embjCAA91399] - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein, cDNA EST EMBL: C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695955, 265020, 265021, 264511, 265009, 264490, 264558, 264259, 264557, 56182323, 264658, 264559, 18108383, 29331824, 18108385, 33657109, 29331826, 21906754, 28331827, 28331828, 33657349, 87168518, 265018, 264905, 284482, 264448, 264486, 264389, 264288

2745	87740125 (5489, 5490)	Novel Protein sim. GBank gij4405795igpAAD19826] - (AF038863) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - helicase domain	35696286, 264508, 264905, 264907, 264908, 264909, 264510, 264512, 265008, 264759, 264801, 265017, 264604, 264763, 264288, 264886, 264769, 264693, 35698423, 35695855, 264634, 264636, 264563, 264564, 264565
2746	85418601 (5491, 5492)	Novel Protein sim. GBank gij4758738refINP_004680.1pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 264907, 264908, 264909, 52644045, 285008, 60170831, 264588, 55812038, 265018, 264683, 264286, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 33857023, 264693, 33857109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gij4557803refINP_000282.1pNPC1 - Niemann-Pick disease, type C1	glycoprotein	264569, 52644507, 18108394, 22278995, 35696286, 22278997, 22278998, 52645080, 29331824, 56182181, 29331826, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109954, 55811386, 87168474, 265010, 87168559, 264603, 265019, 264760, 264688, 264768, 21906769, 35695917, 60170815, 264692, 33857023, 52645129, 27488264, 60431528, 18108374, 35698423, 35695855, 264556, 56182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gij4191272[emb]CAA08984] - (AJ012295) epaG protein [Rhizobium elii]	Contains protein domain (PF00646) - F-box domain.	65274572, 29331828, 264112, 264511, 285019, 264760, 264767, 264768, 264769, 21906768, 21906769, 265020, 27486262, 56526486, 87168518, 22279000
2749	87346307 (5497, 5498)			264259, 264908, 264510, 265008, 265009, 264760, 264399, 264768, 264593
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gij1872488 (U74297) - PIUS [Oryctolagus cuniculus]	UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33857084, 265011, 265019, 18108351, 264288, 264686, 264769, 264868, 55811957, 264693, 27488264, 18108370, 18108374, 264558, 18108385, 264482, 264593
2751	87057465 (5501, 5502)		UNCLASSIFIED	29331822, 29331824, 265017, 33857023
2752	88082675 (5503, 5504)	Novel Protein sim. GBank gij3041859 (AC004534) - OG-2 homeodomain protein-like; similar to U65067 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	

2753	94138972 (5505, 5508)	Novel Protein sim. GBank gi 3851648 (AF098301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00846) - F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278998, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 264288, 56181562, 21908767, 21908768, 265021, 264693, 18108374, 65274791, 264632, 56182323, 22278002, 264563, 264567
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	22278998, 66714117, 29331827, 35695052, 29331828, 264908, 264908, 264909, 265011, 265017, 265018, 265019, 264288, 21908765, 21908767, 265022, 33657023, 264693, 56182323, 18108382, 22278000
2755	88001472 (5508, 5510)	Novel Protein sim. GBank gi 2896653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465908 (5511, 5512)	Novel Protein sim. GBank gi 1173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	264594
2757	95361580 (5513, 5514)	Novel Protein sim. GBank gi 3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		eph	85858542, 264693
2758	76637846 (5515, 5516)	Novel Protein sim. GBank gi 2072200 (U94863) - p40 [Borna disease virus]		struct	264693
2759	81005312 (5517, 5518)	Novel Protein sim. GBank gi 2072200 (U94863) - p40 [Borna disease virus]			
2760	79824788 (5519, 5520)	Novel Protein sim. GBank gi 4914573 (emb)CAB43885.1 - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	65274572, 35696286, 68714117, 29331828, 264508, 56182435, 21908764, 55811957, 264629, 264636, 56182323, 22279002
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gi 3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	nuclease	264808
2762	87592699 (5523, 5524)	Novel Protein sim. GBank gi 3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	22278998, 29331822, 29331830, 265010, 265019, 264288, 21908765, 21908768, 21908769, 265020, 56182323, 22279002, 264593
2763	87539868 (5525, 5526)	Novel Protein sim. GBank gi 3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box		18108394, 22278998, 264906, 264908, 265006, 265007, 264757, 265010, 265011, 265017, 265019, 18108351, 264448, 264683, 264686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108365, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108389, 87168518, 264389, 35696423
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gi 2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF000370) - FGGY family of carbohydrate kinases	transcriptfactor	5264842, 264259, 29331822, 29331825, 29331826, 29331828, 33656970, 264905, 264907, 29331830, 265006, 265009, 21908754, 265019, 264448, 21908769, 27486282, 56182323, 56526486, 87168518, 264487

2765	94315105 (5528, 5530)	Novel Protein sim. GBank gl 4688672 emb CAA17688.2 - (AL022019) /prediction=(method:; /prediction=(method:; /match=(desc: [Drosophila melanogaster])			264488, 65274572, 22278995, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 35698052, 284508, 284509, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 265008, 264592, 264595, 264758, 55812038, 33108954, 265010, 87168559, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56181562, 21808764, 21808765, 21808768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168518, 22278900, 22279002, 264563, 264482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gl 5441611 emb CAB46854.1 - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 60433356, 264288, 264885, 264889, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264556, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gl 1079451 p j A55463 - Itropomodulin, skeletal muscle - chicken		si_ruct	264112, 2633974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gl 5441322 emb CAB46721.1 - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 2633984, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35698052, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264688, 264768, 18108357, 264769, 264689, 21808766, 21808768, 21808769, 35695917, 265021, 265022, 33657023, 33657109, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264488, 264567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gi 5419859 emb CAB46375.1 - (AL096725) hypothetical protein [Homo sapiens]		tubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264808, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264691, 33657023, 264692, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gi 5701965 emb CAB52157.1 - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	18108398, 22278995, 22278996, 22278999, 264105, 265006, 285019, 18108351, 264687, 21908765, 18108364, 264628, 18108374, 264631, 18108385, 18108388
2771	88084071 (5541, 5542)	Novel Protein sim. GBank gi 3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 28331822, 29331824, 29331825, 264369
2772	95357308 (5543, 5544)	Novel Protein sim. GBank gi 488553 ref NP_005465.1 pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	264259, 28331822, 29331824, 66714117, 60432289, 29331827, 264905, 285009, 264592, 55812038, 65274444, 264766, 21908769, 33657109, 263978, 264555, 264638, 264557, 83373044, 264563, 264564, 264486
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gi 3288888 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 264686, 264687, 263978, 56182435, 264688, 55810764, 21906766, 35686423, 55811576, 65274791, 56181886, 55811957, 35695855, 264110, 265021, 264112, 285022, 265008, 265009, 264092, 264084, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424289, 18108385, 29331828, 29331827, 27486261, 29331828, 35686052, 55811386, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264806, 18108370, 264484, 264682, 20281069, 264448, 66712502, 264683, 264764, 264288, 264684, 264766, 263974
2774	87818808 (5547, 5548)	Novel Protein sim. GBank gi 465852 sp P34388 YLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomalprot	22278995, 35696286, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21908754, 87168559, 265017, 265018, 264288, 21906766, 21908767, 21908769, 35695917, 265020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35695855, 87168518, 22278000, 264482

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi 4989132 gb AAD27775.1 AF07704 - (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - Ribosomal protein S7p/S5e	264488, 22278995, 56984075, 22278998, 35898288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 265007, 21908754, 265017, 265019, 264448, 264682, 264369, 264288, 18108354, 52644229, 264689, 21906765, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 60170815, 264891, 18108370, 35898423, 65274781, 35898555, 264634, 60431850, 60170394, 56182323, 264559, 18108368, 22279000, 264563, 264565, 264486, 264567
2776	87791557 (5551, 5552)			56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21908764, 55811386, 265017, 265018, 264448, 264288, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 265021, 265022, 60170815, 55810764, 55811576, 264555, 56526486, 22278000
2777	78818729 (5553, 5554)		UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)		UNCLASSIFIED	264907, 264593, 264760, 264628
2779	67649729 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297 - (AF132970) CGI-35 protein [Homo sapiens]	UNCLASSIFIED	22278997, 264259, 29331824, 68714117, 35898052, 265008, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94679397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 pHKGK - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 4469352 gb AAD21222 - (AF069502) ubiquitin specific protease UBPA3 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	60424179, 29331824, 60424269, 68714117, 29331828, 56182435, 87168474, 265017, 264784, 56181562, 21906765, 21908766, 21908768, 35695917, 265020, 33657023, 35898555, 58182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN1 - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	65274572, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 62644045, 265009, 265017, 265018, 264804, 265019, 264780, 264683, 264288, 264766, 264685, 264688, 264768, 52644229, 264689, 21908768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016828 (5565, 5566)	Novel Protein sim. GBank gij728831[ep]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]		lm7	284809, 284628, 263978, 263981
2784	87614380 (5587, 5588)				264259, 29331822, 29331824, 29331825, 284482
2785	88071930 (5589, 5570)	Novel Protein sim. GBank gij2134933[p]rj[S58890 - collapsin response mediator protein - human]		UNCLASSIFIED	22278999, 284908, 264758, 265018, 264768, 21806785, 21806768, 21806769, 265020, 284584
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gij2073564 (U80223) - eukaryotic Initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	284905, 265017
2787	87901266 (5573, 5574)	Novel Protein sim. GBank gij5174507[re]NP_006020.1[pMA1] - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21806765, 21806788, 55811957, 22278999, 284093, 60170615, 264259, 29331822, 18108365, 29331824, 33657109, 29331827, 35896052, 284100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 284369, 264288
2788	88090644 (5575, 5576)	Novel Protein sim. GBank gij3252828 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264103, 21806769, 264693
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gij2495729[sp]Q82556[Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0781 (HA6725)]			284488, 264769, 284910, 284631, 284636, 264680, 284691, 284259, 264638, 29331824, 264508, 284509, 284905, 284563, 284906, 264828, 18108370, 264907, 264764, 264908, 264288, 284909
2790	87602784 (5578, 5580)	Novel Protein sim. GBank gij5101772[emb]CAB45135.1] - (AJ242978) p821 [Homo sapiens]		struct	21806764, 18108368
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gij2911266 (AC002550) - Unknown gene product [Homo sapiens]			22278996, 22278987, 284259, 29331822, 29331824, 29331825, 66714117, 29331828, 60432289, 29331827, 35896052, 284906, 66712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 284288, 284369, 264766, 52044229, 21806765, 21806768, 265020, 265021, 33657023, 263974, 18108374, 65274781, 35895855, 284636, 284556, 264558, 55182323, 83373044, 18108385, 56526486, 60432113, 22279000, 264567
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gij2854163[gb]AAC02581.1] - (AF045842) No definition line found [Caenorhabditis elegans]			264259, 60432289, 86712502, 265009, 264636
2793	87425476 (5585, 5586)			UNCLASSIFIED	264589, 265022, 264691, 18108388, 284567
2794	85794830 (5587, 5588)			UNCLASSIFIED	264589, 265022, 264691, 18108388, 284567

2785	05334888 (5589, 5590)	Novel Protein sim. GBank gi 5454148 ref NP_005348.1 PUB2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35686286, 22278988, 22278989, 60432048, 264259, 29331822, 29331825, 66714117, 60432289, 29331826, 29331827, 35696032, 29331828, 264807, 66712502, 56182435, 264511, 285007, 264512, 264810, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 52844150, 33857023, 264683, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56528486, 60432113, 22278002, 264482, 264563, 264484, 264567
2786	94848857 (5591, 5592)	Novel Protein sim. GBank gi 4680651 gb AAD27715.1 AF13284 - (AF132840) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278989, 264480, 60432048, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264908, 264907, 264808, 66712502, 56182435, 264510, 265008, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433358, 264594, 264595, 55612038, 264596, 21906754, 60174639, 87188474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264369, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52844150, 264692, 33857023, 18108362, 264683, 65274620, 33657109, 33657182, 27488265, 33857349, 18108374, 35696423, 65274781, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87188518, 22278000, 264563, 264564, 264565, 264566, 264567
2787	95110780 (5593, 5594)	Novel Protein sim. GBank gi 4838557 gb AAD31040.1 - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278989, 22278986, 22278997, 29331827, 28148489, 264508, 264806, 56182435, 264757, 21906754, 265010, 265017, 265019, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 28148628, 265020, 52844150, 264680, 33657182, 264629, 18108376, 56182323, 22278002, 264563
2788	86198005 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264488, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264486, 264567

2799	86090651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331826, 35696052, 29331828, 264909, 60433356, 33657402, 33109954, 87168474, 264448, 52644228, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 52644150, 35695855, 264634, 604332113, 22279000, 264488, 56984075, 264259, 20281089, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264766, 264686, 60170615, 264691, 264692, 27486285, 264628, 264629, 264636, 264557, 264558, 264559, 87168516, 264564, 264566, 264567, 265007, 264687
2800	88316481 (5598, 5600)	Novel Protein sim. GBank gi 4240301 dbj BAA74829.1 - (AB020713) KIAA0906 protein [Homo sapiens]		glycoprotein	
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (P1Dg143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35696055
2803	79577446 (5605, 5606)				
2804	57111131 (5607, 5608)	Novel Protein sim. GBank gi 458368 gb AAD23029.1 AC00858 - (AC008585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED - peptidase	264639, 264566
2805	87398488 (5608, 5610)				264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 285009, 21906754, 264369, 264288, 264632, 50170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi 1168873 sp P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148628, 265022, 52644150, 56182323

2807	91720702 (5613, 5614)	Novel Protein sim. GBank gl 4469310 emb CAB37891 - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52644507, 52645156, 52646842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 35696052, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433356, 264594, 60433436, 52646317, 21906754, 33109954, 33657084, 52644286, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264763, 264887, 52644229, 21906765, 21906766, 21906767, 21908768, 21908769, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486281, 27486282, 27486284, 27486285, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gl 5541863 emb CAB51071.1 - (AL096857) hypothetical protein [Homo sapiens]		MHC	60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264586
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gl 2772561 - similar to ciliary dynein beta heavy chain; 78% Similarity to P23098 (PID:gl118965) [Homo sapiens]		ATPase associated	18108351
2810	87259032 (5619, 5620)			UNCLASSIFIED	264569, 22278998, 264091, 264259, 29331828, 29146499, 29146629, 29148784, 264693
2811	91235845 (5621, 5622)	Novel Protein sim. GBank gl 3264583 (AC005189) - match to ESTs H97758 (NID:gl118643) and AA085546 (NID:gl1828773) [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 66712502, 264693
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gl 4240273 db BAA74815.1 - (AB020689) KIAA0892 protein [Homo sapiens]		UNCLASSIFIED	264106
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gl 3548791 (AC005620) - R33590.1 [Homo sapiens]		UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87168518, 60432113
2814	90980908 (5627, 5628)	Novel Protein sim. GBank gl 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	65274572
2815	78774521 (5629, 5630)			UNCLASSIFIED	264907, 264908
2816	95358229 (5631, 5632)			UNCLASSIFIED	264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21906765, 264683, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gi 1283846 (U56866) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265008, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811957, 35695917, 33657109, 263978, 264634, 264636, 264639, 264564, 264565, 264566, 264488, 264587 66712502
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gi 549886 (U13149) - possible apospory-associated protein [Pennisetum ciliare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	
2819	87783527 (5637, 5638)	Novel Protein sim. GBank gi 4929773 (gb AAD34147.1) - AF15209 - (AF15209) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)			UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21908754, 265017, 18108351, 264683, 264369, 264686, 264769, 21908769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385 264636
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gi 398144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gi 2224671 (dbj BAA20820) - (AB002363) KIAA0365 [Homo sapiens]			
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gi 398144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433358, 33657402, 265011, 264760, 21908765, 60170815, 264638 264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gi 398144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		complement	
2825	19742170 (5649, 5650)	Novel Protein sim. GBank gi 3859683 (emb CAA22020) - (AL033503) conserved hypothetical protein [Candida albicans]		UNCLASSIFIED	264907
2826	94311905 (5651, 5652)				264760
					52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 52644150, 33657109, 33657102, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695855, 52644332, 18108385, 87169516, 264484

2827	95320519 (5653, 5654)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	284488, 263394, 264489, 65274572, 28331822, 86714117, 28331827, 29331828, 264508, 264805, 264509, 264806, 264907, 284809, 264809, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21908754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35895855, 264631, 264634, 264635, 264555, 264638, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22278002, 264563, 264564, 264565, 264566, 264567, 264486, 18108391
2828	91229615 (5655, 5656)	Novel Protein sim. GBank gi 3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	28331822, 35896052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264766, 264686, 55811957, 18108370, 18108374, 55810764, 35896423, 55811576, 56182323, 83373044, 87188518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4680889 gb AAD27734.1 AF13295 - (AF132959) CGI-25 protein [Homo sapiens]			22278996, 22278997, 264091, 264093, 60432048, 264259, 29331822, 29331825, 29331827, 29331828, 264805, 264509, 68712502, 264510, 264511, 264593, 60433438, 21908754, 265011, 264603, 18108351, 264288, 21908765, 21905768, 21906769, 29148629, 52844150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264486
2830	88087109 (5659, 5660)	Novel Protein sim. GBank gi 2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1			265008, 265019, 264639, 22278002
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278998, 52646317, 264288, 264686, 21908767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264566, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1 - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	264259, 264112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	18108394, 22278987, 22278988, 26331822, 264907, 264908, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21806767, 55811957, 35685917, 18108374, 56182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gij973378 (U31263) - core protein [Hepatitis C virus]	UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2839	85799317 (5677, 5678)	Novel Protein sim. GBank gij1575515 (U64899) - (thrombospondin-related anonymous protein [Plasmodium gallinaceum])	UNCLASSIFIED	264555
2840	87774665 (5678, 5680)	Novel Protein sim. GBank gij2224605[djBAA20790] - (AB002330) KIAA0332 [Homo sapiens]		264509, 264511, 265011, 264288, 264768, 265020, 264634, 264636, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gij2224605[djBAA20790] - (AB002330) KIAA0332 [Homo sapiens]	dna_rna_bind	56182575, 35696052, 264907, 264908, 264909, 264910, 264593, 264595, 264766, 265022, 264691, 33657182, 35695763, 18108370, 35695855, 264631, 264559, 264563, 264567
2842	80080086 (5683, 5684)	Novel Protein sim. GBank gij578957[embjCAB51350.1] - (AL050306) dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]	UNCLASSIFIED	264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gij585123[spjQ08878]FBLC MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)	UNCLASSIFIED	264906, 264907, 264908, 264909, 264910, 264764, 35685855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	homeobox	28146498, 87168474, 264686, 35696423, 83373044, 264564
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gij5306263[gbjAAD41995.1]AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264628, 264556
2846	88318613 (5691, 5692)	Novel Protein sim. GBank R31180.1 [Homo sapiens]	UNCLASSIFIED	264908, 264766, 264769, 264628, 264637, 264566
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gij5262615[embjCAB45747.1] - (AL080156) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264480, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264766, 264686, 264628, 264629, 264555, 264636, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 56526466, 18108390
2849	86084283 (5697, 5698)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	35686286, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000
2850	87623636 (5699, 5700)			

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gl 4321619 gb AAD15788.1 - (AF051089) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264908, 264907, 58182435, 264758, 55811388, 265010, 18108351, 264448, 264359, 21906785, 264691, 264692, 264693, 35998555, 264556, 18108385, 264567, 264591
2852	86887023 (5703, 5704)	Novel Protein sim. GBank gl 1825728 (U88308) - similar to drosophila membrane protein PATCHED SP-P18502 (PID:g129645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gl 2702347 (AF027503) - putative membrane-associated guanylate kinase, 1 [Mus musculus]	Contains protein domain (PF00397) - Kinase WW domain		56182575, 55811150, 264690, 27488282, 27488285, 264632, 56182323, 56526486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gl 2785823 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1078086) [Homo sapiens]	Contains protein domain (PF01344) - dna_rna_bind Kelch motif		35698286, 29331824, 29331826, 28331828, 264808, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gl 1504040 gb BAA13219 - (D86883) similar to D.melanogaster peroxidase (U11052) [Homo sapiens]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		22278994, 29331822, 29331824, 29331825, 264908, 264808, 265009, 33109954, 265018, 265019, 264448, 21906785, 265020, 264690, 27466265, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gl 3284583 (AC005189) - match to ESTs H97758 (NID:g118643) and AA085546 (NID:g1028773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27488282, 265007, 265009, 285017, 264482, 264563, 18108351
2857	95348288 (5713, 5714)	Novel Protein sim. GBank gl 3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - struct PHD-finger		22278995, 35698286, 29331824, 29331825, 35698052, 264103, 264108, 56182435, 21906765, 21906768, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gl 462585 sp P35227 ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)	Contains protein domain (PF00097) - dna_rna_bind Zinc finger, C3HC4 type (RING finger)		264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264508, 264905, 264906, 28331830, 264908, 52844045, 264809, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 284766, 264768, 18108357, 264769, 21906766, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264629, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264564, 264566, 264486, 264567, 60424178, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906787, 21906769, 55811957, 265021, 56182323
2859	90937675 (5717, 5718)	Novel Protein sim. GBank gl 4325320 gb AAD17331.1 - (AF124427) claudin-15 [Mus musculus]	UNCLASSIFIED		

2860	87532589 (5719, 5720)	Novel Protein sim. GBank gl 4469186 emb CAB38414.1 - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial RNA (5-Methylaminomethyl-2-thiouridyate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264510, 264511, 33109954, 18108351, 264683, 264765, 264389, 264686, 21908785, 264591, 264692, 264693, 18108388, 22279002, 264482
2861	86690507 (5721, 5722)	Novel Protein sim. GBank gl 3941730 (AF108083) - BS4 [Homo sapiens]			264369, 264692
2862	87569585 (5723, 5724)	Novel Protein sim. GBank gl 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein		UNCLASSIFIED	264691, 264638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gl 3248088 (AC004473) - Contains similarity to goliath protein gb M87204 from D. melanogaster. [Arabidopsis thaliana]	Contains protein domain (PF000096) - struct Zinc finger, C2H2 type		56994075, 35696286, 22278998, 29331822, 29331824, 35686052, 29331828, 284106, 264511, 55612038, 33657084, 55811386, 265018, 265019, 21906765, 21906766, 21906769, 35695917, 265020, 265022, 33657023, 33657109, 33657348, 284628, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gl 1078451 p J A55463 - Tropomodulin, skeletal muscle - chicken	struct		284259, 264910
2865	95312191 (5729, 5730)	Novel Protein sim. GBank gl 438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 264482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank gl 585703 sp Q07066 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN		glycoprotein	65274572, 22278996, 22278998, 22278999, 284259, 29331824, 29331827, 29331828, 60433438, 21906754, 265018, 264446, 264764, 52844150, 83373044
2867	86908001 (5733, 5734)	Novel Protein sim. GBank gl 4580997 gb A024571.1 AF12108 - (AF121081) CAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264488, 264768, 21906768, 22278998, 265022, 264259, 264508, 264805, 264807, 264511, 264910, 264635, 264636, 264637, 265011, 265017, 265018, 265019, 264583, 264088, 264566, 264764, 264369, 264567, 264486, 264288, 264768

2868	95303283 (5735, 5738)	Novel Protein sim. GBank gi 1282868 emb CAA63923 - (X94232) L-Cell activation protein [Homo sapiens]		18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 284508, 52844045, 264828, 265006, 265007, 265008, 265009, 264591, 60432228, 264593, 60433356, 264595, 21906754, 265017, 265018, 264682, 264368, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108388, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35698423, 35698555, 264632, 58182323, 87188518, 284404, 22278000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88084412 (5737, 5738)		UNCLASSIFIED	264369
2870	84404574 (5739, 5740)		UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	88318821 (5741, 5742)	Novel Protein sim. GBank gi 5306263 gb AAD41995.1 AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gi 112205 pir B39086 - proline-rich protein 15 - rat	kinase	263981
2873	88084252 (5745, 5746)		UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35698423, 35698286, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264556, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264583, 264482, 264509, 264905, 264908, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264486, 264768, 18108391

2874	94313548 (5747, 5748)	Novel Protein sim. GBank gij3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52644507, 52645156, 52646365, 56182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 28331822, 56182181, 29331824, 80424268, 28331825, 66714117, 29331826, 29331827, 35696052, 28331828, 33656970, 66712502, 52644045, 265007, 265009, 60433356, 264758, 55812038, 18108348, 52646317, 33109954, 33857084, 265017, 264604, 265018, 265019, 264682, 264369, 264288, 264688, 52644229, 21906768, 21906767, 21906768, 55811857, 265020, 265021, 265022, 52644150, 33857023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22278000, 22278002, 264563, 264565
2875	88083728 (5749, 5750)	Novel Protein sim. GBank gij2781388 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (P1D:g1736918) [Homo sapiens]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat	22278996, 22278997, 22278999, 29331826, 29331828, 29146499, 66712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108376, 18108377, 55811576, 60170394, 22278000, 264487
2876	88080854 (5751, 5752)	Novel Protein sim. GBank gij2878530 (AC004449) - R33683_2 [Homo sapiens]	Contains protein domain (PF00167) - Igi	
2877	94747029 (5753, 5754)	Novel Protein sim. GBank gij4704208[emb]CAB41646.1] - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]	Fibroblast growth factor	52646365, 56274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424269, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265019, 55811150, 264448, 264369, 21906766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22278000, 22279002, 264563
2878	88085309 (5755, 5756)	Novel Protein sim. GBank gij3876775[emb]CAB03067] - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	Contains protein domain (PF01207) - UNCLASSIFIED Uncharacterized protein family UPF0034	264468, 264259, 29331822, 29331826, 264805, 264508, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567

2879	87869122 (5757, 5768)	Novel Protein sim. GBank gl 4895145 gb AAD32752.1 - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - UNCLASSIFIED Uracil-DNA glycosylase	18108359, 264259, 264905, 18108370, 264829, 264908, 264909, 18108374, 18108377, 265008, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264567, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gl 4680703 gb AAD27741.1 AF13296 - (AF132966) CGI-32 protein [Homo sapiens]		264488, 52846365, 52846842, 22278994, 35698286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331828, 29331827, 35698052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52846317, 52844298, 87168559, 264600, 264604, 264605, 264760, 264784, 264288, 264766, 264768, 264687, 264769, 21906768, 21906769, 35695917, 265021, 264680, 264692, 33657023, 52845129, 33657109, 33657182, 27486282, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52844332, 264558, 264559, 83373044, 264404, 22278000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gl 733571 (U23452) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	22278998, 29331822, 52844045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gl 118112 (U41559) - No definition line found [Caenorhabditis elegans]		264488, 22278998, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21906768, 21906769, 264693, 263967, 18108374, 55811576, 56182323, 22279002, 264566
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gl 468008 gb AAD31087.1 AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - UNCLASSIFIED WD domain, G-beta repeat	264112, 264682
2884	87784843 (5767, 5768)			265018, 264634
2885	83006308 (5769, 5770)	Novel Protein sim. GBank gl 2224697 db BAA20832 - (AB002376) KIAA0378 [Homo sapiens]	UNCLASSIFIED	264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gl 1255889 (U53344) - T07H8.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - complementrecept Sushi domain (SCR repeat)	60432049, 264259, 29331828, 264908, 264511, 264595, 60433438, 264596, 265017, 264605, 263989, 263972, 264555, 83373044, 87168518, 264596
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gl 3882323 db BAA34521.1 - (AB018344) KIAA0801 protein [Homo sapiens]	UNCLASSIFIED	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gl 4508015 ref NP_003447.1 pZNF2 - zinc finger protein 205 [Homo sapiens]	Contains protein domain (PF00098) - transcriptfactor Zinc finger, C2H2 type	264488, 264259, 29331828, 264508, 264908, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87606562 (5777, 5778)				UNCLASSIFIED	56994075, 28331824, 265008, 264760, 18108354, 264288, 264591, 264766
2890	78703853 (5778, 5780)	Novel Protein sim. GBank gl 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	
2891	88084428 (5781, 5782)	Novel Protein sim. GBank gl 3877750 emb CA801508 - (Z78084) predicted using GeneFinder, similar to collagen; cDNA EST EMBL:D65865 comes from this gene; cDNA EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D66028 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...			UNCLASSIFIED	284591, 284595, 284369, 284685, 284693, 284628, 284583, 284568
2892	95418745 (5783, 5784)	Novel Protein sim. GBank gl 492879 gb AAD34140.1 AF15190 - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	65274572, 35686286, 29331828, 284110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21908765, 21908766, 21908769, 55811957, 264680, 65274620, 263967, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	284259, 265010, 284682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gl 5669015 gb AAD46135.1 - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		transcript factor	284259, 265006, 60433438, 52644296, 265011, 264369, 35685917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gl 3924708 emb CAA84646 - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMBL...	Contains protein domain (PF01437) - Plexin repeat			29331824, 265007, 264762, 284636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gl 4885549 ref NP_005456.1 pPKBG - protein kinase B gamma	Contains protein domain (PF00089) - Eukaryotic protein kinase domain		kinase	18108392, 18108394, 18108398, 22278998, 284258, 29331822, 29331824, 29146499, 264906, 284908, 265007, 265009, 265018, 265019, 264369, 264685, 264689, 21908766, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gl 4502877 ref NP_001296.1 pCLDN - Clostridium perfringens enterotoxin receptor 1			UNCLASSIFIED	60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433356, 60433438, 65274444, 55811386, 265018, 18108351, 264448, 284288, 264687, 21908765, 21908766, 21908767, 21908769, 55811957, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 284628, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 284604, 18108385, 284566

2899	80357670 (5797, 5798)	Novel Protein sim. GBank gij4581470[emb CAB40137.1] - (Y18483) SLC7A8 protein [Homo sapiens]		UNCLASSIFIED	284764, 21906764, 284692
2900	84233538 (5789, 5800)			glycoprotein	65274572, 56182575, 35696286, 60432048, 284259, 29331824, 86714117, 29331828, 35698052, 29331828, 68712502, 56182435, 285006, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 284785, 264288, 264768, 21906764, 21906768, 21906769, 265020, 284692, 284693, 32833986, 284631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gij4759272[ref NP_004814.1 pTTC4 - tetra-tricopeptide repeat domain 4		phosphatase	22278895, 22278897, 22278899, 60432048, 29331822, 29331824, 29331825, 29331827, 35698052, 33656970, 284910, 265009, 21908754, 33657084, 87168474, 265010, 265018, 21908764, 21908785, 21908788, 21908767, 21908768, 33657023, 264693, 33857109, 33857349, 35698423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gij2414615[emb CAB16384] - (Z99259) hypothetical protein [Schizosaccharomyces pombe]			284683, 264691
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gij1079318[pri S52241 - XLCL2 protein - African clawed frog			284887, 22278984, 264259, 29331828, 29331828, 264905, 52644045, 56182435, 264511, 265017, 285018, 18108351, 284448, 264683, 264769, 264689, 35695917, 52844150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)	Novel Protein sim. GBank gij5639823[gb AAD45885.1 AF143676) multispinning nuclear envelope membrane protein nurim [Homo sapiens]		UNCLASSIFIED	52844365, 22278898, 264259, 35696052, 265011, 265017, 264683, 264768, 35695917, 285020, 283867, 18108374, 35695855, 264637, 264952, 18108385, 18108387
2905	84449828 (5809, 5810)	Novel Protein sim. GBank gij728837[sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	265009, 284681, 264682
2908	95341051 (5811, 5812)	Novel Protein sim. GBank gij4689256[gb AAD27831.1 AF121855) sorting nexin 8 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	UNCLASSIFIED	22278898, 35696288, 22278988, 264259, 60432289, 29331828, 29331830, 68712502, 265009, 60170831, 33109954, 264448, 264683, 264288, 264689, 21908768, 21908767, 21908768, 55811957, 35695917, 265022, 52644150, 264691, 33657023, 284692, 284693, 35695855, 60432113, 284566

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gi 1707079 (U80451) - contains strong similarity to a DNA-J-like domain (PS:PS00836) [Caenorhabditis elegans]	Contains protein domain (PF00226) - eph DnaJ domain	52644507, 56182575, 56181686, 22278995, 56994075, 35696286, 60432049, 56182181, 35696052, 60431735, 264595, 55812038, 21906754, 55811386, 265019, 264682, 264369, 56181582, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2808	80414246 (5815, 5816)	Novel Protein sim. GBank gi 2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]	helicase	265009, 33109854, 18108351, 264766, 265021, 264691, 264892, 18108374, 264556, 264638, 264557, 264558
2809	87420225 (5817, 5818)		eph	264259, 87168474, 265018, 18108355, 264628
2810	86601075 (5819, 5820)	Novel Protein sim. GBank gi 4539335[emb]CAB37483.1] - (AL035539) putative protein [Arabidopsis thaliana]		22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2811	94216615 (5821, 5822)	Novel Protein sim. GBank gi 4469187[emb]CAB38415.1] - (AL031588) dJ1163J1.3 (novel protein similar to mouse B99) [Homo sapiens]	glucoamylase	52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2812	87731803 (5823, 5824)	Novel Protein sim. GBank gi 4929637[gb]AAD34079.1]AF15184 - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat	52645156, 264082, 60432049, 264259, 52645080, 29331824, 29331825, 68712502, 33109854, 264760, 264683, 264288, 264686, 265021, 264689, 18108368, 263976, 264404
2813	87713823 (5825, 5826)	Novel Protein sim. GBank gi 854065[emb]CAA56337] - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED Zinc finger, C2H2 type	52644507, 52645156, 52646842, 56182575, 35696286, 22278997, 264259, 52645080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264688, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264553
2814	87797300 (5827, 5828)			264557

2915	68081872 (5828, 5830)	Novel Protein sim. GBank gl 5174485 ref NP_008030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain Lectin C-type domain	eph	264569, 264488, 264687, 264768, 21806766, 52648842, 21906767, 21908768, 58182575, 29148829, 35695917, 22278998, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 264259, 60432048, 264892, 52645129, 33657109, 33657182, 29331827, 27488261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657349, 29148498, 29146498, 264908, 264807, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56182323, 18108382, 55812038, 18108385, 33109954, 21908764, 33857084, 87168918, 265010, 265011, 60432113, 265017, 265018, 22279000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264883, 264566, 18108354, 264389, 264288, 264768
2916	95337780 (5831, 5832)	Novel Protein sim. GBank gl 5104851 db GBAA80165.1 - (AP000081) 305aa long hypothetical dTDP-4- dehydrothiamose reductase [Aeropyrum pernix]		dehydrogenase	52645156, 65274572, 22278894, 22278995, 35696286, 22278998, 22278997, 22278998, 22278998, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33856970, 264509, 264908, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33857084, 52644286, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27488261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22278002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gl 3169065 emb CAA19260.1 - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264602, 264882, 87168518, 60432113
2918	85680529 (5835, 5836)	Novel Protein sim. GBank gl 539218 pir J S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)			264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gl 2564955 (AF030001) - unknown [Mus musculus]			66714117, 66712502, 263981

2820	87769523 (5839, 5840)				35696286, 22278997, 264259, 52645080, 29331824, 29331826, 29331827, 264828, 264909, 56182435, 264511, 264758, 33109954, 21908754, 52644286, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52844150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27486265, 35696423, 35695855, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 67168518, 60432113
2821	91639882 (5841, 5842)	Novel Protein sim. GBank gl[4580013]gb[AA24202.1]U83194 - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		35696286, 22278997, 264091, 264092, 264094, 264258, 29331822, 29331824, 29331826, 29331827, 35686052, 29146498, 264104, 264105, 264107, 264508, 264110, 264112, 264512, 60433358, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906768, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108378, 264555, 263881, 56526486, 87168518, 22278990, 22278902, 284906, 264909, 264511, 265006, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29148627, 35695917, 264682, 264628, 263978, 55811576, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264486
2822	87749782 (5843, 5844)	Novel Protein sim. GBank gl[4589514]dbj[BAA78779.1] - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - kinase Glycosyl hydrolases family 38		264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52844150, 264681, 264692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22279000, 264563, 264568
2823	95337789 (5845, 5846)	Novel Protein sim. GBank gl[4835268]emb[CAB42898.2] - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain		265017, 264628, 20281152, 264556
2824	87791807 (5847, 5848)	Novel Protein sim. GBank gl[2133085]pir[IS]Z254 - ribosomal protein L36, mitochondria - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - ribosomal prot		
2825	95090120 (5849, 5850)	Novel Protein sim. GBank gl[2388886]emb[CAB11718] - (Z98980) actin associated protein [Schizosaccharomyces pombe]	UNCLASSIFIED		56182575, 35696286, 264259, 60432289, 29331827, 264508, 52844045, 264910, 264581, 60432228, 55812038, 21906764, 264681, 264448, 264683, 264288, 264685, 52844229, 264689, 21906765, 21906766, 21906768, 21906769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35696423, 65274791, 56182323

2828	95343003 (5851, 5852)	Novel Protein sim. GBank gi 283032 prj S22456 - hydroxyproline-rich glycoprotein - perennial teasinte		28331828, 265011, 264768, 264689, 264764, 264288, 264630, 264637
2827	60408018 (5853, 5854)			
2828	20452179 (5855, 5856)		UNCLASSIFIED	264559
2829	91622820 (5857, 5858)	Novel Protein sim. GBank gi 3413320 emb CAA06915 - (AJ008215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]	UNCLASSIFIED	264559, 264489, 22278994, 35696286, 22278998, 22278999, 264094, 264259, 52845080, 28331822, 29331824, 66714117, 28331825, 28331826, 28331827, 35696052, 35696070, 284109, 29331830, 52844045, 265008, 33109954, 52644288, 87168559, 284760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264587, 264486
2830	95302755 (5859, 5860)		UNCLASSIFIED	56182575, 56181686, 35696286, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52844045, 56182435, 285009, 60170831, 264592, 60432229, 60433356, 87168474, 285010, 265011, 265017, 285018, 265019, 264762, 264448, 264683, 264288, 264768, 21906765, 21906769, 35695917, 60170815, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264587
2831	94312893 (5861, 5862)	Novel Protein sim. GBank gi 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	52645156, 22278997, 22278998, 29331822, 52645080, 28331824, 60432289, 33656970, 60433358, 60433438, 33109954, 21906765, 21906768, 21906769, 33657023, 33657109, 33857182, 52644150, 33657023, 33657109, 33857182, 27486265, 35696423, 35695855, 264555, 87168518, 60432113, 264588, 264906, 264907
2832	78632623 (5863, 5864)			
2833	91720776 (5865, 5866)	Novel Protein sim. GBank gi 3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase	264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52844045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644228, 21906765, 21906768, 21906769, 265022, 52644150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264568, 264569, 264567

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27486282, 264628, 87168518, 22278000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21908754, 265018, 265019, 264448, 264789, 21908764, 21908765, 265021, 264682, 33657023, 33657109, 33657349, 55810764, 22279000, 22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gi4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	56984076, 22278998, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264806, 264908, 264809, 56182435, 265006, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52644228, 21906765, 29148784, 65274791, 264658, 56182323, 60170394, 264558, 60432113, 264565, 264486, 264587, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 265008, 265009, 60432228, 33657402, 60433436, 55812038, 21908754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21908765, 21908787, 21908768, 55811957, 35695917, 265020, 60170815, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263976, 35696423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56526486, 60432113, 22278002
2937	94853096 (5873, 5874)	Novel Protein sim. GBank gi15174409 [NP_006101.1] pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	264907, 265018, 264681, 264685, 264686
2938	95419773 (5875, 5876)	Novel Protein sim. GBank gi3319990 [emb] [CAA76720] - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	
2939	87786622 (5877, 5878)	Novel Protein sim. GBank gi3979900 [emb] [CAA9909] - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	

2840	95011103 (5878, 5880)			UNCLASSIFIED	22278986, 28331822, 28331824, 66714117, 29331826, 29331828, 284905, 284908, 66712502, 29331830, 285011, 285017, 284784, 284369, 21908766, 21908767, 33657023, 33657108, 32833886, 18108374, 18108377, 284634, 83373044, 18108385, 18108387, 284566
2841	21423370 (5881, 5882)	Novel Protein sim. GBank gi 3413872 db BAA32300 - (AB007824) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	284557
2842	87430203 (5883, 5884)	Novel Protein sim. GBank gi 1172845 ep P46829 RB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	264910, 265010, 264768
2843	95314504 (5885, 5886)	Novel Protein sim. GBank gi 4929653 gb AAD34087.1 AF15185 - (AF151850) CGI-92 protein [Homo sapiens]		collagen	60432049, 264258, 60432289, 29331827, 29146488, 265008, 284593, 60433358, 60433438, 285010, 285011, 285017, 265018, 284683, 264768, 18108381, 65274727, 60432113, 264567
2844	95081083 (5887, 5888)	Novel Protein sim. GBank gi 4678282 emb CAB41190.1 - (AL048680) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - ATPase associated Regulator of chromosome condensation (RCC1)		56984075, 22278988, 60432049, 284259, 29331822, 29331824, 60424289, 60432289, 29331826, 29331828, 284905, 264807, 52844045, 284909, 284511, 265008, 285009, 284594, 21908794, 87168559, 284803, 265017, 265018, 18108351, 264682, 284766, 264687, 284689, 21908765, 21908766, 21906767, 21906768, 21906769, 265021, 60170615, 52844150, 264680, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35698423, 35698555, 264835, 264555, 264556, 66182323, 60170394, 264558, 284559, 83373044, 56526486, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2845	94233560 (5889, 5890)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35686052, 264808, 265008, 60433356, 55812038, 264759, 55811386, 265018, 284681, 18108351, 264448, 264683, 264389, 264288, 284687, 56181562, 21908767, 21908768, 21908769, 35695917, 285020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567

2946	94317315 (5891, 5892)	Novel Protein sim. GBank gi 5441952 gb AAD43195.1 AF072864 peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	264488, 264259, 264508, 264509, 264808, 264907, 264909, 264510, 264511, 285007, 284512, 284910, 264591, 284593, 18108351, 264764, 264288, 264684, 264769, 285021, 264692, 33857109, 284628, 284629, 18108374, 284631, 284634, 284636, 284637, 18108380, 284638, 284639, 83373044, 284555, 284556, 264486, 264567
2947	87362952 (5893, 5894)	Novel Protein sim. GBank gi 354028 gb AAC34383.1 - (AF056116) Ail-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432228, 21906754, 285010, 265017, 265019, 264766, 284685, 21906765, 21906766, 21906767, 21906768, 21906769, 285020, 264628, 18108370, 264629, 264630, 18108387, 60432113, 52646842, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264686, 21906767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 264563, 264567
2948	87626527 (5895, 5896)	Novel Protein sim. GBank gi 5566614 gb AAB65654.2 - (AF001533) mitogen-induced [Mus musculus]			22278996, 22278997, 60432288, 29331826, 29331827, 29331828, 35696052, 28146499, 284104, 264107, 264905, 68712502, 284908, 60433356, 60433438, 87168558, 264764, 52844229, 56181562, 21906767, 21906768, 21906769, 265022, 60170615, 33857023, 35696423, 263981, 284558, 60432113, 22279002
2949	88175545 (5897, 5898)	Novel Protein sim. GBank gi 2132923 pir S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264488, 35698286, 284259, 35698052, 284907, 285007, 264910, 265017, 285018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108378, 35698423, 65274791, 35695855, 264556, 56526486, 264486
2950	95080870 (5899, 5900)	Novel Protein sim. GBank gi 466102 sp P34629 YOJ6_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - Cytosol aminopeptidase family	peptidase	264686
2951	87392357 (5901, 5902)	Novel Protein sim. GBank gi 4688902 emb CAB41450.1 - (AJ238248) centaurin beta2 [Homo sapiens]			264683

2952	95329952 (5903, 5904)	Novel Protein sim. GBank gl 5596993 emb CAB51405.1 - (AL098881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - CRAL/TRIO domain.	transcript factor	264887, 52645156, 21908766, 21908769, 22278996, 265020, 264680, 60432048, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27488282, 264508, 264905, 20281149, 264906, 264807, 29331830, 264908, 264809, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433356, 264639, 264758, 87168318, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	86093575 (5905, 5906)	Novel Protein sim. GBank gl 119522 sp P10658 SERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)	Contains protein domain (PF00266) - Aminotransferases class-V	UNCLASSIFIED	18108398, 56994075, 22278896, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264807, 264510, 264591, 264594, 33657402, 264595, 264596, 264758, 52646317, 21908754, 33857084, 52644286, 87168559, 264600, 264760, 264661, 18108351, 264764, 264368, 264288, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 33857023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2954	86086288 (5907, 5908)	Novel Protein sim. GBank gl 486526 ref NP_005251.1 pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Igf Transforming growth factor beta like domain	Igf	
2955	87688426 (5909, 5910)	Novel Protein sim. GBank gl 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 264908, 52644045, 264512, 60432229, 265018, 265019, 5581150, 264769, 21908767, 21908768, 21908769, 265021, 60170615, 55810764, 264567
2956	85789745 (5911, 5912)	Novel Protein sim. GBank gl 489254 gb AAD27830.1 AF12185 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264808, 21908768
2957	90833301 (5913, 5914)	Novel Protein sim. GBank gl 4503023 ref NP_000089.1 pCPT2 - carnitine palmitoyltransferase II precursor		cadherin	22278998, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148829, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gl 4240257 db BAA74907.1 - (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264596, 264661, 264369, 264629, 264631, 264567

2959	95109420 (5917, 5918)	Novel Protein sim. GBank gi 988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - TBC domain	oncogene	263994, 22278997, 264259, 60432048, 29331826, 29331828, 35696052, 29331830, 66712502, 56182435, 265006, 264512, 265008, 265009, 60433356, 60433438, 264586, 265017, 265018, 264683, 264288, 264766, 264769, 21906766, 21906767, 21906769, 265020, 60170615, 264692, 27486285, 18108374, 65274781, 35696555, 83373044, 56528488, 60432113
2960	87420091 (5918, 5920)			UNCLASSIFIED	35696286, 56182435, 67188474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2961	85413416 (5921, 5922)	Novel Protein sim. GBank gi 5596646[embj CA805177.2] - (Z82266) predicted using GeneFinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 5284045, 265006, 33657402, 21906764, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264567
2962	87812700 (5923, 5924)			UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264508, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486
2963	95313464 (5925, 5926)	Novel Protein sim. GBank gi 4240223[dbj BAA74880.1] - (AB020674) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	18108382, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33657023, 264693, 65274620, 33657182, 27486261, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2964	94324617 (5927, 5928)			UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108388, 35696423, 83373044, 18108388

2865	80384762 (5929, 5930)	Novel Protein sim. GBank gi 4885447 ref NP_005452.1 pKRML - Kreiser (mouse) mal- related leucine zipper homolog			transcript factor	284259, 29331826, 284508, 284509, 284805, 284907, 284908, 284909, 284511, 285008, 284910, 284591, 284593, 284594, 33657402, 285011, 284760, 284762, 284764, 284288, 284685, 284766, 284692, 33657109, 284628, 284629, 35895855, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 284639, 284563, 284567, 18108391 60432289, 284662, 284448
2866	91725248 (5931, 5932)	Novel Protein sim. GBank gi 526275 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]				
2867	94658303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]			UNCLASSIFIED	264488, 284508, 284509, 284908, 284909, 264511, 284910, 284594, 284756, 85658542, 284762, 284764, 265021, 284556, 18108381, 284594, 284486
2868	95302776 (5935, 5936)	Novel Protein sim. GBank gi 4929715 gb AAD34118.1 AF15188 - (AF15188.1) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)			284687, 52645156, 21806765, 52646365, 21806767, 18108398, 35866423, 22278999, 3586286, 22278997, 265020, 22278999, 265021, 265022, 284093, 284636, 284680, 52644150, 284258, 33657023, 52645080, 284693, 29331822, 56182181, 29331824, 66714117, 29331825, 33108954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35896052, 27486262, 87168518, 87168474, 265010, 87168559, 265018, 22278000, 265019, 22279002, 284563, 18108351, 264906, 284907, 264448, 66712502, 284588, 284369, 284288
2869	95310957 (5937, 5938)	Novel Protein sim. GBank gi 3024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph		52946842, 22278996, 22278998, 22278999, 60432049, 284258, 29331824, 29331825, 29331826, 29331828, 264509, 284909, 52844045, 56182435, 285008, 60433438, 55912038, 21906754, 265011, 87168559, 265018, 265019, 284448, 264288, 284369, 52944229, 21906766, 21906768, 21906769, 29148784, 265020, 265021, 52644150, 284681, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2870	88088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004755) - fos37502.1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox		

2971	94196830 (5941, 5942)	Novel Protein sim. GBank g1728837sp1P39194/ALU7 SQ WARNING ENTRY III		Im7	264488, 56182575, 35696286, 56984075, 29331824, 29331826, 29146489, 264508, 264905, 264907, 264112, 264910, 21908754, 87168559, 265018, 285019, 18108351, 264689, 21906765, 21906767, 21906768, 265020, 265021, 60170615, 18108364, 284628, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264584, 264567 265017, 35695917, 265021, 33657109, 22278002, 264563
2972	86825943 (5943, 5944)	Novel Protein sim. GBank g1728837sp1P39193/ALU6 SQ WARNING ENTRY III		kinase	
2973	91215301 (5945, 5946)	Novel Protein sim. GBank g17246789 (AF040642) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank g1786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108382, 52644507, 56182575, 56181686, 22278985, 22278986, 35696286, 22278987, 22278988, 22278989, 264259, 52645080, 29331824, 29331825, 86714117, 60424269, 29331826, 29331827, 29331828, 35696052, 66712502, 284908, 52844045, 265007, 284910, 285009, 60433436, 33109954, 21906754, 55811386, 52644286, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264389, 264288, 52844229, 18108358, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 52844150, 264681, 264692, 33657023, 27486262, 27486264, 35695763, 18108370, 18108376, 55810764, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52844332, 264558, 83373044, 18108387, 87168518, 60432113, 22278000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank g13880812[emb]CAA19508] - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85658542, 265011, 265018, 264448, 264288, 264769, 21908767, 265020, 264691, 264559, 83373044
2976	87771202 (5951, 5952)	Novel Protein sim. GBank g15679130[gb]AAD46874.1[AF160934] BCDNA.LD14189 [Drosophila melanogaster]		transport	22278996, 264908, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 284689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank g15262751[emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2878	87332059 (5955, 5956)	Novel Protein sim. GBank gij746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 56182435, 265008, 265007, 265009, 60433398, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21908765, 21908766, 21908767, 21908768, 21906799, 265020, 265021, 265022, 35698423, 264639, 60432113, 22279000, 22279002
2879	81725256 (5957, 5958)	Novel Protein sim. GBank gij5282751[emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement		264488, 65274572, 56994075, 22278998, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2880	88296600 (5959, 5960)			UNCLASSIFIED	265009, 21908767, 263361, 22279000
2881	87376330 (5961, 5962)				264629, 264584
2882	95303675 (5963, 5964)	Novel Protein sim. GBank gij4929767[gb]AAD34144.1[AF151907] CGI-149 protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264598, 33657084, 264448, 21906765, 21906766, 21908767, 21908768, 21908769, 265020, 265022, 18108365, 33657182, 33657349, 35698423, 83373044, 22279000, 22279002
2883	91725258 (5965, 5966)	Novel Protein sim. GBank gij5282751[emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60424178, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33658970, 264905, 52644045, 265006, 60431735, 87188474, 265018, 265019, 18108351, 264448, 21908765, 21908768, 35695917, 33657023, 52645129, 18108370, 35698423, 83373044, 56528486, 60432113, 264404, 22279002
2884	94136487 (5967, 5968)	Novel Protein sim. GBank gij238734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130819) [Homo sapiens]	ATPase associated		
2885	87099072 (5969, 5970)	Novel Protein sim. GBank gij1003160[pir]S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		264910, 55812038, 56181562, 55811957, 264628, 55810764, 264632, 264635, 60432113
2886	86284861 (5971, 5972)				55811957, 264566
2887	80455934 (5973, 5974)		UNCLASSIFIED		264369

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gi 4678028 gb AAD27002.1 - (AF077207) HSPC021 [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 22278995, 22278998, 22278997, 22278999, 264092, 264094, 264259, 60432049, 29331824, 29331828, 60432289, 35696052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265008, 265007, 265008, 60170831, 60432229, 264593, 60433358, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264389, 264288, 264685, 5284229, 21908765, 21908767, 21908769, 35685917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35685855, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264584, 264585, 264566, 264567
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gi 113871 sp P23984 ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII			
2990	87330444 (5978, 5980)	Novel Protein sim. GBank gi 2829836 sp P97348 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	kinase		22278996, 22278997, 264905, 264511, 60170831, 264593, 265019, 21908765, 265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2991	94325361 (5981, 5982)				
2992	85425184 (5983, 5984)				
2993	94325363 (5985, 5986)				
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gi 2486548 sp Q50658 YU02_MYCTU - HYPOTHETICAL 29.7 KD PROTEIN CY339.02		UNCLASSIFIED	264563
				UNCLASSIFIED	264259, 265019, 264689, 18108385
				UNCLASSIFIED	264488, 29331822, 265017, 264761, 21908769, 65274791, 263981, 264565
			transport		22278994, 22278995, 56994075, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21908767, 21908768, 21908769, 265021, 265022, 33657023, 264693, 35695855, 83373044, 18108385, 22279000, 264565, 264568
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]			264805, 264907, 265019, 18108351, 264683
2998	91013798 (5991, 5992)	Novel Protein sim. GBank gi 2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase		65274572, 35696286, 264259, 29331824, 35696052, 29148499, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264766, 264769, 264689, 35685917, 60170815, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484

2997	87627440 (5893, 5994)	Novel Protein sim. GBank gi4598652[djBAA76848.1] - (AB0233221) KIAA1004 protein [Homo sapiens]		homeobox	264488, 56182575, 264259, 56714117, 29331826, 35698052, 264508, 264508, 264907, 264908, 265008, 87168474, 265019, 264448, 264682, 264685, 264766, 21908764, 21908766, 21908768, 21908769, 27488261, 18108374, 35686423, 264634, 264635, 264636, 264557, 18108385, 87168518, 52646365, 22278997, 264508, 264908, 18108351, 21908765, 21908767, 18108370, 18108374, 35686423, 264636, 264639
2998	88095381 (5895, 5996)	Novel Protein sim. GBank gi3947589[emb]CAA22252] - (AL034384) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278996, 29147620, 29331825, 29146498, 29146499, 264905, 68712502, 265006, 265009, 21908754, 85658542, 18108351, 28146627, 29146629, 60170815, 33657109, 27486262, 18108370, 18108374, 264556, 264557, 264558, 60170394, 18108385, 264563
2999	94847055 (5987, 5988)	Novel Protein sim. GBank gi115408[sp]P18835[CC19_CAEEL - CUTICLE COLLAGEN 19		UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35698052, 29146498, 264508, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265008, 265007, 265008, 265009, 264910, 33657402, 284757, 264595, 264596, 264758, 21906754, 265011, 264600, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35695917, 265020, 264691, 264692, 33657023, 264693, 33657108, 33657182, 27466281, 264628, 264629, 18108374, 18108376, 35698423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20798451, 22279002, 264563, 264486, 264567
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gi2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g844442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]		calthepsin	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 264910, 33108954, 52644298, 265017, 265019, 264288, 265020, 265021, 52644150, 264692, 35695783, 55810764, 35698423, 56182323, 18108387, 264563, 264564
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gi3599478 (AF085185) - Myosin-1A [Acanthamoeba castellanii]		UNCLASSIFIED	264488, 29331824, 29331825, 26331826, 29331827, 29331828, 264908, 264510, 265009, 21908754, 264682, 264688, 33657023, 264565

3003	86848079 (6005, 6006)	Novel Protein sim. GBank gij1754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - collagen Collagen triple helix repeat (20 copies)	284512, 284593, 284564, 264567, 264486
3004	88066876 (6007, 6008)	Novel Protein sim. GBank gij2224629[gbjBAA20802] - (AB002342) KIAA0344 [Homo sapiens]		29331830, 21906769, 264681, 33657109, 283972, 18108385
3005	87794843 (6009, 6010)	Novel Protein sim. GBank gij4680659[gbjAAD27719.1]AF13294 - (AF132944) CGI-10 protein [Homo sapiens]	Contains protein domain (PF01360) - Monooxygenase	29331822, 29331824, 29331827, 60433438, 265011, 265019, 21906766, 21906767, 21906768, 265020, 33657023, 33657348, 60170394, 22278002, 264567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gij3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - MHC Ank repeat	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264691, 264555, 264556, 264558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gij2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170815, 18108374, 20281152, 264636, 52844332
3008	80418248 (6015, 6016)		Contains protein domain (PF00501) - AMP-binding enzyme	264805, 284593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gij3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	synthase	52646842, 56182575, 22278995, 22278996, 284259, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109954, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264369, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108368, 27486262, 20281149, 18108370, 55811576, 264637, 264556, 264557, 18108381, 264558, 56182323, 264559, 18108385, 18108388, 22278002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gij4927370[gbjAAD33084.1]AF06797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - Protein of unknown function	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170815, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264908, 55811576, 35695855, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gij5052319[gbjAAD38501.1]AF11883 - (AF118838) citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	35696052, 56182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 284682, 264448, 21906766, 85274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)		UNCLASSIFIED	263972

3013	91238789 (8025, 6026)	Novel Protein sim. GBank gij3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcript factor	264488, 263994, 35696286, 22278997, 264259, 29331824, 60424289, 68714117, 35696052, 264905, 264908, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21908754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264766, 264686, 264768, 264687, 21908767, 35695917, 265020, 33657023, 264692, 264683, 33657109, 264628, 264629, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264565, 264566, 264567
3014	78877263 (6027, 6028)	Novel Protein sim. GBank gij3878374[emb]CAA93081] - (Z88879) Similarity to Yeast Chf12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase-associated	264760
3015	86995468 (6029, 6030)				22278995, 22278998, 22278997, 264259, 29331824, 29331828, 264906, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264564
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gij1168819[sp]P41733[CC81_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52648842, 56994075, 52645080, 29331822, 29331824, 35696052, 33658870, 52644045, 264598, 33657084, 265017, 265019, 52644228, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486284, 33657349, 27486265, 35695763, 35695855, 87188518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gij4589656[db]BAA76851.1] - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278998, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264809, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21908754, 55811386, 265010, 265011, 87188559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21908767, 21908769, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108386, 56526486, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)	Novel Protein sim. GBank glj3219332 (AC004020) - Unknown gene product (Homo sapiens)		264558 264569, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264808, 56182435, 265007, 265009, 60432228, 264593, 60433356, 55812038, 21906754, 87168474, 285011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21906766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 284629, 65274781, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264563
3019	94148231 (6037, 6038)		oncogene	
3020	94318251 (6039, 6040)	Novel Protein sim. GBank glj3414809 (AF061529) - rjs (Mus musculus)	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	264488, 263994, 35696286, 264258, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264486
3021	80478512 (6041, 6042)	Novel Protein sim. GBank glj3880889 (emb) (CAB09005) - (Z95559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL.C13455 comes from this gene; cDNA EST yk329g8.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]		264769, 264628, 264482
3022	87718500 (6043, 6044)			
3023	95305484 (6045, 6046)	Novel Protein sim. GBank glj416582 [sp]P32323JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	UNCLASSIFIED	264259, 29331826, 29331828, 264288, 264566
3024	86675305 (6047, 6048)		Contains protein domain (PF00614) - Phospholipase D. Active site motif	264488, 22278995, 35696286, 22278997, 29331828, 35696052, 264807, 29331830, 52644045, 56182435, 60432228, 264592, 60433356, 60433438, 264689, 21906767, 55811857, 35695917, 265021, 18108378, 263978, 264635, 264558, 22279000
3025	65706628 (6049, 6050)	Novel Protein sim. GBank glj295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]	UNCLASSIFIED	60432048, 264760, 21906769, 55811857, 35695917, 264690, 264555, 264559, 264593, 55811576

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gl 3024052 sp P97924 KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21906765, 29148627, 263887, 20281149, 20281089, 263975, 263977, 20281071, 56526486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gl 4929847 gb AAD34084.1 AF15184 - (AF151847) CGI-89 protein [Homo sapiens]	Contains protein domain (PF01528) - D1HC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 35695917, 265020, 265021, 265022, 52644150, 264692, 27486281, 18108374, 55811576, 35698423, 33657023, 264693, 52645129, 33657109, 65274781, 264638, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56526488, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gl 3080521 emb CAA18650 - (AL022599) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486265, 264628, 264629, 18108374, 35698423, 35695655, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 264534, 264690, 264693, 263989, 18108370, 264558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gl 3757729 emb CAA18782 - (AL022727) dJ80119.1 (olfactory receptor-like protein [hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	lm7	
3031	91877853 (6061, 6062)	Novel Protein sim. GBank gl 4530587 gb AAD22105.1 - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56526488, 22279000, 22279002

3032	94130124 (6063, 6064)	Novel Protein sim. GBank gi 1019951 (U37428) - similar to M. musculus MER5 and other AHPCTSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	22278996, 35696286, 264259, 29331824, 29331828, 264907, 29331830, 264768, 33109954, 87168474, 87168559, 265019, 264286, 21906769, 265021, 264693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gi 5031573 jref NP_005712.1 pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - struct Actin	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264591, 21908754, 265010, 265019, 264681, 264369, 264768, 21908764, 21906768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264638, 264482, 264563
3034	80415373 (6067, 6068)			UNCLASSIFIED
3035	91220682 (6069, 6070)	Novel Protein sim. GBank gi 3738207 emb CAA21262 - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]		264906, 264907, 264510, 264592, 265010, 264762, 264768, 264637, 264638, 264486
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		264636
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi 4406590 gb AAD20040 - (AF131786) Similar to Ena-VASP like protein [Homo sapiens]	kinase	264907, 33657402, 265021
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gi 5360093 gb AAD42865.1 AF155089 NY-REN 18 antigen [Homo sapiens]		265017
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi 4757128 emb CAB42094.1 - (AJ238717) ZRP protein [Rattus norvegicus]	Contains protein domain (PF00627) - UNCLASSIFIED UBA domain	22278996, 22278997, 264259, 264905, 265007, 265009, 60433356, 21906754, 265018, 265019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486262, 264636, 56182323, 18108385, 22278000
3040	90833517 (6079, 6080)	Novel Protein sim. GBank gi 4884278 emb CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]		UNCLASSIFIED
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gi 3876073 emb CAB04122.1 - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...		35696286, 29331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 264628, 18108374, 263977, 35696423, 264584, 18108391, 264682, 264556, 18108382, 18108385, 264567
3042	85748402 (6083, 6084)	Novel Protein sim. GBank gi 790236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]	UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33656970, 33108954, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22278002
			glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank glij84085[embjCAA58337] - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	35868286, 60424268, 35868052, 264508, 264805, 66712502, 56182435, 55811388, 52644296, 55811150, 35895917, 60170815, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank glij4104922 (AF042276) - o251 homolog [Pseudomonas putida]		Contains protein domain (PF01209) - ubiE/COQ5 methyltransferase family	glycoprotein	22278998, 22278998, 22278999, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433356, 33109854, 18108351, 264288, 35895917, 18108368, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank glij458988[dbj]BAA76859.1] - (AB023232) KIAA1015 protein [Homo sapiens]		Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_rna_bind	264488, 264259, 35868052, 264508, 264805, 264509, 264808, 264907, 264909, 264511, 265006, 264591, 264593, 33109854, 264604, 264764, 264683, 264288, 264768, 264768, 21908765, 21908768, 55811957, 35895917, 27486282, 18108370, 264628, 18108374, 35895855, 264630, 264632, 264635, 264583, 264584, 264568
3046	88098247 (6091, 6092)				UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 52646317, 55811957, 60432113, 22278000, 22279002, 264482, 264584
3047	95089824 (6093, 6094)				UNCLASSIFIED	264488, 22278998, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21908768, 21908769, 35895917, 52644150, 33657348, 65274781, 35895855, 264555, 60432113, 22279000, 264568
3048	87629419 (6095, 6096)	Novel Protein sim. GBank glij4588034[gbj]AAD25962.1[AF09287] - (AF092878) zinc RING finger protein SAG [Homo sapiens]		Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264102, 29148784
3049	88228955 (6097, 6098)	Novel Protein sim. GBank glij5454158[ref]NP_006286.1[pvARS] - valyl-IRNA synthetase 1		Contains protein domain (PF01406) - IRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264807, 264758, 87168559, 265018, 264448, 21908766, 265020, 33857109, 35895855, 60432113, 22279000
3050	87643678 (6099, 6100)	Novel Protein sim. GBank glij4589842[dbj]BAA76843.1] - (AB023216) KIAA0999 protein [Homo sapiens]		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264809, 265007, 264512, 265019, 264288, 21908766, 265020, 264693, 18108365, 56526486, 87168518, 22279002, 264566
3051	87505899 (6101, 6102)					22278997, 264595, 265019, 264288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank glij117528[sp]P14755[CRYL_RABIT - LAMBDA-CRYSTALLIN]		dehydrogenase		264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gij3947613jemb CAA19465.1 - (AL023828) cDNA EST EMBL:M89008 comes from this gene. cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21908754, 265010, 87168559, 264803, 265018, 265019, 264763, 264764, 264288, 21906765, 21906766, 21906768, 21906769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264583
3054	86843510 (6107, 6108)	Novel Protein sim. GBank gij1076211 pij S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35696286, 35696052, 29331830, 264808, 264809, 264512, 284910, 265017, 264604, 264766, 265020, 33857109, 264628, 35695855, 264636, 264564, 264566, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gij4680655 gbj AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	60424178, 65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 264259, 60424269, 60432289, 35696052, 56182435, 265006, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265018, 18108351, 264683, 264288, 264369, 264689, 21906768, 55811957, 35695917, 80170815, 33657023, 85274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gij728837 spj P39194 ALU7_SQ WARNING ENTRY IIII		glycoprotein	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264805, 264806, 264907, 264808, 264909, 265006, 264512, 285007, 265008, 265009, 264910, 33857402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264584, 264565, 264566, 264486, 264567

3057	95412748 (6113, 6114)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49086) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353....			264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264486
3058	79646226 (6115, 6116)			UNCLASSIFIED	264693
3059	87629425 (6117, 6118)	Novel Protein sim. GBank gi 4588034 gb AAD25982.1 AF09287 - (AF092876) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264480, 264259, 29331824, 29331825, 29331827, 35896052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	87740964 (6121, 6122)			UNCLASSIFIED	264112, 52844286, 21906768, 33657023, 263974, 18108385
3062	87618465 (6123, 6124)	Novel Protein sim. GBank gi 4454680 gb AAD20963 - (AF070857) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gi 2246532 U93872 - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 264558
3064	91241528 (6127, 6128)	Novel Protein sim. GBank gi 4240315 db BAA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646365, 52646842, 65274572, 56182575, 56181886, 22278995, 22278996, 22278997, 22278998, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52844286, 265018, 264682, 264288, 264686, 264768, 264687, 52844229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811578, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6128, 6130)	Novel Protein sim. GBank gi 5656743 gb AAD45960.1 AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2985487), and genscan [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424288, 66714117, 264100, 264907, 265007, 264591, 60432228, 264593, 265011, 265019, 18108351, 264766, 264767, 21906765, 21906768, 264693, 20281069, 22279000, 22279002, 264482, 264566, 264587

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi 4884268 emb CAB43245.1 - (AL050028) hypothetical protein (Homo sapiens)	UNCLASSIFIED	18108397, 22278995, 56994075, 22278996, 264905, 66712502, 265006, 264512, 264910, 264758, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108384, 18108388, 18108370, 18108377, 18108379, 60170394, 264567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF12185) sorting nexin 9 (Homo sapiens)	Contains protein domain (PF00787) - struct PX domain	264488, 264489, 35696286, 22278996, 56994075, 264259, 29331822, 29331825, 35696052, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264602, 264603, 264604, 264605, 265019, 264760, 264762, 264448, 264763, 264764, 264288, 264369, 264768, 264769, 264687, 264769, 264688, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33857023, 264693, 264628, 60431528, 263977, 35695855, 264630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264567, 264486
3068 3069	85360651 (6135, 6136) 95412753 (6137, 6138)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...	Contains protein domain (PF01926) - struct GTPase of unknown function	264112 22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264766, 52644229, 21906765, 21906768, 21906769, 60170615, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gij387778jemb[CAB05527] - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...	synthase	264488, 22278994, 22278995, 22278996, 59894075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52844045, 58182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33108954, 21806754, 87168474, 265019, 18108351, 264448, 264683, 264288, 52844229, 264689, 21806765, 21806768, 21806767, 21806769, 35895917, 265020, 265021, 60170815, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35895855, 264634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gij4502425jref[NP_001709.1]pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Igf Thiodoxin	264488, 65274572, 18108398, 22278896, 35896286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35896052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 58182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433356, 33657402, 60433438, 33108954, 52644286, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21806765, 21806766, 21806767, 21806768, 21806769, 35895917, 265020, 265021, 265022, 60170815, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264630, 264635, 264638, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
3072	95115802 (6143, 6144)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]	transcriptfactor	56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 264555, 56182323, 60432113, 264564

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gij134840spP22528(CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88080351 (6147, 6148)	Novel Protein sim. GBank gij3419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264693, 18108368, 18108370, 18108374, 284567
3075	88085732 (6149, 6150)	Novel Protein sim. GBank gij4557349refJNP_000456.1(pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 56528486
3076	87818219 (6151, 6152)				
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gij3023958spQ00808(HET1_PODAN - VEGETATABLE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264691, 264693
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gij3900850 (AC004994) - similar to KIAA0600; similar to d1028456 (PID:g3043724) [Homo sapiens]		kinase	65274572, 35696052, 264511, 60170831, 87168474, 264369, 35695917, 33657182, 27466264, 33657349, 35695763, 35695856, 264639
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gij3875410(emb)(CAB02876) - (Zr1052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21906768, 265020, 265021, 264693, 18108376, 264631, 52644332, 22278002
3080	95298274 (6159, 6160)	Novel Protein sim. GBank gij5257221(gijAAD41265.1) - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278998, 22278998, 264490, 264259, 29331824, 68714117, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21908754, 60174639, 265010, 264682, 264448, 264763, 264683, 264764, 264288, 264685, 264769, 264688, 264689, 21806765, 21906767, 21906769, 55811857, 35695917, 265020, 60170815, 52644150, 264692, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264658, 56182323, 60170394, 264482, 264555, 264484
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gij728831spP39188(Alu1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII)		UNCLASSIFIED	18108398, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264784, 55811957, 264555, 264564

3083	88095756 (6165, 6166)	Novel Protein sim. GBank gj1888241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264258, 28331824, 284106, 265008, 264591, 264592, 21806754, 264288, 264767, 21806768, 21806769, 29148784, 264691, 264632, 22279000
3084	87448588 (6187, 6166)	Novel Protein sim. GBank gj147674iprjA37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264369, 264288, 264766, 35695917, 265020, 18108374, 35696423, 264631, 264556, 264555, 264586, 264567, 264486
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gj2565037 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	265011, 264681
3086	87769842 (6171, 6172)	Novel Protein sim. GBank gj3894199 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 284112, 18108351, 264687, 263987, 263974, 55810764, 263981, 18108385, 264487
3087	87462888 (6173, 6174)				52848385, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109854, 21806754, 52646317, 265017, 264682, 264369, 264684, 21806767, 21806768, 265020, 264891, 33657023, 33657109, 52845129, 33657182, 27486262, 35695855, 87168518
3088	81224441 (6175, 6176)	Novel Protein sim. GBank gj3355304 (AF001548) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264591
3089	85361242 (6177, 6178)	Novel Protein sim. GBank gj14689146ipbAAD27782.1 AF07704 - (AF077049) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - dehydrogenase 3-hydroxyacyl-CoA dehydrogenase		18108397, 65274572, 56182575, 56181686, 56994075, 35696286, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21806754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21806765, 21806768, 21806767, 21806768, 265021, 60170615, 27486262, 18108370, 60431528, 35696423, 264556, 264559, 60432113, 264486

3080	95342371 (6179, 6180)	Novel Protein sim. GBank gi 1354050 (U47024) - MEM3 [Mus musculus]		UNCLASSIFIED	60424179, 52645156, 65274572, 56182575, 56181886, 22278995, 35696286, 56984075, 22278998, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264906, 264908, 52644045, 264828, 265008, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21906754, 33109954, 52646317, 55811386, 52644298, 87168474, 265011, 87168359, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 264690, 52644150, 264691, 33657023, 18108385, 65274620, 33657109, 18108388, 33657182, 27486261, 27486285, 35695763, 18108374, 18108376, 55810764, 35696423, 55811576, 65274791, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87169518, 22278000, 22278002, 264563, 264482
3081	95317424 (6181, 6182)	Novel Protein sim. GBank gi 3873932[emb] CAB01859] - (Z79596) Similarity to Bovine espartyl beta hydroxylase (TR:G162694): cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68138 comes f...		UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264768, 265010, 265011, 264683, 264685, 264768, 264768, 264768, 264769, 264693, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3082	95314592 (6183, 6184)	Novel Protein sim. GBank gi 1710756 sp P15880 RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - ribosomal prot Ribosomal protein S5	264488, 60424179, 18108396, 22278995, 56994075, 22278996, 35686286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35686052, 29331828, 29146498, 29146499, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264113, 264510, 264511, 265008, 264512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 264593, 264594, 60433438, 264595, 264758, 21906754, 265010, 265011, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 265019, 264760, 264762, 264681, 18108351, 264763, 264682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 29148784, 35695917, 265020, 265021, 264534, 60170615, 264690, 264691, 264692, 65274620, 33657109, 27486262, 264628, 264629, 18108374, 263978, 18108377, 35696423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264557, 264558, 264639, 60170394, 18108385, 264259, 29331824, 35686052, 264905, 265008, 60432228, 60431735, 264684, 264369, 264288, 264768, 21906767, 35686423, 83373044, 18108385
3083	94318457 (6185, 6186)	Novel Protein sim. GBank gi 5002587 emb CAB44347.1 - (Y17454) LSR1 protein [Homo sapiens]	UNCLASSIFIED	
3084	94316675 (6187, 6188)	Novel Protein sim. GBank gi 400734 sp P31044 PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	18108398, 264259, 60432289, 29331827, 264511, 264763, 264288, 264767, 265022, 264691, 264693, 65274791, 56182323, 264564, 264565

3095	94848162 (6189, 6190)	Novel Protein sim. GBank gl 4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108367, 56182575, 22278995, 35686286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35686052, 33658970, 29148499, 264508, 284905, 284509, 29331830, 284909, 284510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85656542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264368, 264288, 264686, 264768, 264769, 264689, 21906765, 21906766, 21906767, 55811957, 35685917, 265020, 265021, 265022, 62644150, 284691, 284692, 33657023, 264693, 263872, 18108376, 55811576, 35696423, 284952, 60170384, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 284482, 284583, 284584, 264566, 264487, 18108391, 22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 284905, 284908, 265008, 284910, 33657402, 265011, 265017, 265018, 284389, 21906766, 21906767, 21906768, 35695917, 265020, 60170815, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 284594, 55812038, 33109954, 33657084, 87168474, 87168559, 52844229, 21906765, 21906767, 18108376, 35696423, 52844332, 264638, 60432113, 22278902, 264634, 264637, 264565
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gl 3882221 db BAA34470.1 - (AB018283) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - struct Calponin homology (CH) domain	UNCLASSIFIED	264488, 35686286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22278902, 284583
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gl 4468288 emb CAB37981 - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	29331825, 60432289, 284594, 55812038, 33109954, 33657084, 87168474, 87168559, 52844229, 21906765, 21906767, 18108376, 35696423, 52844332, 264638, 60432113, 22278902
3098	80258024 (6195, 6196)	Novel Protein sim. GBank gl 303603 db BAA02145.1 - (D12621) cytochrome P-450L TBV [Homo sapiens]		cyto450	264488, 35686286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22278902, 284583
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gl 1083764 pir B48013 - proline-rich proteoglycan 2 precursor, parotid - rat		UNCLASSIFIED	29331825, 60432289, 35686052, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3100	87602421 (6199, 6200)			UNCLASSIFIED	264908, 284693, 264628, 264630, 264632
3101	79602134 (6201, 6202)			UNCLASSIFIED	

3102	91220892 (6203, 6204)	Novel Protein sim. GBank gll530570[gb]AAD41781.1[AF12853] - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	struct	35696286, 22278998, 22278999, 28331827, 35698052, 264909, 264512, 265008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21908767, 60170615, 284692, 33657023, 284638, 22278000, 264482, 264564 35695917, 264565
3103	90838004 (6205, 6206)	Novel Protein sim. GBank gll484564[sp]P35282[RB17_MOUSE - RAS-RELATED PROTEIN RAB-17]		UNCLASSIFIED	
3104	67340833 (6207, 6208)	Novel Protein sim. GBank gll5032207[ref]NP_005698.1[pTSSC - tumor-suppressing STF cDNA 6]		UNCLASSIFIED	284259, 264684, 264532, 33657182, 284558
3105	94148603 (6209, 6210)				22278997, 264259, 28331824, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264768, 264768, 264687, 264769, 21908766, 21908768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695955, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22278002, 264583, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gll1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264906, 264907, 264908, 52644045, 56182435, 264112, 265008, 265009, 55812038, 265017, 285018, 264883, 264886, 264687, 264768, 52844229, 21908765, 21908768, 21908769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108386, 22278000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gll334144[emb]CAA76851] - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265009, 60433356, 60433438, 265011, 265017, 265018, 21908765, 21908766, 21908767, 21908769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526488, 264482, 264487, 56182435, 264288, 264690, 264564
3108	87340835 (6215, 6216)	Novel Protein sim. GBank gll5032207[ref]NP_005698.1[pTSSC - tumor-suppressing STF cDNA 6]		UNCLASSIFIED	

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gjl5002587[emb]CAB44347.1] - (Y17454) LSPR1 protein [Homo sapiens]	Contains protein domain (PF00096) - zinc finger, C2H2 type	struct	264490, 264908, 265007, 264910, 264593, 264683, 264684, 264687, 21906767, 21906768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95080716 (6219, 6220)	Novel Protein sim. GBank gjl1076211[pir]S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432288, 29331826, 29331827, 29331828, 264908, 264510, 265006, 265007, 265008, 265009, 60432229, 33857402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 264369, 21906768, 21906767, 21906768, 265020, 60170815, 264693, 65274620, 18108370, 264639, 18108384, 22278000, 264583, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gjl3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00096) - zinc finger, C2H2 type	transcriptfactor	264488, 18108398, 66712502, 265017, 265018, 265019, 264448, 21906767, 265020, 33657023, 18108385, 18108388, 35696423, 52644332, 18108385, 18108388
3112	89043639 (6223, 6224)	Novel Protein sim. GBank gjl3800848 (AC005023) - match to EST AA381117 (NID:q2013436) [Homo sapiens]	Contains protein domain (PF00046) - homeobox	homeobox	
3113	86207098 (6225, 6226)	Novel Protein sim. GBank gjl2459910 (AF005856) - anon2A5 [Drosophila yakuba]	Homeobox domain	hm7	18108397, 22278999, 264258, 29331824, 35696052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21906767, 21906769, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22279002
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gjl4988270[gb]AAB52261.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1 [C...]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	hydrolase	264909, 56182435, 264910, 21806754
3115	94117986 (6229, 6230)	Novel Protein sim. GBank gjl5032225[ref]NP_005676.1[pv]BSC - Williams-Beuren syndrome chromosome region 11		transcriptfactor	60424179, 56182575, 284259, 29331824, 60424269, 29331826, 66712502, 264510, 265007, 60431735, 60433356, 55812038, 55811386, 265019, 264288, 264689, 21906769, 264691, 33657023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	76642855 (6231, 6232)			UNCLASSIFIED	264905, 264758, 21906764, 264690
3117	87771288 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264564

3118	94665848 (6235, 6238)	Novel Protein sim. GBank gij3880563[embjCAB01444.1] - (Z78018) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - EGF-like domain	lgf	52845156, 52846842, 65274572, 56182575, 22278995, 56994076, 22278996, 35986286, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 66714117, 29331828, 29331827, 35696052, 29331828, 284905, 284908, 29331830, 52844045, 56182435, 284510, 284511, 265007, 265008, 265009, 284757, 52846317, 21906754, 33657084, 52844286, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 284448, 264882, 264684, 284288, 264766, 56181582, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52844150, 284691, 33657023, 284693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35696423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264486, 265006, 264288
3119	85728786 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase		
3120	87344040 (6238, 6240)	Novel Protein sim. GBank gij5019819[gijAAD37863.1]AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]		UNCLASSIFIED	264488, 284509, 284510, 284511, 284512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gij4501877[etjNP_001088.1]pACR1 - acrosin			52844507, 52845156, 52846365, 52846842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52844045, 265008, 52846317, 87168474, 87168559, 21906765, 52844150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)			UNCLASSIFIED	264638
3123	88083003 (6245, 6246)	Novel Protein sim. GBank gij2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	kinase	18108392, 29331822, 29331824, 28331825, 284905, 265007, 55812038, 265019, 18108351, 264682, 264288, 284766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87766898 (6247, 6248)			UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gij4880826[gijAAD35412.1]AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	56181686, 264259, 66714117, 60432289, 29331826, 29331827, 264907, 284908, 264828, 265009, 60433358, 33657402, 60433438, 284758, 18108351, 264288, 28148827, 29148628, 33657023, 33657109, 18108382, 56528486

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278999, 264490, 264259, 60432049, 28331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264388, 264885, 29148628, 33657023, 264693, 33657109, 18108374, 55811576, 18108385, 60432113, 22279002, 35896286, 22278996, 22278999, 28331826, 264908, 60433438, 87168559, 264604, 21908765, 21906789, 33657023, 33657349, 264628, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gi 2828280 emb CAA16584.1 - (AL021687) putative protein [Arabidopsis thaliana]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gi 3885828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	22278996, 264259, 52644045, 265008, 21908754, 265017, 265018, 21906768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gi 3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 264259, 29331825, 29331828, 52644045, 56182435, 60433356, 264800, 264682, 264763, 264764, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264566, 264636
3130	14993860 (6259, 6260)	Novel Protein sim. GBank gi 3239465 (AF064553) - NSD1 protein [Mus musculus]			
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gi 1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264907, 56182435, 264594, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 264448, 264768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486261, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gi 4680647 gb AAD27713.1 AF13293 - (AF132938) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52644507, 52646842, 52646365, 65274572, 56182575, 22278994, 22278995, 35698286, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432269, 29331826, 29331827, 29331828, 35696052, 264508, 52644045, 56182435, 264910, 60170831, 60432228, 60433356, 33657402, 55812038, 52646317, 21808754, 52644296, 85858542, 87168559, 265017, 265018, 265019, 264448, 264286, 264369, 52644229, 21808765, 21808766, 21808767, 21808768, 21806769, 35695917, 265020, 265021, 60170815, 52644150, 264682, 33657023, 52645129, 33657108, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811578, 35695855, 18108385, 18108387, 56526466, 87168518, 60432113, 22278902
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gi 4507613 ref NP_003738.1 pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265008, 265007, 87168559, 264760, 21808767, 18108374, 22279000, 22279002, 264563 264595, 264369, 264685, 264628, 264566
3134	94648816 (6267, 6268)	Novel Protein sim. GBank gi 1729827 sp P54633 TALA_DICD1 - FILOPODIN (TALIN HOMOLOG)		struct	22278996, 264085, 29331828, 33657402, 18108348, 263974
3135	86389356 (6269, 6270)	Novel Protein sim. GBank gi 3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264698, 265020, 27486262, 263972, 65274781, 264557, 264558
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gi 627101 p S44092 - probable carrier protein c2 - Caenorhabditis elegans		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21808754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264769, 21808765, 21808766, 21808767, 21808769, 55811857, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486
3137	88257847 (6273, 6274)	Novel Protein sim. GBank gi 3342730 (AC005331) - R31341_1 [Homo sapiens]			

3138	94130188 (6275, 6276)	Novel Protein sim. GBank gij4406759[gbjAA020070] - (AC006838) hypothetical protein [Arabidopsis thaliana]			264559, 264488, 264907, 264511, 264593, 3310984, 87168559, 264681, 264684, 264685, 264686, 264687, 264768, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 80432113, 22279000, 22279002
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gij228038[prj1814452C - Hyp-rich glycoprotein [Zea mays]	UNCLASSIFIED		
3140	91222682 (6279, 6280)	Novel Protein sim. GBank gij832[embjCAA37773] - (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]	struct		22278995, 56994075, 35696286, 264908, 264909, 60433356, 21906754, 52644296, 87168474, 87168559, 264683, 264288, 264685, 264686, 265022, 264693, 27486282, 35695855, 264630, 264555, 264566, 56182575, 35696286, 28331828, 264909, 265009, 265018, 18108351, 264369, 21908766, 29148627, 265020, 264828, 264628, 264631, 18108385
3141	87323584 (6281, 6282)	Novel Protein sim. GBank gij3213227 (AF035209) - putative v-SNARE Vti1a [Mus musculus]	UNCLASSIFIED		
3142	95419028 (6283, 6284)	Novel Protein sim. GBank gij2498197[spjQ95245] (C561_PIG - CYTOCHROME B561 [CYTOCHROME B-561])	cytochrome		52645156, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 28331822, 29331824, 29331827, 29148499, 56182435, 265007, 60170831, 60432229, 33657402, 264595, 60433438, 264758, 21908754, 264286, 264766, 264687, 52644229, 21908765, 21908767, 21908768, 60170615, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 80432113, 22279000
3143	95351475 (6285, 6286)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 56182575, 22278998, 22278999, 29331822, 29331824, 60432229, 35696052, 28331828, 264508, 264805, 264908, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265019, 264760, 264763, 264448, 264764, 264684, 264288, 264685, 264686, 264768, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 264690, 33657023, 264693, 263967, 33657109, 264628, 264629, 18108374, 263976, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 80432113, 22279000, 22279002, 264563, 264568, 264488

3144	95336328 (6287, 6288)	Novel Protein sim. GBank gij4884468[emb]CAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264486, 18108396, 22278996, 35696286, 22278997, 22278998, 29331826, 29331827, 35696052, 29331828, 264106, 265009, 265007, 265008, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21906765, 21908766, 21906767, 265020, 265021, 52644150, 27486261, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 284587
3145	86611657 (6289, 6290)	Novel Protein sim. GBank gij3879708[emb]CAB03330] - (Z81118) Similarity to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from L...	UNCLASSIFIED		18108397, 29331824, 29148499, 20281100, 265008, 55812038, 265010, 21906766, 29148627, 21906768, 29148784, 264892, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gij2135746[pir]S68990 - mitogen inducible gene mig-2 - human	Contains protein domain (PF00169) - struct PH domain		264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21906766, 265021, 264892, 33657109, 18108374, 35696423, 35695855, 60432113, 264564
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gij3874279[emb]CAB07315.1] - (Z92825) predicted using Genefinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	56181886, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35698052, 56182435, 265008, 264910, 60431735, 60433356, 60433436, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22279002
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gij5225322[gb]AAD40851.1[AF083108] sirtuin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87168474, 264764, 35698423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gij4200446 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - FYVE zinc finger	eph	29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gij3378454[emb]CAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - Glutathione S-transferases.	transferase	264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gij172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	oncogene	29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21906754, 87168559, 264605, 21906768, 52644150, 27486264, 35696423, 22279000

3153	95317299 (6305, 6308)	Novel Protein sim. GBank gi4895041 gb AAD32705.1 AF14395 - (AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	264488, 5264365, 35698286, 22278996, 22278997, 22278999, 60432048, 264259, 29331826, 60432289, 33656970, 264508, 264908, 33657402, 264595, 60433438, 87168474, 87168559, 264601, 265019, 264448, 264682, 264764, 264288, 264389, 264768, 21808765, 21806766, 21906787, 21906768, 21906769, 29148784, 285021, 285022, 60170615, 52644150, 264690, 264691, 33657023, 65274820, 33657109, 18108370, 35695855, 264638, 60170394, 87168518, 60432113, 22278900, 22279002, 22278998, 264259, 29331824, 66712502, 285008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374, 29331828, 264509, 264805, 264908, 264510, 264511, 264512, 33657402, 264681, 264683, 33657023, 18108370, 264634, 264639, 18108385, 264563, 264486
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi4680661 gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]		ATPase-associated	
3155	87762394 (6308, 6310)	Novel Protein sim. GBank gi728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		UNCLASSIFIED	
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi5630078 gb AAD45821.1 AC006017 N-acetylglucosaminyltransferase; similar to Q10473 (PID:g1709559) [Homo sapiens]	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	56182575, 22278996, 22278997, 22278998, 22278999, 60432048, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21806754, 33109854, 87168474, 265010, 265017, 285018, 265019, 18108351, 264448, 264288, 264689, 21906768, 21908768, 21906769, 35695917, 285020, 265022, 264682, 18108370, 35698423, 56182323, 22279002
3157	88259577 (6313, 6314)				18108396, 264259, 29331826, 35696052, 29146498, 87168559, 265017, 264448, 264288, 264691, 18108366, 52645129, 35698423, 52644332, 264488, 263974
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi5306064 gb AAD41895.1 AF15677 - (AF156778) ASB-3 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	
3159	84124114 (6317, 6318)	Novel Protein sim. GBank gi5531272 emb CAB50897.1 - (AJ243600) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	56182575, 22278998, 29331824, 264106, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21906768, 265020, 264691, 264682, 33657109, 18108374, 35698423, 264555, 60170394, 22279000
3160	80221068 (6319, 6320)	Novel Protein sim. GBank gi3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	struct	18108351, 264555, 264556, 264557, 264558, 264559

3161	88074111 (6321, 6322)				264488, 22278995, 22278997, 22278888, 264259, 28331822, 60432289, 28331828, 52644045, 285017, 265018, 264448, 264288, 21906764, 21906767, 265020, 18108374, 264638, 264568
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U1SMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tubercous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (P)ancreas	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3 (U1SMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (U1MVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hermin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5.1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen 1		

Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences

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 <213> Homo sapiens

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 312

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 <211> 104
 <212> PRT
 <213> Homo sapiens

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 Gly Ser Ser Ala Thr Ser Gly Pro Ala Ser Xaa Asp Pro Ser Ala Ser
 35 40 45
 Pro Pro Pro Ile Ser Ala Ala Arg Leu Ser Arg Met Ser Leu Val Glu
 50 55 60
 Arg Cys Ser Ala Ser Ala Ser Cys Ser Ala Val Leu Arg Asp Trp Ala
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 Cys Ser Ser Ala Leu Val Arg Ala Ala Ser Met Ser Ala Lys Ser Asp
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 Ser Ala Phe Gly Ser Glu Thr Arg
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 <211> 987
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 <213> Homo sapiens

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 Ala Ala Glu Arg Ala Glu Ala Ile Leu Gly Met Asp Ile Lys Gly His
 35 40 45

Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu
 50 55 60
 Tyr Tyr Phe Ser Ile Leu Leu Asp Arg Gly Glu Arg Arg Tyr Leu Ala
 65 70 75 80
 Met Cys Ser Arg Glu Gly Gly Met Asp Ile Glu Thr Leu Ala Lys Glu
 85 90 95
 Arg Pro Glu Ala Leu Ala Lys Val Pro Val Asp Pro Ile Asp Gly Val
 100 105 110
 Asp Asp Ala Lys Ala Arg Glu Ile Leu Ser Glu Ala Gly Phe Pro Asp
 115 120 125
 Ser Glu Gln Asp Ala Ile Val Pro Ala Val Leu Lys Leu Trp Glu Thr
 130 135 140
 Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys
 145 150 155 160
 Thr Gly Asp Gly Arg Ile Leu Ala Ile Asp Gly Lys Met Thr Val Asp
 165 170 175
 Asn Asn Ala Ser Phe Arg Gln Pro Asp Arg Ala Gly Leu Val Asp Arg
 180 185 190
 Ala Thr Thr Asp Pro Leu Glu Leu Arg Ala Gly Glu Leu Gly Leu Asn
 195 200 205
 Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly
 210 215 220
 Leu Val Met Ser Thr Leu Asp Cys Val Ala Tyr Ala Gly Glu Asn Phe
 225 230 235 240
 Pro Gly Ser Pro Ala Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala
 245 250 255
 Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu
 260 265 270
 Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys
 275 280 285
 Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp
 290 295 300
 Lys Ala Val Lys Pro Leu Val Val Arg Leu Asp Gly Asn Ala Val Ala
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 <213> Homo sapiens

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 Pro Met Cys Phe Pro Gln Lys Gly Leu Glu Gly Tyr Tyr Pro Asn Ala
 35 40 45
 Pro Ala Thr Pro Ser Leu Gln Lys Val Ile Cys Asp Leu Gln Gly Leu
 50 55 60
 Thr Ala Arg Cys Asp Val Ser Cys Cys Gln Ala Glu Arg Gly Leu Gly
 65 70 75 80
 Glu Pro Cys Arg Asp Val Met Thr Ser Tyr Val Leu Gly Asn Lys Val
 85 90 95
 Thr Cys Cys Arg Pro Leu Glu Leu Trp Pro Val Lys Thr Pro Gly Asn
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 <213> Homo sapiens

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 Pro Val Arg Glu Trp Cys Val Lys Gly His Leu His Val Gly Lys Arg
 35 40 45
 Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly
 50 55 60
 Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg
 65 70 75 80
 Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg
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<210> 9
 <211> 428
 <212> DNA
 <213> Homo sapiens

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 <211> 138
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<213> Homo sapiens

<400> 10

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Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
 35           40           45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
 50           55           60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
 65           70           75           80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
 85           90           95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
 100          105          110
Gly Asn Phe Gln Gly Met Lys Val Phe Phe Met Val Val Ala Ala Val
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Tyr Ile Leu Tyr Leu Leu Phe Leu Ile Val
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<210> 11

<211> 453

<212> DNA

<213> Homo sapiens

<400> 11

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<210> 12

<211> 130

<212> PRT

<213> Homo sapiens

<400> 12

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Leu	Pro Met Pro Val Ala Val Ser Met Pro Leu Ala Cys Ile Leu Ser				
	50		55		60
Ile	Ser Phe Trp Cys Ser Ala Cys Ile Ala Ala Ser Pro Arg Leu Asn				
	65		70		75
Ser	Cys Ser Asn Trp Pro Leu Leu Thr Ser Thr Lys Arg Thr Val Ser				
		85		90	
Pro	Ala Phe Thr Ser Arg Ala Leu Gly Glu Lys Glu Met Ser Cys Arg				
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<210> 13

<211> 2034

<212> DNA

<213> Homo sapiens

<400> 13

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 960

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<210> 14

<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

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			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
		35				40					45				
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50				55					60					
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
65				70					75					80	
Arg	Gln	Glu	Ala	Gly	Ala	Asp	Ala	Phe	Leu	Ile	Gln	Tyr	Asp	Ala	His

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Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
      20             25             30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
      35             40             45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
      50             55             60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

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65              70              75              80
Ala Lys Lys Tyr Asp Leu Tyr Thr Lys Ile Thr Gly Gly Gln Arg Ile
      85              90              95
Asp Leu Phe Gly Ala Gln Leu His Glu Leu Pro Gln Ile Trp Gly Glu
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Leu Val Asp Ala Gly Phe Glu Thr Gly
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<210> 17
 <211> 682
 <212> DNA
 <213> Homo sapiens

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tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
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240
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682

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<210> 18
 <211> 110
 <212> PRT
 <213> Homo sapiens

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Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
      20      25      30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
      35      40      45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
      50      55      60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

```

```

65              70              75              80
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
              85              90              95
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg
              100              105              110

```

<210> 19
 <211> 515
 <212> DNA
 <213> Homo sapiens

```

<400> 19
cttgctggc agacatggga cctgcttccc tcttacaccc cagtcttggc aaggatcatg
60
cccccatctc aactatgtta gccagtctgg ctgttcactt agtcactaca gtttgcttct
120
cgtctgcagt gcagtcttgg gctataagaa aactggggcc actcaatacc tccccctttt
180
tggcccttct cctcctctgg tccatgggtg gggttggggg gagcccagtt tcagcaccag
240
cagctggagc ccataaccaca ctcatcttct agttctggct gtgggagccc ctcccacagg
300
tttcagttcc ccaagcccca ggctgagtt tttttattg caaaagctgg ttgttgttgt
360
ggctagctcc caggcgtgtg aggtgcagct tgctaagtaa gagctaggaa agagaatagg
420
gtcctgctgt aggtgtccag tctgaaggaa tgctgggat acttcctcaa gcagttcctt
480
ctcacagtct cctggctgct ccgcagtca gatct
515

```

<210> 20
 <211> 130
 <212> PRT
 <213> Homo sapiens

```

<400> 20
Met Gly Pro Ala Ser Leu Leu His Pro Ser Leu Gly Lys Asp His Ala
1      5      10      15
Pro Ile Ser Thr Met Leu Ala Ser Leu Ala Val His Leu Val Thr Thr
20      25      30
Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
35      40      45
Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Trp Ser Met
50      55      60
Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
65      70      75      80
Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
85      90      95
Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Phe Tyr Cys Lys Ser Trp
100     105     110
Leu Leu Leu Trp Leu Ala Pro Arg Arg Val Arg Cys Ser Leu Leu Ser
115     120     125
Lys Ser

```

130

<210> 21
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 21
 gtgcgcacaa aagagcacgt tcgcaagggg aggaagagcg tgccaccggt tctgccgagc
 60
 tagacgcggt gcctatgggt gcggaggacc atggagtga gcgagtaaga ctagatgatg
 120
 caacaaatgt gcctgagggg gaaatggcac gagccagtgc caatgagggc atgacacctg
 180
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg
 240
 atacaatgac tgcttgact gatgggttca caattgagca attggagctt acacgatctc
 300
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctggctcaag
 360
 aattaaagca agttgtccaa ggcattccatn
 390

<210> 22
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala
 1 5 10 15
 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly
 20 25 30
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu
 35 40 45
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly
 50 55 60
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg
 65 70 75 80
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu
 85 90 95
 Leu Lys Gln Val Val Gln Gly Ile His
 100 105

<210> 23
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 23
 ntctcggagg ccgacagcct ggcgggctgg aagccctcgg tgtaccacgt gctgctcatc
 60
 ctgggcctgt tcgccgtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag
 120

ggctgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggttc
 180
 ggggacctgg tgagcagcca gcacgcgcc taccggaacc aggggctcta ccgctgggc
 240
 aacttcctct tcatcctgct cggcgtgtgc tgcatttact cgctcttcaa cgatcatctc
 300
 atcctcatca agcagggtgct caactggatg ctgcgcaagc tgagctgccg ctgctgcgcg
 360
 cgctgctgcc cggctcctgg cgcgc
 385

<210> 24

<211> 128

<212> PRT

<213> Homo sapiens

<400> 24

Xaa	Ser	Glu	Ala	Asp	Ser	Leu	Ala	Gly	Trp	Lys	Pro	Ser	Val	Tyr	His
1				5				10						15	
Val	Leu	Leu	Ile	Leu	Gly	Leu	Phe	Ala	Val	Leu	Leu	Ser	Cys	Cys	Ala
			20					25					30		
Ser	Ala	Met	Tyr	Thr	Ser	Val	Glu	Gly	Trp	Asp	Tyr	Val	Asp	Ser	Leu
		35					40					45			
Tyr	Phe	Cys	Phe	Val	Thr	Phe	Ser	Thr	Ile	Gly	Phe	Gly	Asp	Leu	Val
	50					55				60					
Ser	Ser	Gln	His	Ala	Ala	Tyr	Arg	Asn	Gln	Gly	Leu	Tyr	Arg	Leu	Gly
65				70					75					80	
Asn	Phe	Leu	Phe	Ile	Leu	Leu	Gly	Val	Cys	Cys	Ile	Tyr	Ser	Leu	Phe
			85					90						95	
Asn	Val	Ile	Ser	Ile	Leu	Ile	Lys	Gln	Val	Leu	Asn	Trp	Met	Leu	Arg
		100					105					110			
Lys	Leu	Ser	Cys	Arg	Cys	Cys	Ala	Arg	Cys	Cys	Pro	Ala	Pro	Gly	Ala
		115					120					125			

<210> 25

<211> 337

<212> DNA

<213> Homo sapiens

<400> 25

ccatgggaga gaccgtgcat tttcttctag gtctgcgtgg gaagtcactg cagagtttctg
 60
 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttgttgctt ggaccagtga
 120
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac
 180
 tggaggaaag ctggtcgaat gcactgtgta tttggaggca gaaccagcag agggctctct
 240
 ggggttgagt tagggcaaaa gagaaagaag gcaccaagcc tggggtcttg gttttctctc
 300
 ttacacttgc tgggtggacg gtggtgccac tgaatga
 337

<210> 26

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu
 1 5 10 15
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser
 20 25 30
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu
 35 40 45
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp
 50 55 60
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp
 65 70 75 80
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp
 85 90 95
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn
 100 105 110

<210> 27
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 27
 ccgacgtcga atatccatgc agccgcgcgcg aggatggaga gagcgatgga gcaactcaac
 60
 cgcttgacgc gtcgctgctg cgcgcgcgcg accgtggagt tgcccaggga taatgaaact
 120
 gctgtttata cattaatgcc aatgggttatg gctgatcaac acaggtctgt ttctgaacta
 180
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt
 240
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca
 300
 aatcctaact atcaagatat ttcaggctgt aca
 333

<210> 28
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 28
 Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met
 1 5 10 15
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val
 20 25 30
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met
 35 40 45
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser
 50 55 60
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

```

65              70              75              80
His Ile Ala Ala Asn Cys Gly Ser Val Glu Cys Leu Val Leu Leu Leu
              85              90              95
Lys Lys Gly Ala Asn Pro Asn Tyr Gln Asp Ile Ser Gly Cys Thr
              100             105             110

```

<210> 29
 <211> 375
 <212> DNA
 <213> Homo sapiens

```

<400> 29
ncgccgtccg tgctggctat tatgacggcg ggtagcgacc agggcgagga ggtcaactcg
60
gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgtca gctgccccgc
120
tacaatatca cgatcaagcg cgtcgtgaac atgacgggca agggccgcac gccgagctgg
180
tactcgctcg tcgtggctgg caatggtcgg ggcctcgtgg gctatggcga aggcaaagat
240
actaacatca gccgcgcgaa caaaaaggcg ttccacgccg cggtgaaaaa catggacttg
300
gtatcgggcc accggtcgaa gagtggcgcc aacacgctcg agccccccgt cgagggccgcg
360
tggggcgcta cgcgt
375

```

<210> 30
 <211> 125
 <212> PRT
 <213> Homo sapiens

```

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1      5      10      15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
20     25     30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
35     40     45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
50     55     60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65     70     75     80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
85     90     95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
100    105    110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
115    120    125

```

<210> 31
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 31
 accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc
 60
 gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctgggcccct gagagtgcag
 120
 agattcctgg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggct
 180
 cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc
 240
 ctgcagagtg cacaaacctt gccgcgcttc ctccactgca gcttacgtct ttgcagcagc
 300
 cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca
 360
 tggcctgcat tgttt
 375

<210> 32
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Gln Ala Met Ser Leu Lys Leu His Thr Leu Trp Ser His Arg Trp
 1 5 10 15
 Gln Trp Gln Pro Ile Gly Ser Gly Cys Cys Lys Asp Val Ser Cys Ser
 20 25 30
 Gly Gly Ser Ala Ala Arg Phe Val His Ser Ala Gly Pro Thr Gly Ala
 35 40 45
 Arg Asn Arg Gln Glu Pro Pro Phe Pro Phe Glu Leu Ala Gly Arg Glu
 50 55 60
 Pro Cys Thr Pro Arg Arg Ser Cys Ser Arg Pro Ala Ala Ala Leu Asp
 65 70 75 80
 Pro Gly Ile Ser Ala Leu Ser Gly Ala Gln Glu Ala Ser Leu Thr Arg
 85 90 95
 Arg Leu Val Ser Ala Cys Ser Arg Ser Ser Pro Leu Leu Ala Pro Thr
 100 105 110
 Ser Ile Ser Glu Gln Ser
 115

<210> 33
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 33
 ccatgcagcc caaccgttgg cgataaagtc cgtttagggc ataccaattt atgggcaacc
 60
 attgaacaag atttattaac caaaggtgat gagtgtaaat ttggtggcgg taaaagtgtg
 120
 cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt
 180
 gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatatttgt
 240

attcgcgatg gtcgtattgt cggatcggga caagcaggta accctgacac catggatgac
 300
 gtcacgccaa acatgattat cgggtgctagc acagaagtac ataacgggtgc a
 351

<210> 34
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 34
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn
 1 5 10 15
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys
 20 25 30
 Lys Phe Gly Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly
 35 40 45
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn
 50 55 60
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly
 65 70 75 80
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp
 85 90 95
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu
 100 105 110
 Val His Asn Gly Ala
 115

<210> 35
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 35
 nngctagctg caccaccacc tgttcatgca ggcagagcgg ccacccctca tggaagaaga
 60
 ggaatccact gtattgggca caggcttctt gctggacctt ggcaagcagg tgcttggtgctg
 120
 gtaccaggaa gtccagcgtg tacctcagtg cgtctctccg ataagtcctc tccaccacct
 180
 ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa ggggtggatac agggcgggcga
 240
 gagtgtctctg cacacagtcc tccactggct caggctccat ggctcggcgc cgggcccgcgt
 300
 ccgacgcttg gtcggggcggg cggggccggg cgcgccaccg cctcccttca cgcgt
 355

<210> 36
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 36
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

      1           5           10           15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20           25           30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35           40           45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
      50           55           60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
      65           70           75           80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85           90           95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100          105          110
Thr Ala Ser Leu His Ala
      115

```

<210> 37
 <211> 492
 <212> DNA
 <213> Homo sapiens

```

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggacccgcc
60
gcaaccatga caagggcgat gttgtgatct ggggtggattc cttctccgac atgctcgagg
120
gatcggatct ctccggcgta gtcacggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc gggttgacgt ggatcactac cggtcagctc gacggtgctc
240
ggcgtcggct gcgcgtggt ctccgacgtgc tggcaccctt gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcgtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca ccctcgctag caggccacac cctcgctcgt cagccccatt
480
gtcatcccgc gg
492

```

<210> 38
 <211> 127
 <212> PRT
 <213> Homo sapiens

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
1           5           10           15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20           25           30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35           40           45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

```

      50              55              60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu
65              70              75              80
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met
      85              90              95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser
      100              105              110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala
      115              120              125

```

<210> 39
 <211> 412
 <212> DNA
 <213> Homo sapiens

```

<400> 39
aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgtaaag agcggtccga tcgccgggaa
60
gtgatngca ccgcaaaat gcaggtggtc gaagccgcga gttcaggcaa gattgtcttt
120
gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtagagcaa cttctctgcg
180
caagtcacgc gtggtgataa aattgcgctg attggcccga acggttgtgg taaaacgacg
240
ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
300
aaactggaag ttgcgtactt cgaccagcac cgtgtgagc tggatcctga gcgtacggcg
360
atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
412

```

<210> 40
 <211> 137
 <212> PRT
 <213> Homo sapiens

```

<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1              5              10              15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
      20              25              30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
      35              40              45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
      50              55              60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65              70              75              80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
      85              90              95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
      100              105              110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
      115              120              125
Gln Glu Val Met Val Asn Gly Arg Val

```

130

135

<210> 41

<211> 1080

<212> DNA

<213> Homo sapiens

<400> 41

gaattcaagt ggacacaggg tccacgcccg cgtctcaccg ataagagcta caagcacaac
 60
 tactatgacg agcgggtttc gtcgaagag cgtcttgagc gcaactgtggc taaggatttc
 120
 gtcacgacgg aggtcgagcc catgtgggat gggctgatg tcatgcggat gggtaaggat
 180
 ctcttcatcc agcacgggtct gacgacaaat cggaagtcaa tggagtgggt taagcgttac
 240
 taccgccgatt tccgcgttca cgcgggtgaat ttccctgggg atccgtaccc gatccatc
 300
 gacgcgacct ttgtgcgct tcgtccgggg ctcacatca acaaccgaa tcgtccactg
 360
 ccgcaggagc agaggaagat ctctgaggcc aatgactggc agatcgttga tgctgctcag
 420
 ccggcgacag acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc
 480
 ttggtacttg atccgaagac ggtcatctgc gaggcttcgg aagttcatca gatggagcag
 540
 atggacaagc tgggtatgaa cgtcatcccc gtcgccttcc gtgacgcgta cccattcggt
 600
 ggaggtctcc actgcgccac agctgatgta tatcgcaag gtacctgtga ggactacttc
 660
 ccgaatcagg tcgacgaccc gacctgggtg tgagaaaacc ccgtgggtcat gtcactgctg
 720
 acggatctcg gtggctcggg acggaactta cgttgtccgt taccgggccg ccgggtctga
 780
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc
 840
 aacgtcaaac aggaagtcc aggcgtcggg acgatgaacc agaaagtggg attcgtgtcc
 900
 atgcttcttt ctgcaacggg tatggggttg gtgggtactt tcgggcgtct cagcactcct
 960
 gtggatccca cgacgggcag taagtacatc atcgggtgatt ttttggccac tggtaggatg
 1020
 atagtcgggg tcctgggatt tctgcttatt atcgtcatatc ttggaaaatg gtctgagctc
 1080

<210> 42

<211> 230

<212> PRT

<213> Homo sapiens

<400> 42

Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser
 1 5 10 15
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu


```

      20      25      30
Glu Arg Thr Val Ala Lys Asp Phe Val Thr Thr Glu Val Glu Pro Met
      35      40      45
Trp Asp Ala Ala Asp Val Met Arg Met Gly Lys Asp Leu Phe Ile Gln
      50      55      60
His Gly Leu Thr Thr Asn Arg Lys Ser Met Glu Trp Phe Lys Arg Tyr
      65      70      75      80
Tyr Pro Asp Phe Arg Val His Ala Val Asn Phe Pro Gly Asp Pro Tyr
      85      90      95
Pro Ile His Ile Asp Ala Thr Phe Val Pro Leu Arg Pro Gly Leu Ile
      100      105      110
Ile Asn Asn Pro Asn Arg Pro Leu Pro Gln Glu Gln Arg Lys Ile Phe
      115      120      125
Glu Ala Asn Asp Trp Gln Ile Val Asp Ala Ala Gln Pro Ala His Asp
      130      135      140
Thr Pro Pro Glu Leu Cys Tyr Ser Ser Val Trp Leu Ser Met Asn Cys
      145      150      155      160
Leu Val Leu Asp Pro Lys Thr Val Ile Cys Glu Ala Ser Glu Val His
      165      170      175
Gln Met Glu Gln Met Asp Lys Leu Gly Met Asn Val Ile Pro Val Ala
      180      185      190
Phe Arg Asp Ala Tyr Pro Phe Gly Gly Gly Leu His Cys Ala Thr Ala
      195      200      205
Asp Val Tyr Arg Glu Gly Thr Cys Glu Asp Tyr Phe Pro Asn Gln Val
      210      215      220
Asp Asp Pro Thr Leu Val
      225      230

```

<210> 43
 <211> 358
 <212> DNA
 <213> Homo sapiens

```

<400> 43
gggcccccca catagtggac acaggtttct gggatgtcag catggagtgc caagaggtgg
60
gtgaccacct ggtggggaat aaggcgcttc tgggacatag aggctgcctt ccagctgcgc
120
ctggcagagc tgttgacaca acagcatggt ctgcagtgcc gggccactgc cacgcacacc
180
gatgtccttt aaggatggat ttgggttttc ggattcgcgt ggcctatcag cgggagtccc
240
agatcctgaa ggaagtgcag agcccagagg ggatgatctc gctgagggac acagctgcct
300
ccctccgcct tgagagagac acaaggcagt tgccactgct caccagtgcc ctgcacgn
358

```

<210> 44
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 44
Met Glu Cys Gln Glu Val Gly Asp His Leu Val Gly Asn Lys Ala Leu

```

1	5	10	15
Leu Gly His Arg Gly Cys Leu Pro Ala Ala Pro Gly Arg Ala Val Asp			
20	25	30	
Thr Thr Ala Trp Ser Ala Val Pro Gly His Cys His Ala His Arg Cys			
35	40	45	
Pro Leu Arg Met Asp Leu Gly Phe Arg Ile Arg Val Ala Tyr Gln Arg			
50	55	60	
Glu Ser Gln Ile Leu Lys Glu Val Gln Ser Pro Glu Gly Met Ile Ser			
65	70	75	80
Leu Arg Asp Thr Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln			
85	90	95	
Leu Pro Leu Leu Thr Ser Ala Leu His			
100	105		

<210> 45

<211> 905

<212> DNA

<213> Homo sapiens

<400> 45

gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcggtga ggcgggtttc
 60
 gcggctcctg gaatcccaga gcagtatggt ggcgacggtg cggatgcgat tgcgtccgca
 120
 ataatcatgg aagaggtcgc tcgagtctgt gcgtcgtcgt ccaccgtcat atcgtccaat
 180
 gagcttggtta ccgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt
 240
 tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga
 300
 tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat
 360
 ggcgttaagg cttgggtcac ggaggtggc gaggccaaat acctggtgat atttgcggtt
 420
 actgacccag acgatccgcg ccacagaatc agcgcgttga tgggccatgc agatgacccg
 480
 ggcattagct acggggctcc ggagcacaaa atggggatac gcgggtcagt taccagggaa
 540
 gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgtcg agggcacggt
 600
 ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagtg
 660
 ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt
 720
 ggccagccac tgtccaattt tgaggggaatc cagttcatgc tcgcagacat ggcaatgcgt
 780
 ttggaggcgg cgcgagcgct gacatactct gcagctgacg gtagtgggag ccagactgac
 840
 gatgtgagtt acttcggcgc ggcggccaaa tgtttcgctt ccgacacagc gatggcagtg
 900
 tgcac
 905

<210> 46

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46
 Val Asp Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val
 1 5 10 15
 Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Gly Asp
 20 25 30
 Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg
 35 40 45
 Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr
 50 55 60
 Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu
 65 70 75 80
 Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu
 85 90 95
 Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu
 100 105 110
 Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu
 115 120 125
 Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp
 130 135 140
 Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro
 145 150 155 160
 Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser
 165 170 175
 Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg
 180 185 190
 Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu
 195 200 205
 Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln
 210 215 220
 Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe
 225 230 235 240
 Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp
 245 250 255
 Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala
 260 265 270
 Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala
 275 280 285
 Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys
 290 295 300

<210> 47
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 47
 aagctttag agctagtccg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
 60
 atgcatttta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg
 180
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgctg actgcgttta
 240
 gatttcgaaa aaggactcac caaatcccag ggctgcgcag aagagttcat acccgtcggc
 300
 gaagacgccca gcacgtataa cagacttatg aaagcgctgc gccaacgccca tgatgtcatc
 360
 aaatccggaa agcttgccc
 379

<210> 48

<211> 106

<212> PRT

<213> Homo sapiens

<400> 48

Met	His	Leu	Thr	Ala	Ala	Tyr	Ala	Val	Ala	Thr	Glu	Ala	Gly	Cys	His
1				5					10					15	
Ile	Arg	Leu	Ser	Gln	Tyr	Ala	Arg	Lys	Val	Arg	Gln	Thr	Gln	Leu	Arg
		20						25					30		
Val	Glu	Tyr	Leu	Arg	Leu	Arg	Leu	Ala	Ser	Leu	Pro	Gly	Gly	Asp	Ala
		35					40					45			
Gly	Ala	Ala	Val	Gly	Ile	Asp	Arg	Arg	Leu	Arg	Leu	Asp	Phe	Glu	Lys
		50				55					60				
Gly	Leu	Thr	Lys	Ser	Gln	Gly	Arg	Arg	Glu	Glu	Phe	Ile	Pro	Val	Gly
65					70					75				80	
Glu	Asp	Ala	Ser	Thr	Tyr	Asn	Arg	Leu	Met	Lys	Ala	Leu	Arg	Gln	Arg
				85					90					95	
His	Asp	Val	Ile	Lys	Ser	Gly	Lys	Leu	Ala						
				100				105							

<210> 49

<211> 309

<212> DNA

<213> Homo sapiens

<400> 49

tgatcatgat gctggcatgg actattctgg tcctgttcc tctctcacct gctgaaggac
 60
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttccctctct actgagtctc
 120
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgctctg
 180
 cacattaccc tctgccagct ggctcatttt tctgtctccc ttacagggga aactcttcaa
 240
 aaagttatct ccacctcctt ccatctcatg ttctcttgaa cctgcagtac tgggtgctcc
 300
 ctcccttttg
 309

<210> 50

<211> 101

<212> PRT

<213> Homo sapiens

<400> 50

```

Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1             5             10             15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
          20             25             30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
          35             40             45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
          50             55             60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
65             70             75             80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
          85             90             95
Val Leu Pro Pro Phe
          100

```

<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

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agatctttga agaattgcca cactgtcttc ctccctgctt ataatttctt tattccctag
60
gatgtgatcc ttgttcttgg ggctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgcgtggc attcccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgccctt
300
caaaatcttc tgttgctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggtctg gctggatggg acatcaggtg ggccctctgt ttcatttatg tgacctccca
480
tcaggtcttc tggttggatc ctgctttcta ga
512

```

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Glu Lys Lys Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1             5             10             15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
          20             25             30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

```

          35          40          45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
    50          55          60
Arg Pro Ala Gly Ile Glu Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
65          70          75          80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
          85          90          95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
    100          105          110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
    115          120          125

```

<210> 53
 <211> 474
 <212> DNA
 <213> Homo sapiens

```

<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccggatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gagggccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcctcgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcgggtt acgtaaccgt
300
gaccaagtcg acgggcgctc ccgcggttac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgtcataggc gggc
474

```

<210> 54
 <211> 101
 <212> PRT
 <213> Homo sapiens

```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
  1          5          10          15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
    20          25          30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
    35          40          45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
    50          55          60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
65          70          75          80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
    85          90          95
Ala Lys Ser Ser Trp

```

100

<210> 55
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 55
 ccatggccca ggacagccgg catatcggct acgactacgg tacaccggtg gcgccacagt
 60
 tcggcgcagc caagcccgca gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg
 120
 tgggtgttca ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc
 180
 agcccgatgc caccgcgcag caggtcaatg ccgacaaccc gcactacgtc gggcggttca
 240
 gccgcatcgg catgggcctg gtggatgaca agggccggtg cattaccag ggcgtatcgc
 300
 gcgcgttgaa tgcggcgcgc agcaccaagg cgctgaacct gggaccgagt gacgcggcgc
 360
 agttatcggg gaggcgta
 378

<210> 56
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val
 1 5 10 15
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln
 20 25 30
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr
 35 40 45
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr
 50 55 60
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser
 65 70 75 80
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln
 85 90 95
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn
 100 105 110
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg
 115 120 125

<210> 57
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 57
 agacccaccc gacacagatc aggagtcgtc atgtccagaa agaagaaggt cggcatcctc
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc
 120
 atccgccagc acgacatgga gtcacatcggg attcaggacg gctttcttgg attggcgagg
 180
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggg cggcgaggacc
 240
 atcctgggaa ctagccgtga caaggatcaat cacatgatta tcgacggcga ggaacgggat
 300
 atgggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg
 360
 ggtggcggtg gcaccgcaa gaacgcgt
 388

<210> 58
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 58
 Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys
 1 5 10 15
 Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala
 20 25 30
 Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu
 35 40 45
 Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile
 50 55 60
 Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr
 65 70 75 80
 Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly
 85 90 95
 Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu
 100 105 110
 Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Gly Thr Ala Lys Asn
 115 120 125
 Ala

<210> 59
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 59
 ggtaccatcg gagctcgaca agaaatggtt gggatgaagtc gtggcttctg ctccaccag
 60
 tgcctcatg ggtcagccca cctgaatatc ttcacgctg tgcatttctc ctgatgttca
 120
 cgtgtgccct gtgtttttac gcatctgtga tcgtgcaccc acgcgtctca gagaggagcc
 180
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaacct
 240
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaagggaacc
 300

tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcgtg cagacgggtga
 360
 tgcttttcaga agccccgggag agcgtcttgg gggcagtgct gaaggttgtg ctgtaca
 417

<210> 60
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro
 1 5 10 15
 Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp
 20 25 30
 Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys
 35 40 45
 Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala
 50 55 60
 Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln
 65 70 75 80
 Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu
 85 90 95
 Lys Val Val Leu Tyr
 100

<210> 61
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 61
 agatcttcac agccttagac ttttttcatt ggtgccttac agttttggag gtccctatcc
 60
 gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag
 120
 tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga
 180
 ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc
 240
 tcccctagac cgggccccatg gccaggcctg accacagagc tccattgcc tttcctgcac
 300
 gcgt
 304

<210> 62
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 62
 Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala
 1 5 10 15

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
 20 25 30
 Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
 35 40 45
 Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
 50 55 60
 Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
 65 70 75 80
 Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
 85 90

<210> 63
 <211> 577
 <212> DNA
 <213> Homo sapiens

<400> 63
 cgcgtaagg gggctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg
 60
 ctgacgggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc
 120
 accgtgggtcg ggctggccca aaccctcggc cctccgctgc gagcactggg cgtcgacacc
 180
 gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
 240
 ccggcagcct ggcagatcca ccccgacgac ggtgcccgca ccacaccggg tgatggcccg
 300
 gtggagttgc acatcccggg cagggatttc cagcttgacg tcgccggcgg caccatgtg
 360
 ggtatcatgg cgctcaatc ggtctgtgac gccttggccg aggcgataga ccacggctcc
 420
 gagaccgtct tgaatggggg tcccgccagt cgctcaacc ctgcccacg gcgtcgtctg
 480
 gtgctgggtg ctcgccgctc ccccgaaactg ttcgacgata ctgcccgctg gaacatcgtg
 540
 cttgacagcc agacgactgt cgccaggctg aatgcat
 577

<210> 64
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 64
 Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
 1 5 10 15
 Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
 20 25 30
 Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
 35 40 45
 Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
 50 55 60
 Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
 65 70 75 80

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85                      90                      95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100                    105                    110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115                    120                    125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130                    135                    140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
      145                    150                    155                    160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165                    170                    175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180                    185                    190

```

<210> 65
 <211> 339
 <212> DNA
 <213> Homo sapiens

```

<400> 65
gtcgaccgcg ccttgggata gctcgaagg ggcagcctgg accaggtagc ggaagaagtc
60
aagaaggccg ctttcaagat caccgcgcgc gggcaactag tgggcacccat ggcctccgag
120
cgccttggcg tacccttcgg catcatcgac ctttcgcttg ccctactgc cgaattggga
180
gattcggggg cccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggcctgcccc
300
cgcgtcgccg gtttgtctgg ctcttcate ccgggctcc
339

```

<210> 66
 <211> 113
 <212> PRT
 <213> Homo sapiens

```

<400> 66
Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
1      5      10      15
Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
      20      25      30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
      35      40      45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
      50      55      60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
65      70      75      80
Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys Lys Gly Gly Met
      85      90      95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
      100      105      110

```

Ser

<210> 67

<211> 446

<212> DNA

<213> Homo sapiens

<400> 67

tgatcataaa ccacgcgtca ccgaggggat gtggcacacc tacctgcgcg tcgcagatgc
 60
 cgcacaggca cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg cgaccggtga
 120
 caaggggtcc ttcgacgcc aagagcttgc cgtaactcct gatactgaca ccgtcatcca
 180
 gggagtcggg cccgccctag cctcctcga ttcagcgtgg ggacgccaga tccacgtgga
 240
 gacaacaggg tgtcccagtg ccgtggctctg gaatccacgc tcctcgtcga cacatgccga
 300
 taacccgaca gcccaggcat ggcgcgattt cgtatgcgtc gagaccgggg cctgcaagga
 360
 caatgcggtc attgttgccc cacacagcga cctcaccatg tccacacgga ttagcgtcga
 420
 aacgttgtga tcgctgcatg gatatt
 446

<210> 68

<211> 133

<212> PRT

<213> Homo sapiens

<400> 68

Met	Trp	His	Thr	Tyr	Leu	Arg	Val	Ala	Asp	Ala	Ala	Gln	Ala	Arg	Val
1				5				10					15		
Arg	Gly	Val	Arg	Gly	Ala	Ser	Trp	His	Asn	Phe	Ala	Thr	Gly	Asp	Lys
		20					25					30			
Gly	Ser	Phe	Asp	Ala	Asn	Glu	Leu	Ala	Val	Thr	Pro	Asp	Thr	Asp	Thr
		35					40					45			
Val	Ile	Gln	Gly	Val	Gly	Pro	Ala	Leu	Ala	Leu	Leu	Asp	Ser	Ala	Trp
	50					55				60					
Gly	Arg	Gln	Ile	His	Val	Glu	Thr	Thr	Gly	Cys	Pro	Ser	Ala	Val	Val
65					70				75					80	
Trp	Asn	Pro	Arg	Ser	Ser	Ser	Thr	His	Ala	Asp	Asn	Pro	Thr	Ala	Gln
			85						90					95	
Ala	Trp	Arg	Asp	Phe	Val	Cys	Val	Glu	Thr	Gly	Ala	Cys	Lys	Asp	Asn
		100						105					110		
Ala	Val	Ile	Val	Ala	Pro	His	Ser	Asp	Leu	Thr	Met	Ser	Thr	Arg	Ile
		115					120					125			
Ser	Val	Glu	Thr	Leu											

<210> 69

<211> 552

<212> DNA

<213> Homo sapiens

<400> 69

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nnaagggtaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg
60
ccctcaagga ggagccaaaa gaagacccca gtggagcagc tgtgcccag atgccaaaaa
120
agtcctccaa gattgccagc ttcattccca aaggggggaa gctcaacagt gccaagaagg
180
agcnccatgg ccccttcctt cagtggata ccaaaaccag gaatgaaaag catgcccggg
240
aaatccccaa gtgccccagc gccttccaag gaaggggagc ggagccggag tgggaagctg
300
agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttcctcttcc
360
agcctggcgt cctcagaagg aaaaggccca ggagggaacca ccctgaacca cagcatcagc
420
agccagactg tcagtgggtc tgtcgggacc acccagacca caggaagcaa tnnaccgtca
480
gtgttcagct acctcagccc cagcagcaat acaaccatcc caacactgcc acggttgca
540
ctttcctgta ca
552

```

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

```

Xaa Arg Val Arg Arg Lys Ala Arg Thr Leu Gln Arg Glu Pro Leu Cys
1      5      10      15
Arg Arg Gly Trp Pro Ser Arg Arg Ser Gln Lys Lys Thr Pro Val Glu
20      25      30
Gln Leu Cys Pro Arg Cys Gln Lys Ser Pro Pro Arg Leu Pro Ala Ser
35      40      45
Ser Pro Lys Gly Gly Ser Ser Thr Val Pro Arg Arg Ser Xaa Met Ala
50      55      60
Pro Ser Leu Ser Gly Ile Pro Lys Pro Gly Met Lys Ser Met Pro Gly
65      70      75      80
Lys Ser Pro Ser Ala Pro Ala Pro Ser Lys Glu Gly Glu Arg Ser Arg
85      90      95
Ser Gly Lys Leu Ser Ser Gly Leu Pro Gln Gln Lys Pro Gln Leu Asp
100     105     110
Gly Arg His Ser Ser Ser Ser Ser Ser Leu Ala Ser Ser Glu Gly Lys
115     120     125
Gly Pro Gly Gly Thr Thr Leu Asn His Ser Ile Ser Ser Gln Thr Val
130     135     140
Ser Gly Ser Val Gly Thr Gln Thr Thr Gly Ser Asn Xaa Pro Ser
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<210> 71
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 <212> DNA
 <213> Homo sapiens

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 <213> Homo sapiens

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 35 40 45
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val
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 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly
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<213> Homo sapiens

<400> 74

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Val	Asp	Gly	Ala	Gln	Phe	Val	Pro	Arg	Val	Thr	Val	Val	Thr	Pro	
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Pro	Trp	Asn	Phe	Ala	Leu	Ser	Ile	Thr	Ala	Gly	Ser	Thr	Leu	Ala	Ala
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Leu	Ala	Ala	Gly	Ser	Ser	Val	Leu	Leu	Lys	Pro	Ala	Pro	Gln	Ala	Arg
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His	Cys	Ala	Ala	Val	Ile	Ser	Glu	Cys	Leu	Trp	Glu	Ala	Gly	Ile	Pro
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Arg	Asp	Val	Leu	Gln	Leu	Val	Asp	Val	Glu	Glu	Asn	Glu	Ala	Gly	Lys
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<211> 405

<212> DNA

<213> Homo sapiens

<400> 75

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<210> 76

<211> 135
 <212> PRT
 <213> Homo sapiens

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 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr
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 Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln
 65 70 75 80
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg
 85 90 95
 Leu Pro Ala Asp Met Val Val Thr Ser Lys Ala His Arg Asp Ile Ala
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<210> 77
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<210> 78

<211> 799

<212> PRT

<213> Homo sapiens

<400> 78

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Thr	Ala	Ser	Ile	Ile	Gly	Asp	Val	Met	Gly	Pro	Thr	Leu	Asn	His	Leu
		35				40						45			
Asn	Asn	Leu	Leu	Arg	Leu	Pro	Phe	Gly	Cys	Gly	Glu	Gln	Asn	Met	Ile
	50					55					60				
His	Phe	Ala	Pro	Asn	Val	Phe	Val	Leu	Lys	Tyr	Leu	Gln	Lys	Thr	Gln
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Gln	Leu	Ser	Pro	Glu	Val	Glu	Arg	Glu	Thr	Thr	Asp	Tyr	Leu	Val	Gln
			85					90					95		
Gly	Tyr	Gln	Arg	Gln	Leu	Thr	Tyr	Lys	Arg	Gln	Asp	Gly	Ser	Tyr	Ser
		100					105					110			
Ala	Phe	Gly	Glu	Arg	Asp	Ala	Ser	Gly	Ser	Met	Trp	Leu	Thr	Ala	Phe
		115				120					125				
Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Ser	Phe	Ile	Phe	Val	Asp	Pro
	130					135					140				
Arg	Glu	Leu	Ala	Ala	Ala	Lys	Ser	Trp	Ile	Ile	Gln	Gln	Gln	Gln	Ala
145				150					155					160	
Asp	Gly	Ser	Phe	Leu	Ala	Val	Gly	Arg	Val	Leu	Asn	Lys	Asp	Ile	Gln
			165					170					175		
Gly	Gly	Ile	His	Gly	Ile	Val	Pro	Leu	Thr	Ala	Tyr	Val	Val	Val	Ala
		180					185					190			
Leu	Leu	Glu	Thr	Gly	Thr	Ala	Ser	Glu	Glu	Glu	Arg	Gly	Ser	Thr	Asp
	195					200						205			
Lys	Ala	Arg	His	Phe	Leu	Glu	Ser	Ala	Ala	Pro	Leu	Ala	Met	Asp	Pro
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Tyr	Ser	Cys	Ala	Leu	Thr	Thr	Tyr	Ala	Leu	Thr	Leu	Leu	Arg	Ser	Pro
225				230					235					240	
Ala	Ala	Pro	Glu	Ala	Leu	Arg	Lys	Leu	Arg	Ser	Leu	Ala	Ile	Met	Arg
			245					250					255		
Asp	Gly	Val	Thr	His	Trp	Ser	Leu	Ser	Asn	Ser	Trp	Asp	Val	Asp	Lys
		260					265					270			
Gly	Thr	Phe	Leu	Ser	Phe	Ser	Asp	Arg	Val	Ser	Gln	Ser	Val	Val	Ser
	275					280					285				
Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Ala	Leu	Leu	Thr	Tyr	Thr	Leu	Leu
	290					295					300				
Gly	Asp	Val	Ala	Ala	Ala	Leu	Pro	Val	Val	Lys	Trp	Leu	Ser	Gln	Gln

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 Phe Glu Leu His Arg Thr Asn Gln Lys Val Leu Gln Thr Ala Ala Ile
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 Pro Ser Leu Pro Thr Gly Leu Phe Val Ser Ala Lys Gly Asp Gly Cys
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 Cys Leu Met Gln Ile Asp Val Thr Tyr Asn Val Pro Asp Pro Val Ala
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 Lys Pro Ala Phe Gln Leu Leu Val Ser Leu Gln Glu Pro Glu Ala Gln
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 Gly Arg Pro Pro Met Pro Ala Ser Ala Ala Glu Gly Ser Arg Gly
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 Asp Trp Pro Pro Ala Asp Asp Asp Asp Pro Ala Ala Asp Gln His His
 450 455 460
 Gln Glu Tyr Lys Val Met Leu Glu Val Cys Thr Arg Trp Leu His Ala
 465 470 475 480
 Gly Ser Ser Asn Met Ala Val Leu Glu Val Pro Leu Leu Ser Gly Phe
 485 490 495
 Arg Ala Asp Ile Glu Ser Leu Glu Gln Leu Leu Leu Asp Lys His Met
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 Gly Met Lys Arg Tyr Glu Val Ala Gly Arg Arg Val Leu Phe Tyr Phe
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 Asp Tyr Tyr Glu Pro Ala Phe Glu Ala Thr Arg Phe Tyr Asn Val Ser
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 Glu Val Glu Arg Ala Pro Ala Arg Gly Pro Gly Trp Phe Pro Gly Glu
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 Ser Gly Pro Ala Val Ala Pro Glu Glu Gly Ala Ala Ile Ala Arg Cys
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 Gly Cys Asp His Asp Cys Gly Ala Gln Gly Asn Pro Val Cys Gly Ser
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 Asp Gly Val Val Tyr Ala Ser Ala Cys Arg Leu Arg Glu Ala Ala Cys
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 Glu Asp Arg Val Thr Ala Gly Pro Arg Pro Pro Val Ser Ser Gly Asn
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 Leu Glu Ser Ser Thr Gln Ser Ala Ser Pro Phe His Arg Trp Gly Gln

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Thr Pro Ala Pro Gln Arg His Ser Gly Arg Val Val Gly Ala His Arg
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Pro Gly Leu Leu Ser Pro Val Phe Val Tyr Ser Pro Ala Phe Gln Ser
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<210> 79
 <211> 346
 <212> DNA
 <213> Homo sapiens

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 <211> 101
 <212> PRT
 <213> Homo sapiens

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 Asn Asp Phe Met Ala Leu Ser Ile Asp Ala Val Ala Ser Ala Asp Ala
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 Tyr Ser Val Gly Phe Pro Gly Phe Gly Gly Met Asn Leu Ala Pro Ile
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 <212> DNA
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<210> 82

<211> 79

<212> PRT

<213> Homo sapiens

<400> 82

Gly	Trp	Leu	Arg	Trp	His	Cys	Leu	Gly	Ala	Ala	Cys	Thr	Cys	Val	Cys
1				5				10					15		
Met	Xaa	Val	Cys	Met	Cys	Val	Cys	Thr	Cys	Xaa	Cys	Val	Pro	Val	Cys
			20					25					30		
Met	Cys	Pro	Cys	Ala	Cys	Leu	Cys	Cys	Val	Cys	Ala	Cys	Met	Cys	Ala
		35					40					45			
Cys	Leu	Cys	Val	Xaa	Val	Cys	Val	Arg	Ala	Cys	Val	Cys	Thr	Cys	Val
	50					55					60				
His	Val	His	Val	Cys	Ala	Pro	Val	Cys	Met	Ser	Val	Cys	Thr	Arg	
65					70					75					

<210> 83

<211> 411

<212> DNA

<213> Homo sapiens

<400> 83

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 120
 ggaaaagacgc gatccgtaga taaaataggg ccgctttatc gcaaattggct ttatggttac
 180
 cgtttccgca tcgatttgca gctgcggaaa aaaaggcctg tggtcgatgc cgttgtggat
 240
 gatttcgatt ttcgctttgt cgatgccaa gccctatcaaa tcgtttcgca aaaactcgct
 300
 cgcggcgacg atcttttgca cctttgtaag cccccgcttt atctgcatgc gcatcatgcg
 360
 gtcgctcttt tctttgagca tgacggaaac gatggaattg acgacggcga c
 411

<210> 84
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 84
 Met Leu Lys Glu Lys Ser Asp Arg Met Met Arg Met Gln Ile Lys Arg
 1 5 10 15
 Gly Leu Thr Lys Val Gln Lys Ile Val Ala Ala Ser Glu Phe Leu Arg
 20 25 30
 Asn Asp Leu Ile Gly Leu Gly Ile Asp Lys Ala Lys Ile Glu Ile Ile
 35 40 45
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp
 50 55 60
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe
 65 70 75 80
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu
 85 90 95
 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro
 100 105 110
 Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His
 115 120 125

<210> 85
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 85
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 atcctcgacg cggtgaaact gctgagttcg ctcggcttca aggtgatcgc cacctcgggc
 120
 acccagcggt tcttggtgga gaacggagta ccggcggaag agatcaacaa ggtgctggaa
 180
 ggccgcccgc acattgttga cgcaattacc aacggcgagg tgcaactcgt tttcaatacc
 240
 accgaggggc cacaggcgct ggctgacagc cgctcgttgc gacgcgctgc cctcttgcac
 300
 aaagtgccat attacaccac tctttcaggt gca
 333

<210> 86
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 86
 Xaa Arg Val Pro Arg Lys Gly Thr Met Phe Val Ser Val Arg Glu Thr
 1 5 10 15
 Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly
 20 25 30
 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

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```

      35      40      45
Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
      50      55      60
Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
65      70      75      80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
      85      90      95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
      100      105      110

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<210> 87
 <211> 355
 <212> DNA
 <213> Homo sapiens

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<400> 87
acgcgtgagg aaatgggggc cgcaggcctg gatcgcaagg tatggcagtg cccggtcgtc
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ctcctgagcg atgttcattc ggtaggggta cagggtgacg ggcgtactta tggttctccc
120
attgtgcttc gcccggtgac gagtgaggac gccatgactg cggactgggc acgtatccca
180
tatgacgtac tggaaaagat ctcgactcgc attacgaatg cgtgtccgca aatcaaccgg
240
gtgggtactcg atatcacatc taaaccgccc gccaccatcg agtgggaatg agccccgtct
300
caccgtgaac atgacatggc cgcacacctt cttggggcgg gccatgccgt gttag
355

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<210> 88
 <211> 96
 <212> PRT
 <213> Homo sapiens

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<400> 88
Thr Arg Glu Glu Met Gly Ala Ala Gly Leu Asp Arg Lys Val Trp Gln
1      5      10      15
Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
      20      25      30
Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
      35      40      45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
      50      55      60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
65      70      75      80
Val Val Leu Asp Ile Thr Ser Lys Pro Pro Ala Thr Ile Glu Trp Glu
      85      90      95

```

<210> 89
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 89

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nacgcgtcaa caccaggcta cgggtgggtat gatcatgata agggctggga cccgcaggag
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 agggcaagag ttatataata gacgggtgta tgggtttaag gtatacatgg tgatgagaca
 120
 ggtgattgga taaggccaga ggggtgggcg ggggttctgcc cctgctgaag cctgggtgggg
 180
 cccaggtctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg
 240
 caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgacgtaacc
 300
 caggctcatc gcagccggcc agaactcaca actcgagcgg tccatcagat c
 351

<210> 90
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 90
 Ser Leu Val Gly Pro Arg Ser Val Ile Trp Asp Arg Asn Asn Thr Ser
 1 5 10 15
 Ala Leu Gly Leu Leu Asp Val Ala Gln Ala Leu Glu Gln Asn His Ser
 20 25 30
 Leu Lys Ser Met Pro Leu Pro Leu Asn Asp Val Thr Gln Ala His Arg
 35 40 45
 Ser Arg Pro Glu Leu Thr Thr Arg Ala Val His Gln Ile
 50 55 60

<210> 91
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 91
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 60
 acgtcgaagc ccagcagggc ctctgcagg tccctggggc agccagcaca cacaaagtcc
 120
 cggaaggggc tgtagactcc ctgccagcgg ctttcccggg gaaggcacc acgcccagct
 180
 gcctcttgca ggtactgctc ggggtctggtg ggagggcagc cgtgtccagc acaccctgtg
 240
 tgtgcagtcc tctccctgcc cactgccga acgagccctc cacggtgaag ccattggggg
 300
 acgtgacatt gcccttcccc atgaggt
 327

<210> 92
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 92
 Met Gly Lys Gly Lys Val Thr Phe Pro Asn Gly Phe Thr Val Glu Gly

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```

1           5           10           15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
      20           25           30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
      35           40           45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
      50           55           60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
65           70           75           80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
      85           90           95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
      100          105

```

<210> 93
 <211> 394
 <212> DNA
 <213> Homo sapiens

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<400> 93
nccgcgtacg acaagcagta cctcgagggg cgttacggtg cggacccata cctgagcaac
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atgctcgaat gggacggcgg acatgagcaa taggccgcca aagcacagcg agaggaaggc
120
ggcgcgctct ggggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgac
180
ttttgtaccg ataaatcccg ggcgccacct gatcgtgacc gaggttacga aaacggaacc
240
gctctatttc gaggtatca ggttgctgt caacaaccgt tatcacggcc agtgggtgac
300
aatggaagtt gtcgttaccg gcaagcatac caggggactt ctcgatcgtg cagtcactct
360
ggcggaagaa agtgccacag gattcactca cgta
394

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<210> 94
 <211> 109
 <212> PRT
 <213> Homo sapiens

```

<400> 94
Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
1           5           10           15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
      20           25           30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
      35           40           45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
      50           55           60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
65           70           75           80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
      85           90           95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

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100

105

<210> 95
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 95
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 tgcttggatc ctaaaatgga ctggtcttgg gtgtgtaacc ccggtgaagt tatagcctcc
 120
 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat
 180
 cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc
 240
 tggggctctg cttggccata ggcactgcac attgtgccac ctgctcatca cctcctctag
 300
 tctcacactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag
 360
 gctgagcatg gagctcacc ccatgcatag ggtgtgggaa gagggcacag gaggcctcat
 420
 ccatggggga aaggggttag gatggacatg ggtggggaga gggcatagac atcccttcct
 480
 aatctctgtt cccaccacat ttcataggag atgagttagg agatgacagc t
 531

<210> 96
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser
 1 5 10 15
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr
 20 25 30
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp
 35 40 45
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe
 50 55 60
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu
 65 70 75 80
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val
 85 90 95
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg
 100 105 110
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu
 115 120

<210> 97
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 97
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 tcgcggtgcc ttgcgcgcgg gctggtaggt ggagaagccg cgcgagtacg cgccgtagag
 120
 cgacatcgtg tctgagacgt cgaagctcag gccagcttt ggcgccagg cgcgctcggt
 180
 cggtccgccc tcttgccgca attgattcag cgcaatcccg gccatcacat gccagcgctt
 240
 gtccagggtc atgaaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag
 300
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt
 360
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat
 405

<210> 98
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 98
 Met Ala Ser Gly Asp Leu Phe Pro Gly Asn Val Phe Ser Pro Arg Val
 1 5 10 15
 Pro Phe Pro Ser Ser Asp Ile Thr Pro Asn Ile Glu Arg Leu Ser Asn
 20 25 30
 Ser Pro Leu Arg Ser Ser Arg Ala Tyr Ala Gln Asp Phe Met Thr Leu
 35 40 45
 Asp Lys Arg Trp His Val Met Ala Gly Ile Ala Leu Asn Gln Leu Pro
 50 55 60
 Gln Glu Gly Gly Pro Thr Glu Arg Ala Trp Thr Pro Lys Leu Gly Leu
 65 70 75 80
 Ser Phe Asp Val Ser Asp Thr Met Ser Leu Tyr Gly Ala Tyr Ser Arg
 85 90 95
 Gly Phe Ser Thr Tyr Gln Pro Ala Arg Lys Ala Pro Arg Ala Tyr Gly
 100 105 110
 Pro Ser Ala Ala Arg Pro Ser Lys Arg Glu
 115 120

<210> 99
 <211> 545
 <212> DNA
 <213> Homo sapiens

<400> 99
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 60
 tgccccgacg acccagcaaa cgtccccggc tgttcctcat tgaccacgcc gaccggatcg
 120
 tcgatcccat cactcgggat ttgctggaat ccttggttcg cgaagccggc gaggctgcgg
 180
 tgatcttggg tgcccagcgt cgcgggtcgca tcgattgggt ctccccacag atcatccaca
 240

acctggccga acaccatttt gagtcgtcct ctggagggtac tcgatgatga ctgaacgttc
 300
 ccattccacg atcagggttaa ggtggccggc ggtggtggtt ctctcctcg ttccgctgct
 360
 ggtggtcgcc ggattggtcc gggacgacct ggcataccac cgaccggttg ggccgggtga
 420
 aagcggccgt cgtcaacgag gacaaggccg tcaagggtgcg tggacaactg gttccgatgg
 480
 gccgccaact caccgccgcc ttgatggact ctggctcgca caccactgat ggccacaccg
 540
 tcgac
 545

<210> 100

<211> 101

<212> PRT

<213> Homo sapiens

<400> 100

Met	Gly	Thr	Phe	Ser	His	His	Arg	Val	Pro	Pro	Glu	Asp	Asp	Ser	Lys
1				5					10					15	
Trp	Cys	Ser	Ala	Arg	Leu	Trp	Met	Ile	Cys	Gly	Glu	Ser	Gln	Ser	Met
			20					25					30		
Arg	Pro	Arg	Arg	Trp	Ala	Pro	Lys	Ile	Thr	Ala	Ala	Ser	Pro	Ala	Ser
		35					40					45			
Arg	Thr	Arg	Asp	Ser	Ser	Lys	Ser	Arg	Val	Met	Gly	Ser	Thr	Ile	Arg
	50					55					60				
Ser	Ala	Trp	Ser	Met	Arg	Asn	Ser	Arg	Gly	Arg	Leu	Leu	Gly	Arg	Arg
65					70					75				80	
Gly	Arg	Trp	Val	Ser	Thr	Val	Ile	Ala	Glu	Arg	Ser	Ser	Ser	Thr	Thr
			85						90					95	
Ser	Gly	Ala	Asp	Ala											
				100											

<210> 101

<211> 619

<212> DNA

<213> Homo sapiens

<400> 101

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 120
 aagctgccgg gggtgactat ctcatcctcg ccacggattc cggacgcaag ggatacacga
 180
 ccgcccgtcc tcacgaggcc ggcggaacac gctattacca acctggacca gatccgcgaa
 240
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatggtccag
 300
 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact
 360
 ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc
 420

gtcgacattg tccacgccaa agatgtccat aaggagatgg ccgacaagct tttgcctggc
 480
 gagatcacct ggtccgaagg cattcgcgcc gggatgttcg caccatcgg cgacgggtgat
 540
 atcgactttg cagccatcgt gaggtcctt gatgaagcgg gggttcgatgg ttattacgtc
 600
 ctagagcagg acatcatga
 619

<210> 102
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 102
 Thr Arg Ser Leu Thr Pro Ser Lys Leu Pro Gly Val Thr Ile Ser Ser
 1 5 10 15
 Ser Pro Arg Ile Pro Asp Ala Arg Asp Thr Arg Pro Pro Val Leu Thr
 20 25 30
 Arg Pro Ala Glu Asn Ala Ile Thr Asn Leu Asp Gln Ile Arg Glu Val
 35 40 45
 Cys Ala Ser Arg Asn Val Thr Ala Cys Leu His Pro His Trp Gly Thr
 50 55 60
 Met Val Gln Asn Arg Asp Glu Val Ile Arg Val Leu Glu Asn Ser Ser
 65 70 75 80
 Ile Gly Leu Cys Leu Asp Thr Gly His Leu Ala Cys Gly Gly Thr Asp
 85 90 95
 Val Val Glu Leu Val Arg Lys Tyr Ala Asn Arg Val Asp Ile Val His
 100 105 110
 Ala Lys Asp Val His Lys Glu Met Ala Asp Lys Leu Leu Pro Gly Glu
 115 120 125
 Ile Thr Trp Ser Glu Gly Ile Arg Ala Gly Met Phe Ala Pro Ile Gly
 130 135 140
 Asp Gly Asp Ile Asp Phe Ala Ala Ile Val Arg Leu Leu Asp Glu Ala
 145 150 155 160
 Gly Phe Asp Gly Tyr Tyr Val Leu Glu Gln Asp Ile Met
 165 170

<210> 103
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 103
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 gccattgggg ggagaccct gccgtgggga aagaccctg ccatggggga gaccctgcc
 120
 actgggggga gaccctgcc gctgggggga gaccgagcc attgggggga gaccctgcc
 180
 atggggaaag acccctgcca ttgggggaga ntacctgcca ttgggggaga tccctgccgt
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 300

agtggttggg gcgaagaccc c
321

<210> 104
<211> 107
<212> PRT
<213> Homo sapiens

<400> 104
Xaa His Gly Gly Arg Gln Gln Pro Cys Gly Gly Asp Pro Ser His Trp
1 5 10 15
Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr
20 25 30
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu
35 40 45
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp
50 55 60
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg
65 70 75 80
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu
85 90 95
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro
100 105

<210> 105
<211> 344
<212> DNA
<213> Homo sapiens

<400> 105
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ccgggtcaac gagggtttgg cgcacggtcc actccgtggc gcccggggtg atgtgcaaca
120
gggcggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat
180
ccagcgcattc gcccagcgg tcggcatccc agccgtggtc gccgtcgagc gcccagggg
240
cctcaatgtc gtcacggcg gccagttcca cccggcggaa catctcgttg cggaccatga
300
cccgaaggc gcgggaattc tcggtcagtt tcggcgggtgc cggc
344

<210> 106
<211> 62
<212> PRT
<213> Homo sapiens

<400> 106
Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser
1 5 10 15
Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His
20 25 30
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His

35 40 45
 Arg Arg Pro Val Pro Pro Gly Gly Thr Ser Arg Cys Gly Pro
 50 55 60

<210> 107

<211> 549

<212> DNA

<213> Homo sapiens

<400> 107

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 60
 gccgcttaat aaccgaccaa catgaaactc aagggtgcc ccttcctagc ggggaccctg
 120
 cacagaccgc aaaataaggg gttttgctct gccctcctca gttcacgtgg gcaccttgga
 180
 acactgaaga aggcattttc cgaactcact gtcctacgga cttattctcc gcactgtttt
 240
 cgctccttc gccctgttct cgtgactgac aggagcaggg gtcacaagca ggcagcccga
 300
 gagctctgct cacctggaaa agcatttttg tgtagcttaa atgtgaaggc ctcaggcagt
 360
 ggctctgtgt cctcctccac atgcgcccat cttactctt tcattgtgact ggctgtttt
 420
 tgaaggcaag gccctgtca cccttggtta ggccaggat gttctgcacc gaaaatggcc
 480
 ctgccctctg cattggatgg ctagctctta ggttggttta ttttagcaaa taagcgttac
 540
 agggtaggc
 549

<210> 108

<211> 108

<212> PRT

<213> Homo sapiens

<400> 108

Met Lys Leu Lys Gly Cys Pro Phe Leu Ala Gly Thr Leu His Arg Pro
 1 5 10 15
 Glu Asn Lys Gly Phe Cys Ser Ala Leu Leu Ser Ser Arg Gly His Leu
 20 25 30
 Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr
 35 40 45
 Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg
 50 55 60
 Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys
 65 70 75 80
 Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu
 85 90 95
 Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met
 100 105

<210> 109

<211> 748

<212> DNA

<213> Homo sapiens

<400> 109

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nngaattcag atttactttt tgcatttcct tgaatataaa ataggcagta aactaaccta
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aagtcagaag acttatttgt tctggtacct attctgctgt taataaattg ataaatgagt
120
gatattgggg taagttacca atttacttta cagcccttaa gtaaataatc tgctttcctc
180
agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
240
cagtcagtga aaggaataat tctctttaca aagtaaatgc agttgtttta ttttagacaa
300
gagtgttcta aacttcgtga agagttaagg cttcaacatg aagaggataa gaagtcagca
360
atgtctcaac ttttgagtt gaaagatcga gagaaaaatg cagcaagaga ttcatggcag
420
aagaaagtag aagatctctt aaaccagatt tccttgctga aacagaatct ggagatacag
480
ctttcccagt ctcagacttc tttgcaacaa ctgcaagccc agtttacgca agaacgacag
540
cggcttacgc aagagcttga agaattagag gagcaacatc agcaaagaca caaatcatta
600
aaagaagcac atgtccttgc atttcaaact atggaagagg aaaaggaaaa ggagcaaaga
660
gctcttgaaa atcatttaca acagaagcat tctgcagagc ttcaatcact aaaagatgca
720
cacagagagt caatggaggg cttccgga
748

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<210> 110

<211> 157

<212> PRT

<213> Homo sapiens

<400> 110

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Met Gln Leu Phe Tyr Phe Arg Gln Glu Cys Ser Lys Leu Arg Glu Glu
1      5      10      15
Leu Arg Leu Gln His Glu Glu Asp Lys Lys Ser Ala Met Ser Gln Leu
20     25     30
Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
35     40     45
Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
50     55     60
Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
65     70     75     80
Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
85     90     95
Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
100    105    110
Val Leu Ala Phe Gln Thr Met Glu Glu Glu Lys Glu Lys Glu Gln Arg
115    120    125
Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

```

130 135 140
 Leu Lys Asp Ala His Arg Glu Ser Met Glu Gly Phe Arg
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 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu
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 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro
 85 90 95
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val
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<212> DNA

<213> Homo sapiens

<400> 115

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<211> 1062

<212> PRT

<213> Homo sapiens

<400> 116

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Cys	His	Leu	Ser	Pro	Ser	Ser	Leu	Ser	Pro	Phe	Ser	Val	Ala	Glu	Arg				
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Lys	Pro	Pro	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile				
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Ala	Gln	Asn	Glu	Ser	Pro	Val	Leu	Gln	Ser	Gly	His	Trp	Ser	Glu	Tyr				
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Phe	Arg	Asn	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Asp	Arg				
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Pro	Thr	Ser	Glu	Val	Leu	Leu	Lys	His	Arg	Phe	Val	Leu	Arg	Glu	Arg				
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Arg	Glu	Leu	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Ile	Leu	Phe				
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Gln	Glu	Ala	Pro	Asn	Gly	Pro	Gly	Ala	Glu	Ala	Pro	Glu	Glu	Glu	Glu				
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Ser	Ser	His	Ser	Val	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	Ser				
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Ser	Ser	Val	Asn	Ser	Leu	Ala	Asp	Ala	Ser	Asp	Asn	Glu	Glu	Glu	Glu				
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Gln	Ile	Gln	Glu	His	Glu	Gln	Asp	Ser	Ala	Leu	Arg	Glu	Gln	Leu	Ser				
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435 440 445
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 Tyr Phe Glu Leu Gln Cys Arg Gln Tyr Lys Arg Lys Met Leu Leu Ala
 465 470 475 480
 Arg His Ser Leu Asp Gln Asp Leu Leu Arg Glu Asp Leu Asn Lys Lys
 485 490 495
 Gln Thr Gln Lys Asp Leu Glu Cys Ala Leu Leu Leu Arg Gln His Glu
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 Ala Thr Arg Glu Leu Glu Leu Arg Gln Leu Gln Ala Val Gln Arg Thr
 515 520 525
 Arg Ala Glu Leu Thr Arg Leu Gln His Gln Thr Glu Leu Gly Asn Gln
 530 535 540
 Leu Glu Tyr Asn Lys Arg Arg Glu Gln Glu Leu Arg Gln Lys His Ala
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 Glu Arg Arg Ile Leu Gly Lys Glu Gly Ala Thr Leu Glu Pro Lys Gln
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 Gln Arg Ile Leu Gly Glu Glu Ser Gly Ala Pro Ser Pro Ser Pro Gln
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 Lys His Gly Ser Leu Val Asp Glu Glu Val Trp Gly Leu Pro Glu Glu
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 Val Gly Gln Glu Glu Ala Gly Thr Trp Ser Leu Trp Gly Lys Glu Asp
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 Ala Leu Thr Pro Val Pro Glu Glu Glu Glu Glu Glu Glu Glu Ala
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 Pro Ile Gly Thr Pro Arg Asp Pro Gly Asp Gly Cys Pro Ser Pro Asp
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 Gln Leu Pro Gly Leu Leu Ser His Gly Leu Leu Ala Gly Leu Ser Phe
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Gln	Gly	Leu	Ala	Ser	His	Leu	Pro	Pro	Trp	Ala	Ile	His	Thr	Leu	Ala	
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Leu	Pro	Gly	Thr	Leu	Ala	Gly	Arg	Arg	Ser	Arg	Thr	Arg	Gln	Ser	Arg	
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<210> 117
<211> 471
<212> DNA
<213> Homo sapiens
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<212> PRT
<213> Homo sapiens
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<400> 118

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 35 40 45
 Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser
 50 55 60
 Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn
 65 70 75 80
 Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly
 85 90 95
 Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp
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 Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly
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<210> 119

<211> 302

<212> DNA

<213> Homo sapiens

<400> 119

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<211> 98

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<213> Homo sapiens

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 Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr
 35 40 45
 Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

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<210> 121
 <211> 318
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 cctaaaggat ttgccgcatt acaggaaagt tttttggtta gtttgggggtt gtttctgtgc
 120
 tgtgtgagaa ggagtagaag cagctccagt agagtgggcc ttttcatttt tatccagagg
 180
 aaattttagtag gctgtggcta ttacttcctt ttttttcttt tttttttttg ttttagagaca
 240
 gagtctgnct ctgtcgccag gctggagtga agtggcacga tctcagctca ctgcaacctc
 300
 tgcctcccag gttcaagc
 318

<210> 122
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 122
 Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly
 1 5 10 15
 Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu
 20 25 30
 Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser
 35 40 45
 Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
 50 55 60
 Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Cys Leu Glu Thr
 65 70 75 80
 Glu Ser Xaa Ser Val Ala Arg Leu Glu
 85

<210> 123
 <211> 338
 <212> DNA
 <213> Homo sapiens

<400> 123
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 60

cgggcagagg cagggcagct gtgtgccaca ttctgccag ggctggtcag gccccggctc
 120
 tcaccactcc tcttcctgc tttgaacctg tggaacaaag ggccctgca ccccaactca
 180
 ttctcttttg ccacataagg gcctcaagtc atgctgtccc ctctgcctgg gttgctttt
 240
 ctcctctgc ttgggtcact gttcacacca ctggccactt tctcagga agggccctca
 300
 ctgcccacac acctaaacat gccccctgct cctccata
 338

<210> 124

<211> 96

<212> PRT

<213> Homo sapiens

<400> 124

Met Leu Gly Thr Gly Arg Gly Arg Ala Ala Val Cys His Ile Pro Ala
 1 5 10 15
 Arg Ala Gly Gln Ala Pro Ala Leu Thr Thr Pro Pro Pro Cys Phe Glu
 20 25 30
 Pro Val Glu Gln Arg Ala Pro Ala Pro Gln Leu Ile Pro Leu Cys His
 35 40 45
 Ile Arg Ala Ser Ser His Ala Val Pro Ser Ala Trp Val Ala Phe Ser
 50 55 60
 Pro Ser Ala Trp Val Thr Val His Thr Thr Gly His Phe Pro Gln Gly
 65 70 75 80
 Arg Ala Leu Thr Ala His Thr Pro Lys His Ala Pro Cys Ser Ser Ile
 85 90 95

<210> 125

<211> 280

<212> DNA

<213> Homo sapiens

<400> 125

ccatggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc
 60
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga
 120
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca
 180
 ttcccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg
 240
 gcttctgctg tcttggecca ttctggatag gcctgatcta
 280

<210> 126

<211> 92

<212> PRT

<213> Homo sapiens

<400> 126

Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc
 120
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag
 180
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tgggnnacgt
 240
 cgccgggggtg acctgctggg acgggttact gccgacgtcg acgcggtgtt ggacatggtc
 300
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggtcctt
 360
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggc
 416

<210> 132

<211> 126

<212> PRT

<213> Homo sapiens

<400> 132

Ser	Gly	Ala	Ser	Val	Ala	Leu	Met	Gly	Val	Ser	Ala	Trp	Leu	Leu	Ser
1				5					10					15	
Arg	Ala	Ala	Glu	Ile	Pro	Pro	Val	Leu	Tyr	Leu	Glu	Ala	Ala	Ala	Val
			20					25					30		
Gly	Val	Arg	Phe	Phe	Gly	Ile	Ser	Arg	Gly	Val	Phe	Arg	Tyr	Ala	Glu
	35					40					45				
Arg	Leu	Val	Gly	His	Asp	Leu	Ala	Leu	Arg	Met	Gln	Gly	Ala	Leu	Arg
	50					55				60					
Met	Arg	Val	Tyr	Asp	Arg	Leu	Ser	Arg	Thr	Xaa	Pro	Ala	Gly	Xaa	Arg
65					70					75				80	
Arg	Arg	Gly	Asp	Leu	Leu	Val	Arg	Val	Thr	Ala	Asp	Val	Asp	Ala	Val
			85						90					95	
Leu	Asp	Met	Val	Val	Arg	Val	Ile	Val	Pro	Ala	Cys	Ala	Ser	Ser	Leu
		100						105					110		
Val	Ile	Ile	Gly	Thr	Thr	Val	Leu	Leu	Cys	Pro	Arg	Glu	Gly		
		115					120						125		

<210> 133

<211> 327

<212> DNA

<213> Homo sapiens

<400> 133

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 gcgttgaaga gactcgccga catctaccag ggtcgtgttc acacagtagt atccaccgcg
 120
 gccgaaattg cgaaggcgct agaaaccgct gacgttgatga tcggttctgt ccttattccg
 180
 ggtagttcta ccccgaaagct tggtactacc gatatgggtg ctcacatgca gcctgggtct
 240
 gttcttattg atattgctat agaccaagge ggctgcttcg aggattcgca cccaccact
 300
 tacgatgacc ccactttcac tgtgcac
 327

<210> 134
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 134
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp
 1 5 10 15
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg
 20 25 30
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu
 35 40 45
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr
 50 55 60
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser
 65 70 75 80
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser
 85 90 95
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His
 100 105

<210> 135
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 135
 taagatgtgg tcctgccctg ttcctgaagg ggctgcagct ctgatggaaa atacagggat
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 ttacactcag ggctacagcc acggggggct gaggcccaag gctgcaatct cgggggaagg
 120
 ggaagtggc ttttctggt ggattggaaa catcctcttg gaggcaaaga cttttcctgg
 180
 atcttacaga cttcccgga ttttttagatt agaattattgg gggcaaagga ggctgtcttg
 240
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag
 300
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt
 360
 ccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa
 420
 atgacatctt gtcttcatgc tcgagagaga attacttcac tggctccact tggagtcca
 480
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 540
 acttccaagt cccacgcgt
 560

<210> 136
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 136

Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1 5 10 15
 Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
 20 25 30
 Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
 35 40 45
 Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
 50 55 60
 Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
 65 70 75 80
 Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
 85 90 95
 Ile Ser Ser Gly
 100

<210> 137

<211> 429

<212> DNA

<213> Homo sapiens

<400> 137

accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
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 gaggcaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcata gcccttgagc
 120
 aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
 180
 gactgctggc gggtcgcaac gcgcatgata ggcagcgccct ggctggcgcc ctggctgagc
 240
 cagcgcgtcg gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
 300
 aggtacacca catggtcggt catgcagaat gtttcgcccc agccgggata acggcaagt
 360
 ccggcgctgt aatggcaacg ttcggggctc atgatgcaca ggccacactg ggccagcttg
 420
 gtcatgccc
 429

<210> 138

<211> 141

<212> PRT

<213> Homo sapiens

<400> 138

Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1 5 10 15
 Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
 20 25 30
 Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
 35 40 45
 Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
 50 55 60
 Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln


```

65          70          75          80
Gln Ser Gly Phe Val Glu Asp Leu Phe Arg Ser Gln Val Ala Asp Lys
          85          90          95
Thr Asn Trp Arg Ala Leu Leu Lys Gly Asp Ala Gln Ser Val Asp Leu
          100          105          110
Lys Gln Val Arg Asp Gln Leu Phe Ala Ser Cys Ala Glu Gly Leu Leu
          115          120          125
Ser Leu Gln Glu Arg Phe Gly Leu Gln Ala Ile Gln Pro
          130          135          140

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<210> 139

<211> 341

<212> DNA

<213> Homo sapiens

<400> 139

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acgcgtcggt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc
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ttgtgaacag cagaatcaag ccgctggtaa atcttcctgg gagcttcata ggcgggggatg
120
ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
180
tttgagcct gtaacgactg agggttcgga tggaaaaaca catgctccag gatgggaccg
240
acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtagcgcgaa
300
tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
341

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<210> 140

<211> 113

<212> PRT

<213> Homo sapiens

<400> 140

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Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
1          5          10          15
Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
          20          25          30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
          35          40          45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
          50          55          60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65          70          75          80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Leu Phe Thr Ser Cys Gly
          85          90          95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
          100          105          110
Ala

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<210> 141

<211> 324

<212> DNA

<213> Homo sapiens

<400> 141

gaattcctct tggatagctt cgggtaaatg ggtacagcaa atatcaggag cgcaaccgca
 60
 acctttactt actggtacat gaacaccatt tacattacag ctatcggtact caccacacgt
 120
 catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc
 180
 gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcatagaact cctttgacca
 240
 tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca
 300
 gcagttatca ccgccatac gcgt
 324

<210> 142

<211> 106

<212> PRT

<213> Homo sapiens

<400> 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5					10					15	
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
		20					25					30			
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
	35					40					45				
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
	50				55					60					
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65				70					75				80		
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
			85				90						95		
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
			100				105								

<210> 143

<211> 1325

<212> DNA

<213> Homo sapiens

<400> 143

nacgcgtgga tctgccagct gagcctggag ctgtgcaggc agctgccctg ctacgatgag
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 gcaccccagg agaagaactt cctgtacaaa tgcataggca ccaccctggg tgctgcttca
 120
 agtaaggagg tggtgaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag
 180
 gaggcagaac gcgagggcct cgcctgctgc ttcgggatct gtgccatctc ccacctcgag
 240
 gacacgctgg ccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc
 300

attctcaaca tttttaagga tcgaagtga aacgaagtgg agaaggtgaa gagtgtctctg
 360
 atcctgtgct atgggcacgt ggcgccccgg gccccccggg agctgggtgct ggccaaggta
 420
 gagtccagaca tcctccggaa catcntgcca gcacttcagc acnncaagga cccagccctg
 480
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgcg ccatctgcag cagcaccag
 540
 gctggctcct tccacttcac ccggaagca gagctgggtg cacagatgat ggagtccatc
 600
 agggcagagc ccccgactc cttgaggaca cctattcgga agaaagccat gctcacctgc
 660
 attacttggt tctccgtgga gccagcgtg gacgagcagg cccgggcgga tgtgatccat
 720
 ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc
 780
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 840
 cagcggaaca tgacccccca aggcctgcag atcatgattg agcacctgag cccatggatc
 900
 aagtcctcaa gaggtcacgt agcggcgctg gccctaggcc tgagcgccct cctcgtgcgc
 960
 tacttcctgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag
 1020
 cccaggatcc tgtgcaatgg ccctggtgcc cttccacaac ctgggccttc tcatcgccct
 1080
 cttctcccca cgggtgtgcg accctgtggc tgccaccgc caggaggcgg tggactgtgt
 1140
 ctactccctg ctgtacctcc agctcggtta tgagggttc tcccgggact accgcgatga
 1200
 cgtggcggag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct
 1260
 cttccacacc tgccacagtg taggccagat tattgccaag cgctccccc cagcccttca
 1320
 cgcgt
 1325

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Xaa	Ala	Trp	Ile	Cys	Gln	Leu	Ser	Leu	Glu	Leu	Cys	Arg	Gln	Leu	Pro
1				5					10					15	
Cys	Tyr	Asp	Glu	Ala	Pro	Gln	Glu	Lys	Asn	Phe	Leu	Tyr	Lys	Cys	Ile
		20						25					30		
Gly	Thr	Thr	Leu	Gly	Ala	Ala	Ser	Ser	Lys	Glu	Val	Val	Arg	Lys	His
		35					40					45			
Leu	Gln	Glu	Leu	Leu	Glu	Thr	Ala	Arg	Tyr	Gln	Glu	Glu	Ala	Glu	Arg
	50					55					60				
Glu	Gly	Leu	Ala	Cys	Cys	Phe	Gly	Ile	Cys	Ala	Ile	Ser	His	Leu	Glu
65				70					75					80	
Asp	Thr	Leu	Ala	Gln	Leu	Glu	Asp	Phe	Val	Arg	Ser	Glu	Val	Phe	Arg

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400> 145
cggccgtcta ggtccggctc agtgcgctgt tgctcgccgt agaacacgag gctgcgcaag
60
cataagcaga cgtagagagt ggtcacatcc atgtcgatgg tgtgcgcgta atgaaggctc
120
acatcacctt ggtgaaggcc tgcaccacta gcgtcggcac catttccccg cgtcggacaa
180
gacatcatgc cccatatctt gacagaatgt ctgacatgag tatgccacgc cgagcagcac
240

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cagaggacga caccgatctg gcggacgccg cccgttcattg gcgcagatac ctcacccctcg
 300
 tcatttggtg cgttatcgct gctgtccctg gactaggcat tttcgggtat cttgcgtggt
 360
 ggtcattgtg cgatcaagct gccgggggtct gtcagcgtgg tgaaccogtt atgtactggt
 420
 gttcgggtgt ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc
 480
 tggagaagcg ctggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccg
 540
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 600
 tattgatctc cgttttatcg gctcctagca gccgtggtca acgtatcgct atcaagcgat
 660
 acaggactcg tcgttcgcat cgttggtgtg ctgctgggaa acaatcccag cgatctactc
 720
 ggctaccgcc agacagttca ctcaaaccc ctcacgccgg cgcagacatc aaatcccatt
 780
 ctcgatagac ggccacacc ac
 802

<210> 146

<211> 151

<212> PRT

<213> Homo sapiens

<400> 146

Met	Lys	Val	Tyr	Ile	Thr	Leu	Val	Lys	Ala	Cys	Thr	Thr	Ser	Val	Gly
1				5					10					15	
Thr	Ile	Ser	Pro	Arg	Arg	Thr	Arg	His	His	Ala	Pro	Tyr	Leu	Asp	Arg
		20						25					30		
Met	Ser	Asp	Met	Ser	Met	Pro	Arg	Arg	Ala	Ala	Pro	Glu	Asp	Asp	Thr
		35					40					45			
Asp	Leu	Ala	Asp	Ala	Ala	Arg	Ser	Trp	Arg	Arg	Tyr	Leu	Ile	Leu	Val
	50					55					60				
Ile	Cys	Gly	Val	Ile	Val	Ala	Val	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Tyr
65					70				75					80	
Leu	Ala	Trp	Trp	Ser	Leu	Cys	Asp	Gln	Ala	Ala	Gly	Val	Cys	Gln	Arg
				85				90					95		
Gly	Glu	Pro	Val	Met	Tyr	Trp	Cys	Ser	Val	Val	Ser	Leu	Ala	Ile	Leu
			100					105					110		
Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Gln	Ile	Trp	Leu	Glu	Lys	Arg	Trp
		115					120					125			
Trp	His	Met	Leu	Ala	Ile	Val	Ile	Pro	Ala	Val	Phe	Ile	Val	Ala	Gly
		130				135					140				
Ile	Phe	Phe	Trp	Leu	Ala	Val									
145						150									

<210> 147

<211> 368

<212> DNA

<213> Homo sapiens

<400> 147

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 ttacacagct gggcattagt agcccgcat gttcatgaca ttcctgggtct acgaaaagtt
 120
 attggtcaga aagtaccttg tgttgacgtg acgggggtcgg aaaaggtgct tcataaaaag
 180
 gattactggg atctagcaac acctatgccca attgctgggg gtacaacgga ccgaacagtt
 240
 attgctgatg cacgacgtac aatccccacc acggagtggg atataccttgc aagactacgt
 300
 ccacgcctag aagaggttcg caagcaacgt aatgatgtat tgctcctcaa cgaggaggat
 360
 ccccccta
 368

<210> 148
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Thr Leu Leu Ala Leu Val Asp Leu Ser Lys Lys Pro Asp Glu Phe
 1 5 10 15
 Thr Gln Trp Ala Leu Val Ala Arg Asp Val His Asp Ile Pro Gly Leu
 20 25 30
 Arg Lys Val Ile Gly Gln Lys Val Pro Cys Val Ala Val Thr Gly Ser
 35 40 45
 Glu Lys Val Leu His Lys Lys Asp Tyr Trp Asp Leu Ala Thr Pro Met
 50 55 60
 Pro Ile Ala Trp Gly Thr Thr Asp Arg Thr Val Ile Ala Asp Ala Arg
 65 70 75 80
 Arg Thr Ile Pro Thr Thr Glu Trp Asp Ile Leu Ala Arg Leu Arg Pro
 85 90 95
 Arg Leu Glu Glu Val Arg Lys Gln Arg Asn Asp Val Leu Leu Leu Asn
 100 105 110
 Glu Glu Asp Pro Pro
 115

<210> 149
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 149
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 120
 gcggtggatg gtagctgta ccgaagtgcg gatgaaggca agtcgtgggc cccaattaag
 180
 gggcctgaac agggtcaggc gcaccttttc gtgtccatc cctacgacaa gactcaagcg
 240
 tatattctga cgcgcagcac tcagcattgg cgcacgtcga accgtggcga gacgtggcag
 300

tcattctcaa cgctcatcc gctacgacc ttgaaagcta tgctctgga ctttcatccg
 360
 acgcatcatg actggatcct tttcacgggc caggcttgca cggtaaa
 407

<210> 150
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 150
 Xaa Leu Ala Trp Thr Leu Val Thr Gln Ala Ala Ile Pro Glu Val Lys
 1 5 10 15
 Val Thr His Phe Pro Asn Met Ala Ala Gln Ile Gln Tyr Phe Glu Asp
 20 25 30
 Ser Ser Val Val Ile Trp His Asp Ala Val Asp Gly Ile Val Tyr Arg
 35 40 45
 Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln
 50 55 60
 Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala
 65 70 75 80
 Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly
 85 90 95
 Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys
 100 105 110
 Ala Met Pro Leu Asp Phe His Pro Thr His His Asp Trp Ile Leu Phe
 115 120 125
 Thr Gly Gln Ala Cys Thr Val
 130 135

<210> 151
 <211> 448
 <212> DNA
 <213> Homo sapiens

<400> 151
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 gcttttcgcg catccagggtc ccagcccca gctactgggtg cgccccgagc ccctaggtgc
 120
 cagagcggtg gtcggccggg ctctgcccc gtctcggtc ctccctctc cccaccagaa
 180
 ggaaaaactt gggcccttcg agaacctgt ggaatgttct ttgtaatcaa ctgtacatcc
 240
 gcttccaagg cacggcctcg tgcaaaatcg cgggtttcgg ggccttgag caaattgcgc
 300
 ttgtcagcgg cgacgtcagg aggacaaggg gaggggttcg cggctgaaac tgcagcttcg
 360
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 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly
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<212> PRT

<213> Homo sapiens

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Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala		
1185	1190	1195
Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe		1200
1205	1210	1215
Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys		
1220	1225	1230
Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe		
1235	1240	1245
Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser		
1250	1255	1260
Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr		
1265	1270	1275
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg		1280
1285	1290	1295
Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met		
1300	1305	1310
Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr		
1315	1320	1325
Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu		
1330	1335	1340
Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg		
1345	1350	1355
Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly		
1365	1370	1375
Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys		
1380	1385	1390
Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr		
1395	1400	1405
Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val		
1410	1415	1420
Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys		
1425	1430	1435
Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly		1440
1445	1450	1455
Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg		
1460	1465	1470
Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe		
1475	1480	1485
Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys		
1490	1495	1500
Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu		
1505	1510	1515
Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu		1520
1525	1530	1535
Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala		
1540	1545	1550
Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser		

1555
Ser Ser Val Val
1570

1560

1565

<210> 159
<211> 540
<212> DNA
<213> Homo sapiens

<400> 159
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tccgctcatc tgcagaatgg gtgatgctgt cggctacttcg tggcatacag gaaagtgtccc
120
agcatgggtca gcctcagtga gaggtggcca gtggggagtg gtggccactg tacacctggc
180
acagcccaga gatgcatgtg ccactctgtt gtgtgcttca accaaggggc gctctggcag
240
ggcttgggtg ggacttccca aagggtcatgg aaaagttccc agtcaatgag atccatggag
300
acccatggga gtgggggtca gcccagcct aagaggaccc ccagccctgc cctgtgcccc
360
aggacacacc aggcactgtc ccttgtcgcc ttcccagaca acctgtaccc tccaggccac
420
cagttctcgt ccatgacaaa gaaaggagcc ttctaaataa gtgcccgcga gaggtgcac
480
gcttccctgc cccttcggg tggacctggg tttcaaagag aagctgccag tgcaacgcgt
540

<210> 160
<211> 110
<212> PRT
<213> Homo sapiens

<400> 160
Met Val Ser Leu Ser Glu Arg Trp Pro Val Gly Ser Gly Gly His Cys
1 5 10 15
Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe
20 25 30
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala
35 40 45
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly
50 55 60
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg
65 70 75 80
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro
85 90 95
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe
100 105 110

<210> 161
<211> 351
<212> DNA
<213> Homo sapiens

<400> 161
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 60
 cgcgcttgge tcgcagcgac gatgaagggc gacgacagca gcaagatcac ccacaagatc
 120
 gcccggggcga agcgcgaggg ccgcgtatgg tggagctttg agtacttccc gccgcgcacg
 180
 ccgcagggca tgcagaattt gtatgaccgt atcgagcgca tgagtcagct gggccccgag
 240
 tttgtggaca ttacgtggaa tgccgggggc cggacgtcgg atatgacgac gcagctggtc
 300
 aagacggtgc atgcgtactt tgggtgctgag acgtgcatgc atctgacgtg c
 351

<210> 162
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 162
 Xaa Arg Val Arg Leu Ser Ala Glu Glu Gly Thr Trp Ala Gly Ala Ser
 1 5 10 15
 Phe Ala Gly Arg Arg Ala Trp Leu Ala Ala Thr Met Lys Gly Asp Asp
 20 25 30
 Ser Ser Lys Ile Thr His Lys Ile Ala Arg Ala Lys Arg Glu Gly Arg
 35 40 45
 Val Trp Trp Ser Phe Glu Tyr Phe Pro Pro Arg Thr Pro Gln Gly Met
 50 55 60
 Gln Asn Leu Tyr Asp Arg Ile Glu Arg Met Ser Gln Leu Gly Pro Glu
 65 70 75 80
 Phe Val Asp Ile Thr Trp Asn Ala Gly Gly Arg Thr Ser Asp Met Thr
 85 90 95
 Thr Gln Leu Val Lys Thr Val His Ala Tyr Phe Gly Val Glu Thr Cys
 100 105 110
 Met His Leu Thr Cys
 115

<210> 163
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 163
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 60
 gacacctaca ccctgcgctca gcccatcggc gtatgcgag gcactactcc gttcaacttc
 120
 ccggcgatga ttccactgtg gatgttcccg atggcgattg cctgcggtaa cactttcgtg
 180
 ctcaaaccgt ccgaacaaga ccctctgtcg acgatgctgc tggtagaact ggcgctggaa
 240
 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcg
 300

ctgtgcaccc ataaagatat caaggcagtt tctttcgtcg gttcgaccgc cgttgggtacc
360

<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

Ala	Cys	Ser	Ile	Gly	Thr	Leu	Gln	Met	Gly	Glu	Phe	Ala	Glu	Asn	Val
1				5					10					15	
Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
		20						25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
		35				40						45			
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55					60				
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65					70					75				80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
				85				90					95		
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
			100					105					110		
Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
			115				120								

<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

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tcccagcgag ggacgcccgg ggctgggggt gccggtcgag cccggggcaa cagcttcacc
120
aagtttggca accgcaacgt cttcatgaag gacaacagct cttcttccag cacagactcc
180
cgctcccgt cctcctccag gtccccgacg cgccacttcc gcagaagtga ctcccactca
240
gactccgaca gctcctactc aggggaatgag tgtcaccctg tgggcccgcag gaaccgcccc
300
cctaagggcc ggggagggtcg agggggcccat atggatcggg gccgaggcag ggcgcagcgt
360
gggaagaggc acgatctggc gccaccaaag cgcagtcgaa agaagatggc ggcgctggag
420
tgtgaggacc cggagcgaga gctgaagaag cagaagcggg cagcccgtt ccagcacgga
480
cactcccgcc gcctgcgcct cgagcccctg gtgctgcaga tgagcagcct ggagagcagt
540
ggggctgacc ctgactggca ggagctgcag atcgtgggca cctgccctga catcaccaag
600
cactacctgc gcctcacctg tgcccccgac ccgtccacg tgccgctgt ggcattccct
660

gtggcaggtt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaaag agaagcagga
 720
 ctacgcgt
 728

<210> 166
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 166
 Ala Ser Ser Leu His Pro Pro Arg Gly Ala Gly Ser Ala Thr Arg Gly
 1 5 10 15
 Gly Gly Ala Pro Ser Gln Arg Gly Thr Pro Gly Ala Gly Gly Ala Gly
 20 25 30
 Arg Ala Arg Gly Asn Ser Phe Thr Lys Phe Gly Asn Arg Asn Val Phe
 35 40 45
 Met Lys Asp Asn Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser
 50 55 60
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser
 65 70 75 80
 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg
 85 90 95
 Arg Asn Pro Pro Pro Lys Gly Arg Gly Gly Arg Gly Ala His Met Asp
 100 105 110
 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro
 115 120 125
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro
 130 135 140
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly
 145 150 155 160
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser
 165 170 175
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val
 180 185 190
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala
 195 200 205
 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe
 210 215 220
 Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly
 225 230 235 240
 Leu Arg

<210> 167
 <211> 510
 <212> DNA
 <213> Homo sapiens

<400> 167
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 gcaacacaga attgtcaggt cctgtgccgt gaccaccac cctcggggcca tgccaggtgc
 120

tggtaggggg caggtggctc ccgccaggcg cctgctggcc tgaccgcact ccgtccacag
 180
 gtcctcatgg gcgtcctccg gctgggcttc gtgtccgcct acctctcaca gccactgctc
 240
 gatggctttg ccatgggggc ctccgtgacc atcctgacct cgcagctcaa acacctgctg
 300
 ggctgcgga tcccgcggca ccagggggcc ggcatgggtg tcctcacatg gctgagcctg
 360
 ctgctggcg ccgggcaggc caacgtgtgc gacgtgggtca ccagcacggg gtgcctggcg
 420
 gtgctgctag ccgcaagga gctctcagac cgctaccgac accgcctgag ggtgccgctg
 480
 cccacggagc tgetgggtcat cgtgggtggc
 510

<210> 168
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 168
 Gly Ala Gly Gly Ser Arg Gln Ala Pro Ala Gly Leu Thr Ala Leu Arg
 1 5 10 15
 Pro Gln Val Leu Met Gly Val Leu Arg Leu Gly Phe Val Ser Ala Tyr
 20 25 30
 Leu Ser Gln Pro Leu Leu Asp Gly Phe Ala Met Gly Ala Ser Val Thr
 35 40 45
 Ile Leu Thr Ser Gln Leu Lys His Leu Leu Gly Val Arg Ile Pro Arg
 50 55 60
 His Gln Gly Pro Gly Met Val Val Leu Thr Trp Leu Ser Leu Leu Arg
 65 70 75 80
 Gly Ala Gly Gln Ala Asn Val Cys Asp Val Val Thr Ser Thr Val Cys
 85 90 95
 Leu Ala Val Leu Leu Ala Ala Lys Glu Leu Ser Asp Arg Tyr Arg His
 100 105 110
 Arg Leu Arg Val Pro Leu Pro Thr Glu Leu Leu Val Ile Val Val Ala
 115 120 125

<210> 169
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 169
 gaattccacc gcatgtcgtg tctggacgta tgtaggtcgc ggtagtgtgc gaccgccggg
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 gccttaaagg agagcgggca tcggcgttgc agtacgagag gggaagggtg gcggatactt
 120
 attgtcggtg cggcatcgtc catccacacc gttcgatggg tcaatggact ggtcaagcgg
 180
 ggtcacgagg ttcacctggc atcagtccat ccggcggggc gtcactccat tgatccccga
 240
 gttcggatcc acctggcccc acacggcggg aaggcaaaat acgtcgtcaa tgccggctgg
 300

ctgcgatcag tggcggctgg ggtgcaacct gacatcgta acgtccacta tgcgaccggt
 360
 tatgggtctgc tcgctcgtct tgcccatatt gacgccccga cgctgctgtc ggtgtgggga
 420
 agtgacgttt acgattcccc ccgggcaaat cccctcatgc gtcacatggt ccgatccaac
 480
 ttggtctcag ctactcggat cgcacgcaca agccactgca tggcgcgtgt caccgct
 537

<210> 170

<211> 164

<212> PRT

<213> Homo sapiens

<400> 170

Cys	Ala	Thr	Ala	Gly	Ala	Leu	Lys	Glu	Ser	Gly	His	Arg	Arg	Cys	Ser
1				5					10					15	
Thr	Arg	Gly	Glu	Gly	Val	Arg	Ile	Leu	Ile	Val	Gly	Ala	Ala	Ser	Ser
		20						25					30		
Ile	His	Thr	Val	Arg	Trp	Val	Asn	Gly	Leu	Val	Lys	Arg	Gly	His	Glu
		35					40					45			
Val	His	Leu	Ala	Ser	Val	His	Pro	Ala	Gly	Arg	His	Ser	Ile	Asp	Pro
	50					55					60				
Arg	Val	Arg	Ile	His	Leu	Ala	Pro	His	Gly	Gly	Lys	Ala	Lys	Tyr	Val
65				70					75					80	
Val	Asn	Ala	Gly	Trp	Leu	Arg	Ser	Val	Ala	Ala	Gly	Val	Gln	Pro	Asp
			85					90					95		
Ile	Val	Asn	Val	His	Tyr	Ala	Thr	Gly	Tyr	Gly	Leu	Leu	Ala	Arg	Leu
		100						105					110		
Ala	His	Ile	Asp	Ala	Pro	Thr	Leu	Leu	Ser	Val	Trp	Gly	Ser	Asp	Val
		115					120					125			
Tyr	Asp	Ser	Pro	Arg	Ala	Asn	Pro	Leu	Met	Arg	His	Met	Val	Arg	Ser
	130					135					140				
Asn	Leu	Val	Ser	Ala	Thr	Arg	Ile	Ala	Ser	Thr	Ser	His	Cys	Met	Ala
145				150					155					160	
Arg	Val	Thr	Arg												

<210> 171

<211> 391

<212> DNA

<213> Homo sapiens

<400> 171

ctagacaagc tcgcgcgggt gggcttcgac actcttggtc tacagacctt cctaactgcg
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 ggggagaagg agtcccgcgc atggacgatt cacaagggcg acaccgcccc tgaggctgct
 120
 ggcgatcatcc ataccgactt ccagaagggg ttcataaggg ccaggtggt gtccttcggc
 180
 gaccttggtg aatttggcgg cgaaaaggag gccaggctg ctgggaagct gcggttggag
 240
 ggcaaggagt acgttatgca ggacgggtgac gtagtggaat tccgatttaa cgtgtagctc
 300

tgggttgata cttacttggc ttaaccgcat ctgagatccg tcatatcttt ggcgtagcct
 360
 tattggtatg aataacatgc cgtagccaaa g
 391

<210> 172
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 172
 Leu Asp Lys Leu Ala Arg Val Gly Phe Asp Thr Leu Gly Leu Gln Thr
 1 5 10 15
 Phe Leu Thr Ala Gly Glu Lys Glu Ser Arg Ala Trp Thr Ile His Lys
 20 25 30
 Gly Asp Thr Ala Pro Glu Ala Ala Gly Val Ile His Thr Asp Phe Gln
 35 40 45
 Lys Gly Phe Ile Lys Ala Gln Val Val Ser Phe Gly Asp Leu Val Glu
 50 55 60
 Phe Gly Gly Glu Lys Glu Ala Gln Ala Ala Gly Lys Leu Arg Leu Glu
 65 70 75 80
 Gly Lys Glu Tyr Val Met Gln Asp Gly Asp Val Val Glu Phe Arg Phe
 85 90 95
 Asn Val

<210> 173
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 173
 ccatggagtg tcccttgtgc gagcattttg agagctatac caacacccat ccctgcaggt
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 cccagagccg agccatttct caggagagca ggaagggagc aggccgaggg gtgctcccag
 120
 ccagccccgg aacccgaggt ctggggacgc agccgaccag cctccttgt ctgggcctct
 180
 gtttcctctt cgacacaggg aagcagggag gggccgatca gcgacttagg cctgttggct
 240
 gtgggtgggg cccctgcgtt tctgggaagc cacggaccct gggatgtacc tgggtttcat
 300
 tcgcagtga
 309

<210> 174
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 174
 Met Glu Cys Pro Leu Cys Glu His Phe Glu Ser Tyr Thr Asn Thr His
 1 5 10 15
 Pro Cys Arg Ser Gln Ser Arg Ala Ile Ser Gln Glu Ser Arg Lys Gly


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<400> 175
nnacttttttt tttttttttt catttatgct atggagaaac cagcatggag atgtcatggg
60
agagcatgca caggccccgc cctagggagt ggtgatgtgt ttggggaggt gcttgtttcc
120
aggtccatcc cacacgttgt ccagttggat cctatggcag gctggctgtg gctttctctc
180
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240
gccaaggact ggtggatggg tggctggaag cagcgcacat gctccacagt ggaactgtct
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360
tacttctga tccggctcggc catcttcttc aggggcacat tcttaatgat ttcctcttc
420
ccgtcttgcc tctgcacttt tagcaggtgg taacagaagt cgaacaggtc aaagcgacgc
480
tgctggccca gcaggacaat gatggagcaa ccagcccagt tcaagccatc gccgaaacac
540
tgctcagctg tgaactcggt ggttcccaca gggatgcagt acacgaactg catggcgctc
600
cacagccggt ggaactccac aactcatcg acgtgcatga cgccattggt gggcggtggg
660
ccccgccaga tggggtcctg caggtagctc cgaatgcggg tcaggatgac ctcaaacatg
720
gacaggccac agcacagccg ctcttggtc aggaggtcac cctcgcgagc aatggcgatt
780
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840
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900
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960
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ctgttttgag ctctgcgtac tcaatgatgt ccttcagctg gtggtggaag aactccagga
1080

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tccctgggga gccataactca tgctggggca agcggcatat cttgggcatc acctctatca
1140
gtgttttcac atactggaga atggttcctt ggagcaagct cttcacaatc tttagcagtt
1200
cctccatgac cacagcgatg ccctgataac ccaggagtct gcagatagtc ttgaaagtgt
1260
ggagggtccca cgaagtccg gtagctgccg taaatgctgg agtaggcca gttcaaagcc
1320
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1380
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1440
aggaagtcac agttgagctc ccagaagacg tgcagggtga tcctcccgta gggcgctgac
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1560
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1620
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1680
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1800
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1860
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1920
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1980
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2160
agcgtttcac tgaaatttat caagtgagtg tagaagaatg actctcgatg aaagtcctct
2220
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2280
tctgcaatga gtgattcaag catggttctc accatgtaca gctgtgtgct ggatggcccc
2340
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2400
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2460
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2520
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2580
aagacgtct ccatcctgcc catgagcacc tgcaggcctt tgatcatggc gatcacctca
2640
acgaaggcaa atttttctc actgggtgtaa ttgtagcgtg tggtctctc atattcctcc
2700

gcggtgccag gacagtcctt gttgcagaac ttgtctgtgg gatgaaccag cttccaagag
2760
tacacctcca tgacgtgggc gctccacttg gatagaagct gcagaccccg cagggctagg
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2880
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2940
tgaaccatct gctcgcagat attgtactgg gggctgatgc tgctctgggt gcacgtccat
3000
cgagatttat tttcctcgta gtgggcgctg gtcttgatat atcttgccag ttctatttgc
3060
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3120
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3180
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3240
ttctcgtagt aatccacaca cagattcaca atatctgcca ggagctcttc gtagccagaa
3300
atcacttcga gctgctgctg cagagactgt gtgatcttgt tatgattggc caggaacatg
3360
gacagattct gcgattcctg gatggactgt ggatctgcca ttttacgtaa aaactgtgct
3420
gccctcttgt aggcagagtg gtcgttcttg acgctgcact tcatgttctt cagatcgtcc
3480
agcacagcga acatgttgat gaatttgccc agtgtgatca ggtaggcttc tgacacgaag
3540
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<210> 176

<211> 1393

<212> PRT

<213> Homo sapiens

<400> 176

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Ser	Met	Tyr	Leu	Ala	Met	Pro	Val	Thr	Asn	Ala	Phe	Leu	Ser	Ser	Lys
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Phe	Val	Ser	Lys	Leu	Ala	Trp	Tyr	Met	Met	Glu	Glu	Gly	Gly	Gly	Ser
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Met	His	Gly	Cys	Trp	Ser	Gly	Arg	Gly	Ser	Ser	Ser	Ser	Arg	Ser	Thr
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Leu	Asp	Arg	Ala	Ser	Ser	Arg	Val	Thr	Cys	Val	Val	Met	Ala	Ala	Val
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Ser	Val	Phe	Cys	Thr	Gly	Ser	Ala	Ala	Gly	Pro	Gly	Glu	Gly	Pro	Glu
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Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro Pro Ser Ser Ile
165      170      175
Met Tyr Gln Ala Asn Phe Asp Thr Asn Phe Glu Asp Arg Asn Ala Phe
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Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr Val His Ser Ser
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Met Asn Glu Met Leu Glu Glu Gly His Glu Tyr Ala Val Met Leu Tyr
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Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val Lys Cys Asn Glu
225      230      235      240
Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val Glu Val Leu Glu
245      250      255
Pro Glu Val Thr Lys Leu Met Asn Phe Met Tyr Phe Gln Arg Asn Ala
260      265      270
Ile Glu Arg Phe Cys Gly Glu Val Arg Arg Leu Cys His Ala Glu Arg
275      280      285
Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Ile Thr Leu Gly Lys Phe
290      295      300
Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn Met Lys Cys Ser
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Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala Gln Phe Leu Arg
325      330      335
Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln Asn Leu Ser Met
340      345      350
Phe Leu Ala Asn His Asn Lys Ile Thr Gln Ser Leu Gln Gln Gln Leu
355      360      365
Glu Val Ile Ser Gly Tyr Glu Glu Leu Leu Ala Asp Ile Val Asn Leu
370      375      380
Cys Val Asp Tyr Tyr Glu Asn Arg Met Tyr Leu Thr Pro Ser Glu Lys
385      390      395      400
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Ser Val Ser Asn Ile Tyr Lys Leu Asp Ala Lys Lys Arg Ile Asn Leu
420      425      430
Ser Lys Ile Asp Lys Tyr Phe Lys Gln Leu Gln Val Val Pro Leu Phe
435      440      445
Gly Asp Met Gln Ile Glu Leu Ala Arg Tyr Ile Lys Thr Ser Ala His
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Tyr Glu Glu Asn Lys Ser Arg Trp Thr Cys Thr Ser Ser Gly Ser Ser
465      470      475      480
Pro Gln Tyr Asn Ile Cys Glu Gln Met Ile Gln Ile Arg Glu Asp His
485      490      495
Met Arg Phe Ile Ser Glu Leu Ala Arg Tyr Ser Asn Ser Glu Val Val
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Thr Gly Ser Gly Arg Gln Glu Ala Gln Lys Thr Asp Ala Glu Tyr Arg
515      520      525
Lys Leu Phe Asp Leu Ala Leu Gln Gly Leu Gln Leu Leu Ser Gln Trp
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 Glu Val Ile Ala Met Ile Lys Gly Leu Gln Val Leu Met Gly Arg Met
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 Glu Ser Val Phe Asn His Ala Ile Arg His Thr Val Tyr Ala Ala Leu
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 Gln Asp Phe Ser Gln Val Thr Leu Arg Glu Pro Leu Arg Gln Ala Ile
 625 630 635 640
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 675 680 685
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 690 695 700
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 Met Glu Tyr Val Leu Tyr Ser Leu Asp Leu Tyr Asn Asp Ser Ala His
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 Lys Arg Leu Arg Ser Glu Cys Lys Asn Gln Gly Ala Thr Ile His Leu
 865 870 875 880
 Pro Pro Ser Asn Arg Tyr Glu Thr Leu Leu Lys Gln Arg His Val Gln
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 Ser Glu Asp Leu Thr Ser Ile Val Glu Leu Asp Gly Leu Leu Glu Ile
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 Asn Arg Met Thr His Lys Leu Leu Ser Arg Tyr Leu Thr Leu Asp Gly
 945 950 955 960
 Phe Asp Ala Met Phe Arg Glu Ala Asn His Asn Val Ser Ala Pro Tyr
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 1285 1290 1295
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 <212> DNA
 <213> Homo sapiens

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<210> 178
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 178
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 35 40 45
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu
 50 55 60
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala
 65 70 75 80
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu
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 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu
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 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser
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 <211> 362
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 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala
 50 55 60
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe
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 <211> 297
 <212> DNA
 <213> Homo sapiens

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<210> 182
 <211> 99
 <212> PRT

<213> Homo sapiens

<400> 182

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Trp Ala Ser Val Glu Phe Trp Gln Gln Gly Ile Cys Arg Val Ile
      35             40             45
Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln
      50             55             60
Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met
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Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp
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Ala Asn Gln

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<210> 183

<211> 351

<212> DNA

<213> Homo sapiens

<400> 183

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<210> 184

<211> 117

<212> PRT

<213> Homo sapiens

<400> 184

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Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp
      35             40             45
Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His
      50             55             60
Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly
65             70             75             80
Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

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Asn	His	Phe	Gly	Asp											
	115														

<210> 185
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 185
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 gctgttggtg gcaattgtgt ttatgcaggc catgaaacca aagcaatgct gaacaacagt
 120
 gggccacggt ataagcgag caaattagaa agaagagcaa acacagatgt cctctggtgt
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 240
 aggtatgaaa agatgcattt tttcaatggt cccgagcctg atggacatat catatcacca
 300
 ctggtggcag gattttatat gttttggacc gtgatcattt tggtacaggt cttgattcct
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<210> 186
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 186
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 Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
 20 25 30
 Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
 35 40 45
 Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
 50 55 60
 Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
 65 70 75 80
 Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
 85 90 95
 Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
 100 105 110
 Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
 115 120 125
 Ile Val Lys Leu
 130

<210> 187
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 187

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 gacactccgt tgtccgagct cttegtctcg accagcaacg ccagggtgcc gttggccgtt
 300
 gtcgacgagg acttccacct catgggtgtc atctctcggg tgaccctgct cgacgcgatg
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 ctt
 423

<210> 188

<211> 141

<212> PRT

<213> Homo sapiens

<400> 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
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Ser	Arg	Ser	Ala	Glu	Pro	Arg	Arg	Val	Gln	Arg	Ile	Leu	Asp	Gln	Arg
		20						25				30			
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
	35						40				45				
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50					55					60				
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70					75					80	
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85						90				95		
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
		100						105					110		
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
	115						120					125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
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<210> 189

<211> 429

<212> DNA

<213> Homo sapiens

<400> 189

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 180
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 240
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 300
 gaagggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca
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 429

<210> 190
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Met Gly Ala Gly Pro Leu Val Ala Gly Leu Ala Leu Gly Leu Gly
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 20 25 30
 Pro Leu Gly Ala Pro Phe Ala Val Ala Ser Ala Val Tyr Met Gly His
 35 40 45
 Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala
 50 55 60
 Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg
 65 70 75 80
 Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly
 85 90 95
 Asn Ala Gly Ile Phe Lys His Phe Thr Ala Ser Pro Arg Gly Ala Ile
 100 105 110
 Ala Ala Arg Thr Val His Met Leu Val Asn His
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<210> 191
 <211> 4845
 <212> DNA
 <213> Homo sapiens

<400> 191
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 180
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg
 240
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 300

atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaac
360
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420
gtttacgtcc tgcaaagtta cgcagagggg tggaaagaag ggacctggga agagaagggtg
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780
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 4845

<210> 192

<211> 428

<212> PRT

<213> Homo sapiens

<400> 192

Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly
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 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro
 20 25 30
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

35 40 45
 Tyr Leu Leu Tyr Asp Val Asn Pro Pro Glu Gly Phe Asn Leu Arg Arg
 50 55 60
 Asp Val Tyr Ile Arg Ile Ala Ser Leu Leu Lys Thr Leu Leu Lys Thr
 65 70 75 80
 Glu Glu Trp Val Leu Val Leu Pro Pro Trp Gly Arg Leu Tyr His Trp
 85 90 95
 Gln Ser Pro Asp Ile His Gln Val Arg Ile Pro Trp Ser Glu Phe Phe
 100 105 110
 Asp Leu Pro Ser Leu Asn Lys Asn Ile Pro Val Ile Glu Tyr Glu Gln
 115 120 125
 Phe Ile Ala Glu Ser Gly Gly Pro Phe Ile Asp Gln Val Tyr Val Leu
 130 135 140
 Gln Ser Tyr Ala Glu Gly Trp Lys Glu Gly Thr Trp Glu Glu Lys Val
 145 150 155 160
 Asp Glu Arg Pro Cys Ile Asp Gln Leu Leu Tyr Ser Gln Asp Lys His
 165 170 175
 Glu Tyr Tyr Arg Gly Trp Phe Trp Gly Tyr Glu Glu Thr Arg Gly Leu
 180 185 190
 Asn Val Ser Cys Leu Ser Val Gln Gly Ser Ala Ser Ile Val Ala Pro
 195 200 205
 Leu Leu Leu Arg Asn Thr Ser Ala Arg Ser Val Met Leu Asp Arg Ala
 210 215 220
 Glu Asn Leu Leu His Asp His Tyr Gly Gly Lys Glu Tyr Trp Asp Thr
 225 230 235 240
 Arg Arg Ser Met Val Phe Ala Arg His Leu Arg Glu Val Gly Asp Glu
 245 250 255
 Phe Arg Ser Arg His Leu Asn Ser Thr Asp Asp Ala Asp Arg Ile Pro
 260 265 270
 Phe Gln Glu Asp Trp Met Lys Met Lys Val Lys Leu Gly Ser Ala Leu
 275 280 285
 Gly Gly Pro Tyr Leu Gly Val His Leu Arg Arg Lys Asp Phe Ile Trp
 290 295 300
 Gly His Arg Gln Asp Val Pro Ser Leu Glu Gly Ala Val Arg Lys Ile
 305 310 315 320
 Arg Ser Leu Met Lys Thr His Arg Leu Asp Lys Val Phe Val Ala Thr
 325 330 335
 Asp Ala Val Arg Lys Glu Tyr Glu Glu Leu Lys Lys Leu Leu Pro Glu
 340 345 350
 Met Val Arg Phe Glu Pro Thr Trp Glu Glu Leu Glu Leu Tyr Lys Asp
 355 360 365
 Gly Gly Val Ala Ile Ile Asp Gln Trp Ile Cys Ala His Ala Arg Cys
 370 375 380
 Leu Pro Thr Ser Leu Ser Ala Glu Ser Gly Ser Gly Gly Phe Gln Arg
 385 390 395 400
 Phe Phe Cys Pro Lys Tyr Ser Val Ser Glu Gln Met Val Ala Cys Val
 405 410 415
 His Ser Gly His Phe His Thr Val Cys Leu Leu Val
 420 425

<210> 193

<211> 350

<212> DNA

<213> Homo sapiens

<400> 193

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cgtgccagca tcagccccga ggaggtcaag ggcgagacca tgttgatgtt gggcacgggc
180
ccctggtttc cccgggccccg cgggtgggggt ttggcccga tttggcgcgt ttctccagcg
240
ccgttaaggg catacgccgc agtttcgagg gctcgtcgtt ggagaccatc aagcacatcg
300
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350

<210> 194

<211> 116

<212> PRT

<213> Homo sapiens

<400> 194

Ala	Gly	Glu	Leu	Asp	Cys	Ala	Ile	Met	Ala	Glu	Pro	Phe	Pro	Asp	Thr
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Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
		20					25					30			
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35				40					45				
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50				55				60						
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65				70				75					80		
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
			85				90					95			
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
			100				105					110			
Val	Arg	Ala	Ala												
			115												

<210> 195

<211> 495

<212> DNA

<213> Homo sapiens

<400> 195

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cgcgaaatag cacgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgcgg
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<210> 196
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 196
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 Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp
 20 25 30
 Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala
 35 40 45
 Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser
 50 55 60
 Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln
 65 70 75 80
 Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His
 85 90 95
 Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala
 100 105 110
 Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu
 115 120 125
 Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile
 130 135 140
 Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala
 145 150 155 160
 Phe Pro Leu Met Asp
 165

<210> 197
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 197
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 120
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 180
 gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaacgt
 240
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt
 300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta
 360
 tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc
 402

<210> 198
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 198
 Gln Ala Met Leu Asp Ala Val Val Glu Tyr Leu Pro Ala Pro Thr Asp
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 Ile Pro Ala Ile Lys Gly Ile Asn Pro Asp Glu Thr Glu Gly Glu Arg
 20 25 30
 His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala
 35 40 45
 Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly
 50 55 60
 Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg
 65 70 75 80
 Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu
 85 90 95
 Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys
 100 105 110
 Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile
 115 120 125
 Leu Glu Arg Met Glu Phe
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<210> 199
 <211> 507
 <212> DNA
 <213> Homo sapiens

<400> 199
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 caatagtga atccccgaga acccagctat ggaagggttt ccagatgctc gaaggcctgt
 180
 cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagttg actcgccggt
 240
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 300
 gcctgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgat ttgagcctct
 360
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 480
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 507

<210> 200
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 200
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 Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu
 20 25 30
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile
 35 40 45
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg
 50 55 60
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr
 65 70 75 80
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu
 85 90 95
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu
 100 105 110
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu
 115 120 125
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser
 130 135 140
 His Arg Ser Met His Asp Phe Thr Arg
 145 150

<210> 201
 <211> 527
 <212> DNA
 <213> Homo sapiens

<400> 201
 gatgtggcta ttatccctgt ttcccagggtg agaaacaggg tcagtgatag agctgggatg
 60
 tgtgcctgca ggctcaccag ccagtcacct ctcaccaag gatgatgttc tccgtgggtga
 120
 gctggctcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat
 180
 ccttctccat ctctttggct agctgcaagt tctggagctg ctggttgagg tctgtgatct
 240
 catccacctg ctggttgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg
 300
 ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc
 360
 gctggtaccg ggctagccgg tctccagggt ctcggtatctg gatgtggtag aactccttca
 420
 tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cttttcttct
 480
 tgacttcaag ctcttgctt gccttgctca cactcttttt gggaggc
 527

<210> 202

<211> 70
 <212> PRT
 <213> Homo sapiens

<400> 202

```

Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro
 1           5           10           15
Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly
          20           25           30
Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr
          35           40           45
Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro
          50           55           60
Ser Cys Pro Leu Ser Ser
65           70

```

<210> 203
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 203

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ngtgcaccgg tggatcatgga caacgccgcc tacgtggtct acacctcggg atccaccggc
60
cgacccaagg gagttgtcgt caccacacac ggactcgaca gtttcgcact cgaccagcag
120
cgtcgattcc acgcagatca ccactctcga accctgcact tcgccacccc cagcttcgac
180
ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcgtcccg
240
accgacatct acggcggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac
300
gcgt
304

```

<210> 204
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 204

```

Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser
 1           5           10           15
Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu
          20           25           30
Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His
          35           40           45
Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe
          50           55           60
Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro
65           70           75           80
Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu
          85           90           95
His Val Thr His Ala

```


100

<210> 205
 <211> 356
 <212> DNA
 <213> Homo sapiens

<400> 205
 nngaattcag caatgataac tggctcaatt gaaggtaaga caacaattga gggaattaat
 60
 gcacaattaa atacagtgtt aactttattt tcaccacaat caaaagataa agatttaatc
 120
 atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga
 180
 cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt
 240
 atcattcaaa gatttggacg gattgatcga attgggtcga agaataaatg tgtacaatta
 300
 gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt
 356

<210> 206
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 206
 Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile
 1 5 10 15
 Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
 20 25 30
 Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile
 35 40 45
 Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
 50 55 60
 Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
 65 70 75 80
 Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
 85 90 95
 Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
 100 105 110
 Ile Asp Leu Lys Gly Arg
 115

<210> 207
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 207
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
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 catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg
 120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt
 180
 gtgcacatgt gcactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc
 240
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt
 300
 gtatgcatgg taatgtgcac gtgt
 324

<210> 208
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 208
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys
 20 25 30
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val
 35 40 45
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys
 50 55 60
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys
 65 70 75 80
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys
 85 90 95
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys
 100 105

<210> 209
 <211> 168
 <212> DNA
 <213> Homo sapiens

<400> 209
 nnctccagag gttatgaggt tggaagcccc gtttttttca ggtgcagaaa aggetaccat
 60
 attcaagggt ccacgactcg cacctgcctt gccaatataa catggagtgg gatacagacc
 120
 gaatgtatac ctcatgcctg cagacagcca gaaacccccg cacacgcg
 168

<210> 210
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 210
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg
 1 5 10 15
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn
 20 25 30
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40 45
 Gln Pro Glu Thr Pro Ala His Ala
 50 55
 <210> 211
 <211> 354
 <212> DNA
 <213> Homo sapiens
 <400> 211
 tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgttgg aggcaatgtc
 60
 cagctggcag ctgagacct tgcacaccat ggaggaagcc tcccacccga cctgcagttc
 120
 tcaggagagg actcctcccc cacaccgtcc acatcccat ctgactctgc agggacctct
 180
 agtgcctcga cagatgaaga catggagacg gaggtgtgca acgaaatcct ggaggacatt
 240
 ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct
 300
 gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gac
 354

<210> 212
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 212
 Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe
 1 5 10 15
 Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly
 20 25 30
 Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr
 35 40 45
 Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr
 50 55 60
 Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile
 65 70 75 80
 Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu
 85 90 95
 Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala
 100 105 110
 Xaa Lys Glu Gln Leu Ile
 115

<210> 213
 <211> 669
 <212> DNA
 <213> Homo sapiens

<400> 213
 attgcccaat ctgagagtgt ccaggaaagc ctggagagcc tggtgcagtc tattggggaa
 60

gttgaacaaa acctggaagg gaaacaggtg tcatcactct catcaggagt catccaggaa
 120
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag
 180
 gccacccgtg agatggtgac ccgattcatg gagacagcag acagtactac agcagcagtg
 240
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa
 300
 gaaaaggaga gctccctaaa gaagcttcta cccagggcag agatgtttga acacctctct
 360
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca
 420
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttgga aatggaagac
 480
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt
 540
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag
 600
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat
 660
 gaattccgg
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile	Ala	Gln	Ser	Gln	Ser	Val	Gln	Glu	Ser	Leu	Glu	Ser	Leu	Leu	Gln
1				5				10					15		
Ser	Ile	Gly	Glu	Val	Glu	Gln	Asn	Leu	Glu	Gly	Lys	Gln	Val	Ser	Ser
		20					25					30			
Leu	Ser	Ser	Gly	Val	Ile	Gln	Glu	Ala	Leu	Ala	Thr	Asn	Met	Lys	Leu
		35				40					45				
Lys	Gln	Asp	Ile	Ala	Arg	Gln	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Arg	Glu
	50				55					60					
Met	Val	Thr	Arg	Phe	Met	Glu	Thr	Ala	Asp	Ser	Thr	Thr	Ala	Ala	Val
65				70				75					80		
Leu	Gln	Gly	Lys	Leu	Ala	Glu	Val	Ser	Gln	Arg	Phe	Glu	Gln	Leu	Cys
		85					90						95		
Leu	Gln	Gln	Gln	Glu	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Leu	Leu	Pro	Gln
	100						105					110			
Ala	Glu	Met	Phe	Glu	His	Leu	Ser	Gly	Lys	Leu	Gln	Gln	Phe	Met	Glu
	115					120					125				
Asn	Lys	Ser	Arg	Met	Leu	Ala	Ser	Gly	Asn	Gln	Pro	Asp	Gln	Asp	Ile
	130				135					140					
Thr	His	Phe	Phe	Gln	Gln	Ile	Gln	Glu	Leu	Asn	Leu	Glu	Met	Glu	Asp
145				150				155					160		
Gln	Gln	Glu	Asn	Leu	Asp	Thr	Leu	Glu	His	Leu	Val	Thr	Glu	Leu	Ser
		165					170						175		
Ser	Cys	Gly	Phe	Ala	Leu	Asp	Leu	Cys	Gln	His	Gln	Asp	Arg	Val	Gln
	180						185					190			
Asn	Leu	Arg	Lys	Asp	Phe	Thr	Glu	Leu	Gln	Lys	Thr	Val	Lys	Glu	Arg

	195		200		205									
Glu	Lys	Asp	Ala	Ser	Ser	Cys	Gln	Glu	Gln	Leu	Asp	Glu	Phe	Arg
	210					215						220		

<210> 215
 <211> 814
 <212> DNA
 <213> Homo sapiens

<400> 215
 aaatttcgta cccgctccgg cacagtacga gcccttgacg atgtgagcct ggctattaag
 60
 agagggttcca tctcagccgt tatcgggcac tccggagccg gcaaattccac cctgggttcgc
 120
 ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc
 180
 tcgcagctct cggacaaagc gatgcgcccc ctacgcgcag acatcgggat gatcttccaa
 240
 cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg
 300
 gtcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg
 360
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcggggt
 420
 ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg
 480
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa
 540
 ctagggttga cggtcgtcgt catcaccac gagatggagg tcgtccgctc gattgcccag
 600
 caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcgcccg ccaggtcttc
 660
 gtcattccac agtcagagac caccagcgt ttcttggcga cgattatcgg ccagcaccgc
 720
 agtggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgacgtc
 780
 agttcgggtg ccagtcactc gttcgggtgac gcgt
 814

<210> 216
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 216
 Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser
 1 5 10 15
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly
 20 25 30
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro
 35 40 45
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser
 50 55 60
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln

```

65          70          75          80
Gln Phe Asn Leu Phe Gly Ser Arg Thr Ile Tyr Asp Asn Val Ala Tyr
          85          90          95
Pro Leu Lys Leu Ala His Trp Lys Lys Ala Asp Glu Lys Lys Arg Val
          100          105          110
Thr Glu Leu Leu Ser Phe Val Gly Leu Thr Ser Lys Ala Trp Asp His
          115          120          125
Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg
          130          135          140
Ala Leu Ala Thr Lys Pro Ser Ile Leu Leu Ala Asp Glu Ser Thr Ser
145          150          155          160
Ala Leu Asp Pro Glu Thr Thr Ala Asp Val Leu Ser Leu Leu Lys Arg
          165          170          175
Val Asn Ala Glu Leu Gly Val Thr Val Val Val Ile Thr His Glu Met
          180          185          190
Glu Val Val Arg Ser Ile Ala Gln Gln Val Ser Val Leu Ala Ala Gly
          195          200          205
His Leu Val Glu Ser Gly Ser Ala Arg Gln Val Phe Ala His Pro Gln
          210          215          220
Ser Glu Thr Thr Gln Arg Phe Leu Ala Thr Ile Ile Gly Gln His Pro
225          230          235          240
Ser Gly Glu Glu Gln Ala Arg Leu Gln Ser Glu Asn Pro Asp Ala Arg
          245          250          255
Leu Val Asp Val Ser Ser Val Ala Ser His Ser Phe Gly Asp Ala
          260          265          270

```

<210> 217
 <211> 500
 <212> DNA
 <213> Homo sapiens

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<400> 217
nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
60
agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
120
tttctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
180
ctgttcacta tccaaggctc ggaccccagc ttgcagccct acctgctgat ggctcacttt
240
gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
300
gatggcgtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
360
caggccttgg agctcctgct gatcaggaag tacatcccc gaagatcttt cttcattttc
420
ctgggcatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
480
tcaagggcgc tccagctagc
500

```

<210> 218
 <211> 166
 <212> PRT

<213> Homo sapiens

<400> 218

```

Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
      20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
      35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
      50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
      85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
      100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
      115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
      130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145          150          155          160
Ser Arg Gly Val Gln Leu
      165

```

<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

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acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caagggtccgc acgctcccat gtccctcggt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgtcg agattgcgcc tgatatcaag cgcatacagg tcaacaaccc cagccccttc
180
acttttttcg gcaccaacag ttatctgatc ggccgcgata cgctggcatt gatcgatccc
240
ggtcgcgttg acgaggccca tcacgcggcg ctgctgctg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgacac gggtttgaaa
360
g
361

```

<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

```

Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```

```

      1             5             10             15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20             25             30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35             40             45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50             55             60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
      65             70             75             80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85             90             95
Ile Pro Val Ser Thr Arg
      100

```

<210> 221
 <211> 401
 <212> DNA
 <213> Homo sapiens

```

<400> 221
agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcatatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagccccaca ctgctgcagc acacctcgct
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgctggc ccagtgaacca cccccccagg gcataccctc ctacagagca
240
ttccccaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagggga cgcttggtga accagcatcc aggctggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

```

<210> 222
 <211> 124
 <212> PRT
 <213> Homo sapiens

```

<400> 222
Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
1             5             10             15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20             25             30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35             40             45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50             55             60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
      65             70             75             80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85             90             95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```


ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct
180
caaatcctcc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg
240
cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaaacc
300
tttgtcaca ctggccctc ttcctggaac atgggcctn
339

<210> 226

<211> 91

<212> PRT

<213> Homo sapiens

<400> 226

Met	Thr	Leu	Ile	Pro	Ser	Cys	Thr	Asp	Gly	Asp	Ser	Ser	Asn	Ser	Tyr
1				5					10				15		
Lys	His	His	Gln	Thr	Asp	Leu	Gln	Glu	Gln	Arg	Asn	Ser	Gln	Ser	Arg
			20					25					30		
Phe	His	Pro	Arg	Arg	Ala	Leu	Lys	Ser	Ser	Arg	Ala	Ala	Cys	Tyr	Gly
		35					40					45			
Gly	Gly	Arg	His	Thr	Leu	Leu	Gly	Ser	Gln	Gly	Leu	Ser	Gln	Pro	Gly
		50				55					60				
Pro	Asn	Gln	Leu	Pro	Ala	Trp	Pro	His	His	Pro	Thr	Ala	Lys	Pro	Leu
65					70					75					80
Leu	Thr	Leu	Ala	Pro	Leu	Pro	Gly	Thr	Trp	Ala					
				85						90					

<210> 227

<211> 353

<212> DNA

<213> Homo sapiens

<400> 227

gtcgaccctc tcgattgtgg cgaactccat ggctgctgcg ggctgctgta ggctctcgag
60
tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatggttc
120
gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccgga
180
ggccaggccg acaagtgctg cctcctgcca cccgctgagc gacgctgcca tgttgagtac
240
ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgtcca ggccgagaga
300
cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg
353

<210> 228

<211> 102

<212> PRT

<213> Homo sapiens

<400> 228

Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

1 5 10 15
 Leu Thr Ser Glu Asp Ala Val Leu Asn Met Ala Ala Ser Leu Ser Gly
 20 25 30
 Trp Gln Glu Ala Ala Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu
 35 40 45
 Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro
 50 55 60
 Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val
 65 70 75 80
 Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Ala Met Glu Phe Ala
 85 90 95
 Thr Ile Glu Gly Val Asp
 100

<210> 229
 <211> 743
 <212> DNA
 <213> Homo sapiens

<400> 229
 nnggctaggg acacggcctc ctcctcaaca ggcagtgcct gtgcaggctc aggggcatca
 60
 tcaaagataa cacagggctg gtcaggggct gctggctgct cctgccccag gactggctcc
 120
 aggatgggca aggctgcctc cctggtagcc agggggagag gggaaggag caccagggag
 180
 tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
 240
 agtaaagtgt ctgccccagg ggtgctcaca gcccaggacc gggtagttgg aaagccagcc
 300
 cagcttggca ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
 360
 gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaag
 420
 agagattcac tgggtaccta cagtagtcga gatgtaagcc ttggggactg ggaatttggg
 480
 aagagagatt ctctgggtgc ttatgccagc caagatgcca acgagcaggg ccaagatttg
 540
 gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
 600
 ttccagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
 660
 caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
 720
 cttgacgccc aggacagaag ctt
 743

<210> 230
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 230
 Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

1	5	10	15
Ser Gly Ala Ser Ser Lys Ile Thr Gln Gly Trp Ser Gly Ala Ala Gly			
20	25	30	
Cys Ser Cys Pro Arg Thr Gly Ser Arg Met Gly Lys Ala Ala Ser Leu			
35	40	45	
Val Ala Arg Gly Arg Gly Glu Gly Ser Thr Arg Glu Trp Ala Ser Arg			
50	55	60	
Cys Gly Ile Gly Gln Glu Met Glu Ala Ser Ser Ser Gln Asp Gln			
65	70	75	80
Ser Lys Val Ser Ala Pro Gly Val Leu Thr Ala Gln Asp Arg Val Val			
85	90	95	
Gly Lys Pro Ala Gln Leu Gly Thr Gln Arg Ser Gln Glu Ala Asp Val			
100	105	110	
Gln Asp Trp Glu Phe Arg Lys Arg Asp Ser Gln Gly Thr Tyr Ser Ser			
115	120	125	
Arg Asp Ala Glu Leu Gln Asp Gln Glu Phe Gly Lys Arg Asp Ser Leu			
130	135	140	
Gly Thr Tyr Ser Ser Arg Asp Val Ser Leu Gly Asp Trp Glu Phe Gly			
145	150	155	160
Lys Arg Asp Ser Leu Gly Ala Tyr Ala Ser Gln Asp Ala Asn Glu Gln			
165	170	175	
Gly Gln Asp Leu Gly Lys Arg Asp His His Gly Arg Tyr Ser Ser Gln			
180	185	190	
Asp Ala Asp Glu Gln Asp Trp Glu Phe Gln Lys Arg Asp Val Ser Leu			
195	200	205	
Gly Thr Tyr Gly Ser Arg Ala Ala Glu Pro Gln Glu Gln Glu Phe Gly			
210	215	220	
Lys Ser Ala Trp Ile Arg Asp Tyr Ser Ser Gly Gly Ser Ser Arg Thr			
225	230	235	240
Leu Asp Ala Gln Asp Arg Ser			
245			

<210> 231
 <211> 431
 <212> DNA
 <213> Homo sapiens

<400> 231
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 caggggtgcag cctgctgcagc agctcctcca tcaccttgct gatgaactgt cttccacagg
 120
 ccaccaggac gccactcgcc gctgtgtgcc agtcccagac caggtccttc gtcttggtca
 180
 tctcgctgga ggccaggagg atgatgggtgc tggctgtgtc cttgtccagc tcaactggcg
 240
 gactgctcag gaccctctcc atggccctca ggaccgctgc tcggtatggg tgtgccagct
 300
 tgtcatgctg ccgcagatac tcctcgagc cagggagcgt ctccaccctg ctggacgcc
 360
 tcaccgataa ggacccctg gtgcaggagc aggtctgcag tgcctgtgc tcctcgagg
 420
 aggtgcggcc g
 431

<210> 232
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
 1 5 10 15
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg
 20 25 30
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp
 35 40 45
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr
 50 55 60
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val
 65 70 75 80
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg
 85 90 95
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu
 100 105 110
 Ala Ser Leu Ser Val Ala Asn Ala
 115 120

<210> 233
 <211> 606
 <212> DNA
 <213> Homo sapiens

<400> 233
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 aagggtgggca cccttagcat tccccaaaag caccagccct cctcatcctt cccagcttct
 120
 gtgctggaat gcacccccat cggaaggct cgaaaactca ggacacatta ggatcacctg
 180
 gaaagcatTT gtcaaaacgc atctccctgc gggtcagggt ccaagttaaa atcaaacttc
 240
 aggtgatgct gactcagggt gctccagaaa cacctgggga agcagcactt tggaggctgc
 300
 ctctcacatc cccccacag caagtgggca gggagctagg taaatctcct tcccagttga
 360
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttagctgc
 420
 gaaagtccag cctgcaggct tcctgggcaa gctagtgggc tgaagtatgc cacagcaaca
 480
 ggcttctaga gccggctgcc cagctcctac tctgctctg ccactcactg actgtgtggt
 540
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 600
 acgcgt
 606

<210> 234

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
 1 5 10 15
 Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
 20 25 30
 Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
 35 40 45
 Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
 50 55 60
 Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
 65 70 75 80
 Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
 85 90 95
 Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
 100 105

<210> 235
 <211> 328
 <212> DNA
 <213> Homo sapiens

<400> 235
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 atagcaaaca cttaaaacag cagcagtaca gagctgaaaa ccagattctt ttgaaagaga
 120
 ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atgggtcaag
 180
 aaagaggaaa aagaagggca acttcaggat taaccactgg ggacctgaac ctaactgaaa
 240
 acatttctca aggagataga ataagtgaaa gaaaattgga tttattgagc ctcaaaaata
 300
 tgagtgaagc acaatcaaag aatgaatt
 328

<210> 236
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
 1 5 10 15
 Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
 20 25 30
 Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
 35 40 45
 Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
 50 55 60
 Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

65		70		75		80									
Leu	Asp	Leu	Leu	Ser	Leu	Lys	Asn	Met	Ser	Glu	Ala	Gln	Ser	Lys	Asn
		85						90						95	
Glu															

<210> 237
 <211> 2059
 <212> DNA
 <213> Homo sapiens

<400> 237
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 60
 gagcacgaag ccggcggtcca tagctacggc ccatacggtc atgtctgcc a tggctccgtt
 120
 gatgtcagac tgcacatgaa atcgggttacg gtaccccagg atcatcgcta ccgagtacac
 180
 cccgaacagc acccgctggg cgccgatcag cgtgagggag tgccccacca gtggcacttt
 240
 tcttagatag cggaacccat ccaccacatc cccagtcacc gttctcatcg tccgggaacg
 300
 atccaccagt ggcgggcccaa gctcccgacg tgaaaactgc agcccctagg cgaccgagac
 360
 tgccaagagg gctgcggaga tgcagaaaat gatcgtgtcg gcgtgggtgca caggaatatg
 420
 gcgtccggca atcatgcgca ctgctgcagc aacaaccgca ccgatcatga gccctagcgg
 480
 ccaatcggtg gcatgattga cgatgccgtc aggtagtcgc gcttgctgat ggtgtattcc
 540
 aaccagcga ccaaggcggg gagcaaaaac cggttcaggc tcatcgcgat gagcaaccca
 600
 atgagcaagg ccagggtggga gggcttatcg cgcgaccac cccagaccaa gatccccagc
 660
 ccgaccaggg tgacggcacg cattcatctg cgtattgtcc cgactacacc gtgagggcgc
 720
 tctctgatct gcagctcatc aagggttacg gactgcagta cctcaatgca ctctggcta
 780
 cccgagccca gaacctgcca cagtcccctg agaacaccga cctgcagggt attccaggca
 840
 gccagaccag gtccttggtt gagaagacca ccacagcggc agctttccca gtagcccttt
 900
 ccctctttgg cacagttgga acctccagtt gataaatgac tgtggactag cgcgcgtttt
 960
 ttgttttcag agcacacgta aggggtccagc cacagcaggc ccggcgctcc ggtggaaggc
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 1080
 agatgagcac gtggggagct ggagtgagct gagcagaagt tttgtgccc cctgccccca
 1140
 tcccctccag gccacgtttt agatggccct tgtagttgcg ggtcctgggt gtcctcagaa
 1200
 ctagacatca atgcctggat ccttcagccg gccctgccct cctttaggag acaggagtca
 1260

ccagggcaca gccctccagg cccgcctcag gaaggaatga aaggaatgcc atcatctcta
 1320
 gttcccaggg ccagccttc cctttctccc ccggggcagg gacagtgcgg catattcaga
 1380
 ttcagacctc tttgggctga gccaccttgt gagtgcagtt actgcctttg tgtggccgtg
 1440
 acctctattt gtttgctttt aatttgccaa cctatcgctg ctggcagcac tttttgagca
 1500
 agccgagagc acccattttg gctggggatt cagatcgatg gccttggtcca tgttgctcctt
 1560
 tctggcttcc ctgatgggtg catgtttcag cgcattgcgc ccagcctttc ccatgtgcca
 1620
 aaccagaagc tccactgccc gtaggctgtc cctgtagccc tgctccctcc ctggaggctg
 1680
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 1740
 acctgctgag ttgccactcg cagtgttgct agttcccgtg ttctgagaag aggtcatgcc
 1800
 tgggaggaag ggatcgatc gctgcatcga atcctctctc cgccgtgtgg cccccaggag
 1860
 agtagctgcc tgttgacact gctccacacc tccccacagc ctccctgcag gtgctgtgtg
 1920
 gccgtgatgt gcagagagca gtgagggagg gttcatgaac caggtggatc ctctttaaaa
 1980
 aaaaaaaaaag tttttgttat atctctaaaa tcccatagct aggaacagaa aaaaaggaaa
 2040
 agacttgaaa tgttctaga
 2059

<210> 238

<211> 129

<212> PRT

<213> Homo sapiens

<400> 238

Ala	Glu	Gln	Lys	Phe	Cys	Ala	Arg	Leu	Pro	Pro	Ser	Pro	Pro	Gly	His
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Val	Leu	Asp	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Trp	Val	Ser	Ser	Glu	Leu
		20						25					30		
Asp	Ile	Asn	Ala	Trp	Ile	Leu	Gln	Pro	Ala	Leu	Pro	Ser	Phe	Arg	Arg
		35				40						45			
Gln	Glu	Ser	Pro	Gly	His	Ser	Pro	Pro	Gly	Pro	Pro	Gln	Glu	Gly	Met
	50					55					60				
Lys	Gly	Met	Pro	Ser	Ser	Leu	Val	Pro	Arg	Ala	Gln	Pro	Ser	Pro	Ser
65					70				75					80	
Pro	Pro	Gly	Gln	Gly	Gln	Cys	Gly	Ile	Phe	Arg	Phe	Arg	Pro	Leu	Trp
			85					90					95		
Ala	Glu	Pro	Pro	Cys	Glu	Cys	Ser	Tyr	Cys	Leu	Cys	Val	Ala	Val	Thr
		100						105					110		
Ser	Ile	Cys	Leu	Leu	Leu	Ile	Cys	Gln	Pro	Ile	Ala	Ala	Gly	Ser	Thr
		115					120						125		
Phe															

<210> 239
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 239
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 cctcgaatta atgagatggg ggactggatg agtcaagttc tcgtcggtgc ggcggctgtc
 120
 ggtcagctgc cctectcca cttctgcttc tcggcggtac cccataccgt attggccgcg
 180
 tggtcacctt tgaatgcagc catgtcgctg tctccgtatc gaaatgatgt gccatcgaag
 240
 atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc
 300
 cagcgcaacc gtgtcctcgc acgatacgaa gtgcttgggt atctcagctc tggtacctat
 360
 ggtcgtgtat ataaagcaaa ggaacttn
 388

<210> 240
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 240
 Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly
 1 5 10 15
 Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val
 20 25 30
 Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr
 35 40 45
 Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala
 50 55 60
 Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val
 65 70 75 80
 Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly
 85 90 95
 Arg Val Tyr Lys Ala Lys Glu Leu
 100

<210> 241
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 241
 ncggggggcc gagttgaaag ctgccggcac actggctgtg ctgcttgctt cacttctcgg
 60
 gatgctgctt ccagggcggg cctgggggaa acatcggcct tcccaggcac ccttagcccc
 120
 tcccatctgg gggcccttag cacagtcctt gggacccac atgctgcctt tcaggctgat
 180

gtgggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttcctt
 240
 ggggctaagc cgtgtgctct gaatcaaaag cagtagtggc atcggcggca ctggcgccat
 300
 gggaaacggg ttgacttgca caaccagcac
 330

<210> 242
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 242
 Met Ala Pro Val Pro Pro Met Pro Leu Leu Leu Leu Ile Gln Ser Thr
 1 5 10 15
 Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val
 20 25 30
 Gly Trp Ala Ala Glu Phe Ala His Ile Ser Leu Lys Gly Ser Met Trp
 35 40 45
 Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly
 50 55 60
 Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile
 65 70 75 80
 Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn
 85 90 95
 Ser Ala Pro Arg
 100

<210> 243
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 243
 nnaccttctc tccgcgttat taccaaagat gctatgcacg taactgcgga ggaaattctt
 60
 cacacaggcc accccgcccc cactgcgctc gtcgctaatac ttccctataa cgttgcggta
 120
 cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatggtg
 180
 caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cggtgtcccc
 240
 agcgtcaaag tcaactttta cgggactgtc tcgcgtgcgg gagcaattgg acgcaatgtc
 300
 ttctggccgg ctcccaatgt tgattctggn
 330

<210> 244
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 244
 Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

```

      1           5           10           15
Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
      20           25           30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
      35           40           45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
      50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
      65           70           75           80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
      85           90           95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
      100           105           110

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<210> 245
 <211> 355
 <212> DNA
 <213> Homo sapiens

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<400> 245
tctagatcct gaatcaccca cctcctagtt tcggattcac ctccgccggc gtcacctgaa
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aacaatgtcg agcccgaatg gatgatggta gccacaccca tctcggaag gtggaatgca
120
gcgtgttgca gaaacagaag ttgaccgtcg gaggtaggcg gcattcgctt cggatcgaag
180
cgtcccgagg catccatctc gagttgacga cgaaaatctt tccagtccac gccgtagggg
240
ganttggcaa ccacagcatc gaatttgtcc agaaggaagt ggtcgttggt gagggatttg
300
ccccattcaa tacgcgcac ttcccgaag cgcgcctcta ttgcggccaa cgcgt
355

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<210> 246
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 246
Met Arg Val Leu Asn Gly Ala Ile Pro Ser Pro Thr Thr Thr Ser Phe
1           5           10           15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
      20           25           30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
      50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
      65           70           75           80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
      85           90           95
Lys Leu Gly Gly Gly
      100

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<210> 247
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 247
 atggccgcga atgggcaccg tgtcatggtc gtctctcccc gctacgacca gtacaaggac
 60
 gcctgggaca ccagcgctgt gtccgagatc aagatgggag acaggtacga gacggtcagg
 120
 ttcttcact gctacaagcg cggagtggac cgcgtgttcg ttgaccaccc actgttcctg
 180
 gagagggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac
 240
 agggacaacc agctgcgggt cagcctgcta tgccaggcag cacttgaagc tccaaggatc
 300
 ctgagcctca acaacaaccc atacttctcc gga
 333

<210> 248
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 248
 Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr Asp
 1 5 10 15
 Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys Met
 20 25 30
 Gly Asp Arg Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg Gly
 35 40 45
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp
 50 55 60
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr
 65 70 75 80
 Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu
 85 90 95
 Ala Pro Arg Ile Leu Ser Leu Asn Asn Pro Tyr Phe Ser Gly
 100 105 110

<210> 249
 <211> 5503
 <212> DNA
 <213> Homo sapiens

<400> 249
 atgaccagg ggattttggc cttggtcacg tccactggct gtgcatctgc caatgccctg
 60
 cagtcctca cggatgccat gcacatccca cacctctttg tccagcgcaa cccgggaggg
 120
 tcgccacgca ccgcatgcc cctgaacccc agccccgatg gtgaggccta cacactggct
 180
 tcgagaccac ccgtccgcct caatgatgtc atgctcaggc tggtgacgga gctgcgctgg
 240

cagaagttcg tcatgttcta cgacagcgag tatgatatcc gtgggcttca aagctttctg
300
gaccaggcct cgcggtctggg ccttgacgtc tctttacaaa aggtggacaa gaacattagc
360
cacgtattca ccagcctgtt caccacgatg aagacagagg agctgaatcg ctaccgggac
420
acgcttcgcc gcgccatcct gctgctcagc ccacagggag cccactcctt catcaacgag
480
gccgtggaga ccaacctggc ttccaaggac agccactggg tctttgtgaa tgaggaaatc
540
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720
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780
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840
aggtccatgc tggataccat caaaaagggc cacatcactg gcctcactgg ggtgatggag
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960
gagacttttg gcaaagacat gcgcaagttg gcgacatggg actcagagaa gggcttgaat
1020
ggcagcttgc aagagaggcc catgggcagc cgcctccaag gattgactct taaagtgggtg
1080
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1140
tacaaagggt tctccataga tgtcctggat gcactggcca aggtcttggg ctttaaatat
1200
gagatttacc aagccccctga tggcaggtac ggtcaccagc tccataacac ctcttggaaac
1260
gggatgatcg gggagctcat cagcaagaga gcagacttgg ccatctctgc catcaccatc
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1380
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cgggattctg ctgtatatga gtacttccga gccaaaggga ccaaccccct ggagcaggac
1860

agcacgtttg ctgaactctg gcggaccatc agcaagaacg gaggggctga caactgcgtg
1920
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1980
gtggccgtgg tggaaatcgc agccctgacg gatgacgact gctcggtgac tgtcatcggc
2040
aacagcatca gcagcaaggg ttacgggatt gccctgcagc atggcagccc ctacagggac
2100
ctcttctccc agaggatcct ggagctgcag gacacagggg acctggatgt gctgaagcag
2160
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2220
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2280
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2340
gagaccccc aaggaggaaa agaagtgaac ttggagcagg tccaccggcg catgaacagc
2400
ctcatggatg aagacattgc tcacaagcag atttccccag cgtcgattga gctctcggcc
2460
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2520
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2820
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2880
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3480

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 5280
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 5340
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 5503

<210> 250

<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

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 1 5 10 15
 Ala Asn Ala Leu Gln Ser Leu Thr Asp Ala Met His Ile Pro His Leu
 20 25 30
 Phe Val Gln Arg Asn Pro Gly Gly Ser Pro Arg Thr Ala Cys His Leu
 35 40 45
 Asn Pro Ser Pro Asp Gly Glu Ala Tyr Thr Leu Ala Ser Arg Pro Pro
 50 55 60
 Val Arg Leu Asn Asp Val Met Leu Arg Leu Val Thr Glu Leu Arg Trp
 65 70 75 80
 Gln Lys Phe Val Met Phe Tyr Asp Ser Glu Tyr Asp Ile Arg Gly Leu
 85 90 95
 Gln Ser Phe Leu Asp Gln Ala Ser Arg Leu Gly Leu Asp Val Ser Leu
 100 105 110
 Gln Lys Val Asp Lys Asn Ile Ser His Val Phe Thr Ser Leu Phe Thr
 115 120 125
 Thr Met Lys Thr Glu Glu Leu Asn Arg Tyr Arg Asp Thr Leu Arg Arg
 130 135 140
 Ala Ile Leu Leu Leu Ser Pro Gln Gly Ala His Ser Phe Ile Asn Glu
 145 150 155 160
 Ala Val Glu Thr Asn Leu Ala Ser Lys Asp Ser His Trp Val Phe Val
 165 170 175
 Asn Glu Glu Ile Ser Asp Pro Glu Ile Leu Asp Leu Val His Ser Ala
 180 185 190
 Leu Gly Arg Met Thr Val Val Arg Gln Ile Phe Pro Ser Ala Lys Asp
 195 200 205
 Asn Gln Lys Cys Thr Arg Asn Asn His Arg Ile Ser Ser Leu Leu Cys
 210 215 220
 Asp Pro Gln Glu Gly Tyr Leu Gln Met Leu Gln Ile Ser Asn Leu Tyr
 225 230 235 240
 Leu Tyr Asp Ser Val Leu Met Leu Ala Asn Ala Phe His Arg Lys Leu
 245 250 255
 Glu Asp Arg Lys Trp His Ser Met Ala Ser Leu Asn Cys Ile Arg Lys

[illegible]

690					695					700					
Arg	Ile	Leu	Glu	Leu	Gln	Asp	Thr	Gly	Asp	Leu	Asp	Val	Leu	Lys	Gln
705					710					715					720
Lys	Trp	Trp	Pro	His	Met	Gly	Arg	Cys	Asp	Leu	Thr	Ser	His	Ala	Ser
				725					730					735	
Ala	Gln	Ala	Asp	Gly	Lys	Ser	Leu	Lys	Leu	His	Ser	Phe	Ala	Gly	Val
			740					745					750		
Phe	Cys	Ile	Leu	Ala	Ile	Gly	Leu	Leu	Leu	Ala	Cys	Leu	Val	Ala	Ala
			755			760					765				
Leu	Glu	Leu	Trp	Trp	Asn	Ser	Asn	Arg	Cys	His	Gln	Glu	Thr	Pro	Lys
	770				775					780					
Glu	Asp	Lys	Glu	Val	Asn	Leu	Glu	Gln	Val	His	Arg	Arg	Met	Asn	Ser
785					790					795				800	
Leu	Met	Asp	Glu	Asp	Ile	Ala	His	Lys	Gln	Ile	Ser	Pro	Ala	Ser	Ile
				805					810					815	
Glu	Leu	Ser	Ala	Leu	Glu	Met	Gly	Gly	Leu	Ala	Pro	Thr	Gln	Thr	Leu
			820				825						830		
Glu	Pro	Thr	Arg	Glu	Tyr	Gln	Asn	Thr	Gln	Leu	Ser	Val	Ser	Thr	Phe
		835				840					845				
Leu	Pro	Glu	Gln	Ser	Ser	His	Gly	Thr	Ser	Arg	Thr	Leu	Ser	Ser	Gly
	850				855					860					
Pro	Ser	Ser	Asn	Leu	Pro	Leu	Pro	Leu	Ser	Ser	Ser	Ala	Thr	Met	Pro
865				870						875				880	
Ser	Met	Gln	Cys	Lys	His	Arg	Ser	Pro	Asn	Gly	Gly	Leu	Phe	Arg	Gln
			885					890					895		
Ser	Pro	Val	Lys	Thr	Pro	Ile	Pro	Met	Ser	Phe	Gln	Pro	Val	Pro	Gly
		900					905					910			
Gly	Val	Leu	Pro	Glu	Ala	Leu	Asp	Thr	Ser	His	Gly	Thr	Ser	Ile	
	915				920					925					

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<210> 251
<211> 291
<212> DNA
<213> Homo sapiens
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<400> 251
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gacgtcaacg cgctcgaacg gctgcggttg gccgtgcgcg ccagcgtggt catcctcatc
120
gagtaccacc attcggtgac cctgctgctg cgggtgcgcg ggaactcacc tctggaacga
180
gaggccctcg aggcccgccg ccgtatcgat gcgaagggttc ccgctctcgt cgagagcgcc
240
atcgccgagg gtggtctgcg ctcggatttc actccggggc tcatcacgcg t
291
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<210> 252
<211> 97
<212> PRT
<213> Homo sapiens
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<400> 252
Xaa Ile Ser Arg Gly Val Arg Ala Leu Asp Ser Ala Val Glu Thr Glu

```

      1           5           10           15
Ser Leu Arg Glu Asp Val Asn Ala Leu Glu Arg Leu Arg Leu Ala Val
      20           25           30
Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
      35           40           45
Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
      50           55           60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
      65           70           75           80
Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
      85           90           95
Arg

```

<210> 253
 <211> 327
 <212> DNA
 <213> Homo sapiens

```

<400> 253
gtgcacggat gggagcgctc gcgcgcgtgc tggcgccttc acagcccggc gagcggcgtg
60
cgctcacggc cctgtaccga ccgatctcgc aaccttcgcg agaccgatcc accaaccgcg
120
cccacatgtc ggcagtgatg gcgggcacct tgcggggagaa ggccgggaag gtcgagcgag
180
ccaatgaccg tcgcacggtc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
240
gtctactcgt cgcggtgtcc tccgcggtct ccataccgt ccctgcgaca tggaacgccc
300
acgacttcgg acggcgactc gacgcgt
327

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<210> 254
 <211> 106
 <212> PRT
 <213> Homo sapiens

```

<400> 254
Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
      1           5           10           15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
      20           25           30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
      35           40           45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
      50           55           60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
      65           70           75           80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
      85           90           95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
      100           105

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<210> 255
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 255
 ctagaaatgg ctggctacga atacatggaa gctgaaaata gccacaagc ccacgaaatt
 60
 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc
 120
 atcgagctaa ctcgctcgctt aaagaaagac agcacgacag cagaaatccc tggtatttta
 180
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac
 240
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc
 300
 cgagcgactc cacaaggtat tgatgatcct attgaaattg atggtttaac gcttgatccc
 360
 attagccaac gc
 372

<210> 256
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 256
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln
 1 5 10 15
 Ala His Glu Ile Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp
 20 25 30
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys
 35 40 45
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys
 50 55 60
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp
 65 70 75 80
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys
 85 90 95
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu
 100 105 110
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg
 115 120

<210> 257
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 257
 nnacgcgtag cggtcgaggt tgcggacacc atgcccgaac ccggcctgct cgccatcgag
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 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa
 120

cgggttcgggc tcggcggcat cttcttcggg ctaccgacga tggccacgtc caatcccatg
 180
 ttcgggtcgag ttcgggaatg gctggacgct gtgccagcca aggaccgctc aagcatttcc
 240
 ctgggtcact cgaaagctgg actcaacgag gagtaccagc agctcatgcc gtggaacgcc
 300
 accatggccg tctacgacga aggtgcgggc acgcagcgtg aagcttcggc gatcgtccat
 360
 gagtgggttct tgggcccga ggcgcgcgac ctggccgacc acgtcgtcgg gaccatcgac
 420
 caggcactgt tcaccggtct caaagccaag catgtgggtgt tacgccacct cggctctggcg
 480
 agcaaggctc tcatcattga tgagggtccac gccgccgacg tctatatgcg cgaatacctc
 540
 aaggctcgtc tcgaatggct cggcgcctac cgcacgccag tcatcctcat gtccgcgacg
 600
 ctgccaccgg cccaacgtca tgaactcggc ctagcgtac
 639

<210> 258

<211> 213

<212> PRT

<213> Homo sapiens

<400> 258

Xaa	Arg	Val	Ala	Val	Glu	Val	Ala	Asp	Thr	Met	Pro	Glu	Pro	Gly	Leu
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Leu	Ala	Ile	Glu	Ala	Pro	Met	Gly	His	Gly	Lys	Thr	Glu	Ala	Ala	Leu
			20					25					30		
Met	Cys	Ala	Gln	Val	Leu	Ala	Glu	Arg	Phe	Gly	Leu	Gly	Gly	Ile	Phe
		35					40					45			
Phe	Gly	Leu	Pro	Thr	Met	Ala	Thr	Ser	Asn	Pro	Met	Phe	Gly	Arg	Val
	50					55					60				
Arg	Glu	Trp	Leu	Asp	Ala	Val	Pro	Ala	Lys	Asp	Pro	Ser	Ser	Ile	Ser
65					70					75				80	
Leu	Ala	His	Ser	Lys	Ala	Gly	Leu	Asn	Glu	Glu	Tyr	Gln	Gln	Leu	Met
				85					90					95	
Pro	Trp	Asn	Ala	Thr	Met	Ala	Val	Tyr	Asp	Glu	Gly	Ala	Gly	Thr	Gln
		100						105					110		
Arg	Glu	Ala	Ser	Ala	Ile	Val	His	Glu	Trp	Phe	Leu	Gly	Arg	Lys	Arg
	115						120					125			
Ala	Ile	Leu	Ala	Asp	His	Val	Val	Gly	Thr	Ile	Asp	Gln	Ala	Leu	Phe
	130					135					140				
Thr	Gly	Leu	Lys	Ala	Lys	His	Val	Val	Leu	Arg	His	Leu	Gly	Leu	Ala
145					150					155				160	
Ser	Lys	Val	Val	Ile	Ile	Asp	Glu	Val	His	Ala	Ala	Asp	Val	Tyr	Met
				165					170					175	
Arg	Glu	Tyr	Leu	Lys	Val	Val	Leu	Glu	Trp	Leu	Gly	Ala	Tyr	Arg	Thr
		180						185				190			
Pro	Val	Ile	Leu	Met	Ser	Ala	Thr	Leu	Pro	Pro	Ala	Gln	Arg	His	Glu
		195					200					205			
Leu	Ala	Leu	Ala	Tyr											
				210											

<210> 259
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 259
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
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 ncatgggtgtg tgcacgtgtg cnaactgtgta tgcattggtaa tgtgcacgtg tgcantgtgtg
 120
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggg gtatgcatgg
 180
 tgtgtgcaca tgagcactgt gtggtgtgta tgcattggtgn ggtgcacgtg tgcactgtgt
 240
 atgcaatggg gt
 252

<210> 260
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 260
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val
 35 40 45
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met
 50 55 60
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys
 65 70 75 80
 Met Gln Trp Cys

<210> 261
 <211> 1202
 <212> DNA
 <213> Homo sapiens

<400> 261
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 60
 ctgtggggcg gcatcgtctt cggatcgtcg ggaatcatca acggttacgc gggggcctta
 120
 ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtgggc ctccggtact
 180
 ggcacgggtct accttgccag tctcgtcctg gccatcatga tcccgccaat tatcactgct
 240
 gttagcccg cgtcatgcc ccgaacgccc catgatcaag tcgaggccgc gtcgcccctc
 300
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtcgggcac
 360

atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcaccctc
 420
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc
 480
 ggtggtgaga cattcgcgtc gaagattgcc ggtaacttct ccgaggccat tagcgatccc
 540
 acctcgctgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac cttcgtggtc
 600
 aacgcgactg cccggttgat tgccggcgaag ggggttaagc gatgagcgcc accaccctg
 660
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgctctg
 720
 gtaaaccggac tatcaagagc ggctgcgctt caacattcat gatcgtggcc accgtactgg
 780
 ctgttatccc actggcctgg ctgctcttcg cggcgcgtccg gcgcggcatc ggatcactat
 840
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg
 900
 ccattcacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtac
 960
 cgatcgctct gatgaccgcg atcttcctag tcgagtacgc ccgcggaact aagatcgcca
 1020
 aggtcattag cttcgccgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct
 1080
 tcgtcttcgc cgtagtcgtt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt
 1140
 tggeccctcat gatcctcatg gttccgacgg tgctgcgac aaccgaggaa atgctcaagc
 1200
 tt
 1202

<210> 262
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 262
 Ala Ser Pro Val Ala Phe Val Val Asp Leu Leu Ala Ala Val Pro Ser
 1 5 10 15
 Ile Val Phe Gly Leu Trp Gly Gly Ile Val Phe Gly Ser Ser Gly Ile
 20 25 30
 Ile Asn Gly Tyr Ala Gly Ala Leu Phe Lys Ala Leu Gly Trp Ile Pro
 35 40 45
 Ile Phe Ser Glu Asp Pro Ser Trp Ser Ser Ala Thr Gly Thr Val Tyr
 50 55 60
 Leu Ala Ser Leu Val Leu Ala Ile Met Ile Leu Pro Ile Ile Thr Ala
 65 70 75 80
 Val Ser Arg Asp Val Met Pro Arg Thr Pro His Asp Gln Val Glu Ala
 85 90 95
 Ala Leu Ala Leu Gly Ser Thr Arg Trp Glu Val Ile Lys Leu Ala Val
 100 105 110
 Phe Pro His Ser Arg Ser Gly Ile Ile Ser Gly Ser Met Leu Gly Leu
 115 120 125
 Gly Arg Ala Leu Gly Glu Thr Leu Ala Val Thr Leu Ile Leu Gln Thr

```

      130              135              140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145              150              155              160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
      165              170              175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
      180              185              190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
      195              200              205
Ala Lys Gly Val Lys Arg
      210

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<210> 263
 <211> 424
 <212> DNA
 <213> Homo sapiens

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<400> 263
acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgccg tgaactttcc
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gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcy aacgtacctc ggaagacgtt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcagcag gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaaag
240
gcttatatgg cctcgccatt ccgtgccaat ttggacctgg catacccatc ttcgacgcca
300
caggcccagt cccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
420
gann
424

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<210> 264
 <211> 99
 <212> PRT
 <213> Homo sapiens

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<400> 264
Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
1      5      10      15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
      20      25      30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
      35      40      45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
      50      55      60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
65      70      75      80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
      85      90      95
Lys His Xaa

```


<210> 265
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 265
 ncgtacggcc ctggcgcccg catggacgag ggataccatt ccggcatgac ggtgccgggt
 60
 gccttcgact cccatcatcg caagctcatc atcactgggt atagccgtga gcaagccctg
 120
 gctcgagctg .cccgcgccct cgacgaaatc gtcatcgacg gcatgccgac ggtcattccc
 180
 tttaccagg cgggtggtca cgaccgggt ttcactgccg ccgacggctg cttcggcgtc
 240
 tttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg
 300
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgctg tcgagggtcaa cggtaaacgc
 360

<210> 266
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 266
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met
 1 5 10 15
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr
 20 25 30
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Arg Ala Leu Asp
 35 40 45
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala
 50 55 60
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val
 65 70 75 80
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr
 85 90 95
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val
 100 105 110
 Val Val Glu Val Asn Gly Lys Arg
 115 120

<210> 267
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 267
 natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg
 60
 ttaacgcata ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg
 120

ctagatctcg ggcaccttca ccctagtcgg ccgggactcg tcactatcac cacaactgtc
 180
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa
 240
 aaacttttctg aagctcgcga ttaccgccag attccgatgc ttgcatcacg tcatggctgg
 300
 acagctccat tcattggtga gaccggcgca gcccatgcca tcgaggatgc gatgggcatt
 360
 accatcccaa ctgcgctggc atggatacga accctgctcg ctgagttcag cagaatcacc
 420
 tcacacttca catttttgtc atgggtaggc catcactgtg atgatgccgg c
 471

<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

Xaa	Pro	Gln	Arg	Val	Phe	Ser	Ser	Thr	Arg	Lys	Ile	Met	Phe	Val	Ile
1				5					10					15	
Gly	Ser	Met	Pro	Leu	Thr	His	Pro	Ser	Gln	Ser	Thr	Asp	Gly	Asp	Pro
			20					25					30		
Gly	Lys	Lys	Tyr	Glu	Val	Thr	Trp	Leu	Asp	Leu	Gly	His	Leu	His	Pro
		35				40					45				
Ser	Arg	Pro	Gly	Leu	Val	Thr	Ile	Thr	Thr	Thr	Val	Asp	Asp	Asp	Val
	50					55					60				
Ile	Thr	Ser	Ser	Gln	Val	Asn	Val	Gly	Asn	Leu	His	Arg	Gly	Asp	Glu
65				70					75					80	
Lys	Leu	Phe	Glu	Ala	Arg	Asp	Tyr	Arg	Gln	Ile	Pro	Met	Leu	Ala	Ser
			85					90					95		
Arg	His	Gly	Trp	Thr	Ala	Pro	Phe	Ile	Gly	Glu	Thr	Gly	Ala	Ala	His
		100						105					110		
Ala	Ile	Glu	Asp	Ala	Met	Gly	Ile	Thr	Ile	Pro	Thr	Arg	Val	Ala	Trp
	115					120						125			
Ile	Arg	Thr	Leu	Leu	Ala	Glu	Phe	Ser	Arg	Ile	Thr	Ser	His	Phe	Thr
	130					135						140			
Phe	Leu	Ser	Trp	Val	Gly	His	His	Cys	Asp	Asp	Ala	Gly			
145					150							155			

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

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 120
 tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct
 180
 tggtcggttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggat tcgcttagaa
 300
 ccgggcgttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc
 360
 tcgggggttat tggttcaaact actacgc
 387

<210> 270
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 270
 Thr Arg Val Val Phe Pro Glu Lys Thr Asn Lys Leu Glu Phe Met Val
 1 5 10 15
 Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val
 20 25 30
 Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys
 35 40 45
 Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu
 50 55 60
 Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp
 65 70 75 80
 Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly
 85 90 95
 Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu
 100 105 110
 Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu
 115 120 125
 Arg

<210> 271
 <211> 443
 <212> DNA
 <213> Homo sapiens

<400> 271
 gccggcacca acggaaagtc ctctaccgcg cgcattggcgc attcgctttt gcgtgccttc
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 caccgcccag tgggttttggg aaccagccca cacctgcagc gcgttactga gcgcacggc
 120
 attgatggcc agcccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca
 180
 tttgtggaaa tggtcgatgc cgaatcggac gtgcctatgt ctaagttcga ggtcttcgtg
 240
 ggcctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc
 300
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg
 360
 gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa
 420
 gctggcatta ttaagccacg cgt
 443

<210> 272
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 272
 Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu
 1 5 10 15
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu
 20 25 30
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro
 35 40 45
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met
 50 55 60
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val
 65 70 75 80
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val
 85 90 95
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn
 100 105 110
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr
 115 120 125
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile
 130 135 140
 Lys Pro Arg
 145

<210> 273
 <211> 864
 <212> DNA
 <213> Homo sapiens

<400> 273
 caaagtaaga ctgcttcaaa ttttgtgttc tgctctgcag ctgctcccc cctgctgtcg
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 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt
 120
 ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc ctagacagc
 180
 tgctgcctga gaactggcct ccagccggtg tcttcattcc atggggctcc ctgctgactg
 240
 catttctga tctgggatga tgtttaccag cccaaaacca gtcattgttct tccaaaagct
 300
 tctctttgat agaattttga ggccatgcc cctcccttcc agtccacatg gaattccaga
 360
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaatgtca
 420
 gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg
 480
 gtgggagcaa cccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc
 540
 tggcttgag acttaggtac ttttctcag tggacacact gatcccatcc catattgcat
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg
 660
 tctattgtat ctccttttgag gaaaagaaca cacattttta atggagattg gctgctttca
 720
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt
 780
 ccaccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac
 840
 tcctgactaa tgcccttcac gcgt
 864

<210> 274
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 274
 Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu
 1 5 10 15
 Lys Leu Leu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro
 20 25 30
 Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro
 35 40 45
 Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu
 50 55 60
 Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met
 65 70 75 80
 Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Gly Phe Gly Phe Ser
 85 90 95
 Ser Thr Ala Gly Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys
 100 105 110
 Gln Ser Tyr Phe
 115

<210> 275
 <211> 911
 <212> DNA
 <213> Homo sapiens

<400> 275
 naaatttaaa ggaacctccc ttctataacg gagagtattt attgcagctt tcctttctgt
 60
 ttatttttcag gaatgaaagg aattaccag ctttctgctt ttataacctac agctgaaagt
 120
 aattcctttc agcctcaggt gaagactttg ccatctccaa ttgatgctaa acagcagttg
 180
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccctt gccaggagaa
 240
 tctgcagcaa aaaagtcaga aagtgtctaca agcaatggag tgactaatct tcctaattgga
 300
 aatccttcaa tcctttctcc tcaacctatt ggtatcggtg tggcagctgt ccctagtccc
 360
 attccgggtcc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga
 420

cggcaaaagtt cttccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca
 480
 ggcaccaaag actccccaga acgttccagc agtcctgggtg ggaatcggtc tgcccggcac
 540
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca
 600
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg
 660
 agttctctaa atgtgggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc
 720
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt
 780
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctgggtc caggagcagc
 840
 agtgcggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag
 900
 catcctgtac a
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met Lys Gly Ile Thr Gln Pro Ser Ala Phe Ile Pro Thr Ala Glu Ser
 1 5 10 15
 Asn Ser Phe Gln Pro Gln Val Lys Thr Leu Pro Ser Pro Ile Asp Ala
 20 25 30
 Lys Gln Gln Leu Gln Arg Lys Ile Gln Lys Lys Gln Gln Glu Gln Lys
 35 40 45
 Leu Gln Ser Pro Leu Pro Gly Glu Ser Ala Ala Lys Lys Ser Glu Ser
 50 55 60
 Ala Thr Ser Asn Gly Val Thr Asn Leu Pro Asn Gly Asn Pro Ser Ile
 65 70 75 80
 Leu Ser Pro Gln Pro Ile Gly Ile Val Val Ala Ala Val Pro Ser Pro
 85 90 95
 Ile Pro Val Gln Arg Thr Arg Gln Leu Val Thr Ser Pro Ser Pro Met
 100 105 110
 Ser Ser Ser Xaa Arg Gln Ser Ser Ser Pro Gln Cys Thr Gly Gly His
 115 120 125
 Ser Ala His Ala Val Cys Glu Thr Gly Thr Lys Asp Ser Pro Glu Arg
 130 135 140
 Ser Ser Ser Pro Gly Gly Asn Arg Ser Ala Arg His Arg Tyr Pro Gln
 145 150 155 160
 Ile Leu Pro Lys Pro Ala Asn Thr Ser Ala Leu Thr Ile Arg Ser Pro
 165 170 175
 Thr Thr Val Leu Phe Thr Ser Ser Pro Ile Lys Thr Ala Val Val Pro
 180 185 190
 Ala Ser His Met Ser Ser Leu Asn Val Val Lys Met Thr Thr Ile Ser
 195 200 205
 Leu Thr Pro Ser Asn Ser Asn Thr Pro Leu Lys His Ser Ala Ser Val
 210 215 220
 Ser Ser Ala Thr Gly Thr Thr Glu Glu Ser Arg Ser Val Pro Gln Ile

<400> 278															
Met	Ser	Glu	Val	Pro	Asp	Glu	Leu	Val	Val	Leu	Arg	Gly	Ala	Ile	Asp
1				5					10					15	
Asn	Met	Asp	Ala	Ala	Leu	Ile	His	Leu	Leu	Ala	Glu	Arg	Phe	Arg	Ile
			20					25					30		
Thr	Arg	Glu	Val	Gly	Arg	Leu	Lys	Ala	Glu	Cys	Gly	Leu	Pro	Pro	Ala
		35					40					45			
Asp	Pro	Ala	Arg	Glu	Ala	Glu	Gln	Ile	Ala	Arg	Leu	Arg	Gln	Leu	Ala
	50					55					60				
Val	Glu	Ser	Asn	Leu	Asp	Pro	Glu	Phe	Ala	Gln	Lys	Val	Ile	Thr	Phe
65					70					75					80
Ile	Val	Ala	Glu	Val	Val	Arg	His	His	Glu	Ala	Ile	Ala	Asp	Asp	Ser

85 90 95
 Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly
 100 105 110
 Ser Gly Ser
 115

<210> 279
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 279
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 60
 taccacaatc cttaaaaaga aaagaaagaa aggcataatg aacccttagt tacctctcat
 120
 ccagcttcaa aattgtcagt gcattggtaa tcttgtctta tctgcccctc acccaccctt
 180
 ttccagaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact
 240
 ggaagttggt gttaattgtg catgtattca taaaacctct aggcatttct agtgtccctc
 300
 agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt
 348

<210> 280
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 280
 Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr
 1 5 10 15
 Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp
 20 25 30
 Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg
 35 40 45
 Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp
 50 55 60
 Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser
 65 70 75 80
 Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu
 85 90 95
 Pro Lys Ile

<210> 281
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 281
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 60

aacaaggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg
 120
 aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag
 180
 acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa
 240
 gctgtcaact cagccatggt tccgcttatt aataacgtga caaagaatct tcctaccttg
 300
 caaaaacagg ccaggaatct cgtgtcagtg aacggtaccc tgcagaaccc caacggtgat
 360
 tctgtcatta agattcaaca gacc
 384

<210> 282

<211> 110

<212> PRT

<213> Homo sapiens

<400> 282

Met	Asn	Asn	Lys	Val	Leu	Gly	Ala	Thr	Lys	Ala	Val	Gly	Asp	Ser	Thr
1			5						10				15		
Thr	Thr	Val	Asn	Gln	Val	Asn	Ser	Ala	Leu	Gly	Xaa	Ala	Asp	Ser	Ala
		20					25					30			
Ala	Glu	Lys	Thr	Ser	Ser	Ala	Val	Thr	Gln	Thr	Arg	Val	Gly	Ala	Gln
	35					40					45				
Ala	Ile	Thr	Gly	Ala	Ala	Gln	Asn	Val	Met	Ala	Asp	Ser	Gln	Ala	Val
	50					55				60					
Asn	Ser	Ala	Met	Val	Pro	Leu	Ile	Asn	Asn	Val	Thr	Lys	Asn	Leu	Pro
65					70					75				80	
Thr	Leu	Gln	Lys	Gln	Ala	Arg	Asn	Leu	Val	Ser	Val	Asn	Gly	Thr	Leu
			85						90					95	
Gln	Asn	Pro	Asn	Gly	Asp	Ser	Val	Ile	Lys	Ile	Gln	Gln	Thr		
			100						105					110	

<210> 283

<211> 426

<212> DNA

<213> Homo sapiens

<400> 283

cgcgtagacc aatgtgagac ggccgtcacc aagggtcatgc gcgacaagtc ggttggttagc
 60
 ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat
 120
 ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc
 180
 tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga
 240
 tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta
 300
 cgcacaaagg aagtcttgca tgaaaaaggg gtcattgttc cttccacgct gcgcttgatc
 360
 cgcaacgcgg tgcccaccac ctgccaaatt accatgctca agcctgatac cgaattgtcg
 420

gagaga
426

<210> 284
<211> 142
<212> PRT
<213> Homo sapiens

<400> 284
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
1 5 10 15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
20 25 30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
35 40 45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
50 55 60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Thr Ala Glu Phe Arg
65 70 75 80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
85 90 95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
100 105 110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
115 120 125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
130 135 140

<210> 285
<211> 345
<212> DNA
<213> Homo sapiens

<400> 285 .
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgatttctca gaaatctaca aacgtcagaa ctcgatcttc ggcgatgtaa ggaataactt
120
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggg gtattgcgca agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgtttcttc gcggtgtggc
240
gcatttcgaa ctcgtcggtt tgtttcgaca accctggggg tatacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn
345

<210> 286
<211> 107
<212> PRT
<213> Homo sapiens

<400> 286
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

1	5	10	15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn			
	20	25	30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu			
	35	40	45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly			
	50	55	60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu			
65	70	75	80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile			
	85	90	95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile			
	100	105	

<210> 287

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 287

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nnttaactgc ccctttgcag tctttattct gggacattag cactgtctgg ttatcttgct
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120
gttttgcagg tcacggccag gggctttggg ccgctgttac agtttgccta cactgccaa
180
ctgttactca gcagagaaaa catccgcgag gtcacccgct gtgctgagtt cctgcgcatg
240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgcg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
420
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480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac ccagataca agaaatacca gcttgcatgt
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagttag
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtctgg agatgagcct
780
gacgccaaag acagagcggg ggatgtcgag atggaccgga aacagcccag cctgcccct
840
acccccacgg cccagctgg ggccgcctgc ctggagagat ccaggagcgt ggcctcgccc
900
tcctgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

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ggtgacctta aaactgacta cacccttttc acaggaatt atggacagcc ccacgtgggc
 1080
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct
 1140
 ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctcctc cagcgcttgt
 1200
 gaccaagtga gcacctcggt gcattcttat tctgggggtga gcagtttgga caaagacctc
 1260
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 1320
 gcctactccc acggtgggct gatggccgac cacttgccag gaaggatgcg gcccaacac
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
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Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35				40					45				
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50				55						60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65				70					75				80		
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
			85					90					95		
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105					110		
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
			115					120					125		
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
			130					135					140		
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
145				150					155					160	
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
			165					170					175		
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180						185					190		
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
		195						200					205		
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu
		210				215							220		
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225				230					235					240	
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
			245						250					255	
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260						265					270		
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

Ser	Thr	Ser	Gln	Gln	His	Phe	Ala	Arg	Ser	Pro	Ala	Cys	Pro	Phe	Asp	
	290					295					300					
Lys	Gly	Ile	Thr	Gln	Gly	Asp	Leu	Lys	Thr	Asp	Tyr	Thr	Pro	Phe	Thr	
305					310					315					320	
Gly	Asn	Tyr	Gly	Gln	Pro	His	Val	Gly	Gln	Lys	Glu	Val	Ser	Asn	Phe	
				325					330					335		
Thr	Met	Gly	Ser	Pro	Leu	Arg	Gly	Pro	Gly	Leu	Glu	Ala	Leu	Cys	Lys	
			340					345					350			
Gln	Glu	Gly	Glu	Leu	Asp	Arg	Arg	Ser	Val	Ile	Phe	Ser	Ser	Ser	Ala	
	355						360					365				
Cys	Asp	Gln	Val	Ser	Thr	Ser	Val	His	Ser	Tyr	Ser	Gly	Val	Ser	Ser	
	370					375					380					
Leu	Asp	Lys	Asp	Leu	Ser	Glu	Pro	Val	Pro	Lys	Gly	Leu	Trp	Val	Gly	
385					390					395'					400	
Ala	Gly	Gln	Ser	Leu	Pro	Ser	Ser	Gln	Ala	Tyr	Ser	His	Gly	Gly	Leu	
				405					410					415		
Met	Ala	Asp	His	Leu	Pro	Gly	Arg	Met	Arg	Pro	Asn					
	420						425									

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<210> 289
<211> 822
<212> DNA
<213> Homo sapiens
```

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<400> 289
ngcattaccg ggctgaagac ggggtgctcat gacctcaacg atataggcta ttgctagaac
60
cacgccggcc cacgccgcgc aaagcgcaga cacggcacca ggaggggtca catggctgat
120
agcaagtcga aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg
180
accctgtgctt gcctggcagc cgggggtggag aacctcgtgg aggaggtgca tccggcaacc
240
ctcaagcgtg aagcatctga tcgtgcccgat gattttgtgc aggggtgagtt tgatcaggtc
300
aagagccagg tcaaagatga gaaatggtgg cgcgtgcagc ggatcgcgat ggccgcagga
360
gtgctcgctg ccggcgctgt cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420
ggcgctaccg ctgctcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcgggttcga
480
aaagatgcca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540
ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600
cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg
660
tgagaacagt gccgcctagc aaacagcggg cacagcgcaa aacaggtttg gctccgaccc
720
atggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct
780
gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

```

<210> 290
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 290
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu
 1 5 10 15
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val
 20 25 30
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala
 35 40 45
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys
 50 55 60
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met
 65 70 75 80
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg
 85 90 95
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu
 100 105 110
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln
 115 120 125
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly
 130 135 140
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser
 145 150 155 160
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg
 165 170 175
 Ala Gln Ala Ala Ala Gly Ala
 180

<210> 291
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 291
 ctccacgccg acaagactta cgacgggcgt cgctgccggg ctgagtgccg ggcccgcctcc
 60
 atcacccccc gcatcgctcg ccgcgggcgtg gagaccagcg agcgcttggg ccggtatcgc
 120
 tgggtcgtcg agcgcacctt cgcttggtc aaccgctttc ggcgctcgc catccgctac
 180
 gaggcggtg ctgacatcca cgaagccttc gtgatcctcg gctgcgcct catctgcctc
 240
 aaccagatca gacggttttg ttaggtgctg taaagggaga atggctgcag ctgggctatc
 300
 tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t
 351

<210> 292
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 292

```

Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1             5             10             15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
      20             25             30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
      35             40             45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
      50             55             60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
      65             70             75             80
Asn Gln Ile Arg Arg Phe Cys
                        85

```

<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

```

nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
60
ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcattgtg ctgtcgggtca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaagggt
240
gcgaagactt tcgatgttcc agtgtgcgtc atagctgggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgcattgc ctacgggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcgggtca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
gggggtgttg gtgtgcaggc tcgcactatt cattctgcgg cgttgcggca gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccgggtga gtgattctcg tttctcgatg
540
gtggcgggaga cgacccatcg cattgggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgccgaga tctcgtgggc gaaggctctca aatgtgccga ctgatcaata cgcacccctg
660
gctagggcgg aaggctcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

```

<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

```

Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```

1				5					10					15				
Thr	Ala	Asp	Ala	Ile	Leu	Ala	Ala	Leu	Asp	Leu	Asn	Arg	Phe	Lys	Val			
			20					25					30					
Ala	Lys	Thr	Phe	Asp	Val	Pro	Val	Cys	Val	Ile	Ala	Gly	Ala	Gly	Thr			
		35					40					45						
Gly	Lys	Thr	Arg	Ala	Val	Thr	His	Arg	Ile	Ala	Tyr	Gly	Ala	Ala	Thr			
	50				55				60									
Gly	Lys	Leu	Asp	Pro	Arg	Arg	Thr	Leu	Ala	Val	Thr	Phe	Thr	Thr	Lys			
65					70				75						80			
Ala	Ala	Gly	Thr	Met	Arg	Gly	Arg	Leu	Ala	Asp	Leu	Gly	Val	Val	Gly			
			85					90					95					
Val	Gln	Ala	Arg	Thr	Ile	His	Ser	Ala	Ala	Leu	Arg	Gln	Ile	Lys	Phe			
		100						105				110						
Phe	Trp	Pro	Arg	Ala	Tyr	Asn	Cys	Glu	Leu	Pro	Pro	Val	Ser	Asp	Ser			
	115					120						125						
Arg	Phe	Ser	Met	Val	Ala	Glu	Thr	Thr	His	Arg	Ile	Gly	Leu	Gly	Asn			
	130				135				140									
Asp	Lys	Ala	Leu	Leu	Arg	Asp	Leu	Ser	Ala	Glu	Ile	Ser	Trp	Ala	Lys			
145				150				155						160				
Val	Ser	Asn	Val	Pro	Thr	Asp	Gln	Tyr	Ala	Ser	Leu	Ala	Arg	Ala	Glu			
			165					170					175					
Gly	Arg	Val	Val	Ala	Gly	Val	Ser	Ala	Thr	Asp	Val	Gly	Arg					
		180						185					190					

<210> 295

<211> 417

<212> DNA

<213> Homo sapiens

<400> 295

ttcatatcag gcagtaccg agtccatgcg atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttcag
240
gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggcg
300
cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcg aaaactagga
360
atcgagtcac tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

<210> 296

<211> 139

<212> PRT

<213> Homo sapiens

<400> 296

Phe	Ile	Ser	Gly	Ser	Thr	Arg	Val	His	Ala	Ile	Asn	Asn	Val	Ser	Val			
1				5				10					15					
Ser	Phe	Thr	His	Ser	Gly	Val	His	Leu	Leu	Met	Gly	Glu	Ser	Gly	Ser			


```

      20      25      30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35      40      45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50      55      60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
      65      70      75      80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85      90      95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100      105      110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115      120      125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130      135

```

<210> 297

<211> 378

<212> DNA

<213> Homo sapiens

<400> 297

```

tacaccatcg gtgaccagat tgtcgaagct ctgcaggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccagagtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc aggccagat tctcgatttg ctgcgcgtag cccagcgtga aaccatgcg
300
ggcgtcgtaa tgatcaccca cgacctcggt gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

```

<210> 298

<211> 126

<212> PRT

<213> Homo sapiens

<400> 298

```

Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
1      5      10      15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
20      25      30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
35      40      45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
50      55      60
Asn Asp Pro Asp Leu Ile Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65      70      75      80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Leu Arg Val Ala Gln Arg

```

```

      85              90              95
Glu Thr His Ala Gly Val Val Met Ile Thr His Asp Leu Gly Val Val
      100              105              110
Ala Gly Leu Ala Asp Arg Val Ala Val Met Tyr Ala Gly Arg
      115              120              125

```

<210> 299
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 299
 gtgcacgggtt tcgttggcat gcgcaatgac cgggagaact tgcgttttga tccgagactt
 60
 ccagcccaat ggacgtogat caaacaccac atgctcattg gcgactctca catgctcggt
 120
 ttcttggaac gtgacgcat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
 180
 gtgcgcgggtg agctctacca cattgggggtt gagccgggtga ggggtccggt gtccgatcag
 240
 gggccggtgc gtcctagcct gcgcggttacc catccgatct cggggttgcg tcgagctgac
 300
 gggttctctta tcaactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg
 360
 atctcgac
 368

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

```

<400> 300
Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe
  1              5              10              15
Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu
      20              25              30
Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr
      35              40              45
Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu
      50              55              60
Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln
      65              70              75              80
Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu
      85              90              95
Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile
      100              105              110
Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser
      115              120

```

<210> 301
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 301
 ggccgggtta ttgcccgcgc gtttgtcggg gaaacccggc agaccttcga gcgcaccggc
 60
 aaccggcgcg actattccgt accgccgcgc gaaccgacct tgctcgacag gcttacggac
 120
 gcggggccgga cggatgatcg aatcggaag attggtgata tctacgcgca caaaggcgtg
 180
 tctcagggtgc gtaaggcaat ggcaatattg gccttggtcg atgaaacact cattgccatg
 240
 gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac
 300
 gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggctttcga ccggaaggctg
 360
 ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcctgacagc cgatcatggc
 420
 tgcgaccga ccctcaaggg aaccgaccac acgcgt
 456

<210> 302
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 302
 Gly Arg Val Ile Ala Arg Pro Phe Val Gly Glu Thr Arg Gln Thr Phe
 1 5 10 15
 Glu Arg Thr Gly Asn Arg Arg Asp Tyr Ser Val Pro Pro Pro Glu Pro
 20 25 30
 Thr Leu Leu Asp Arg Leu Thr Asp Ala Gly Arg Thr Val Ile Ala Ile
 35 40 45
 Gly Lys Ile Gly Asp Ile Tyr Ala His Lys Gly Val Ser Gln Val Arg
 50 55 60
 Lys Ala Met Ala Ile Leu Ala Leu Phe Asp Glu Thr Leu Ile Ala Met
 65 70 75 80
 Asp Asp Ala Gln Asp Gly Asp Leu Val Phe Thr Asn Phe Val Asp Phe
 85 90 95
 Asp Met Leu Tyr Gly His Arg Arg Asp Val Pro Gly Tyr Ala Ala Ala
 100 105 110
 Leu Glu Ala Phe Asp Arg Arg Leu Pro Glu Ala Met Ala Lys Leu Arg
 115 120 125
 Thr Gly Asp Leu Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro Thr
 130 135 140
 Leu Lys Gly Thr Asp His Thr Arg
 145 150

<210> 303
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 303
 nncgtgggca tcgaggagtt cctcgacatg aagtatcagg cgacgccgat tcacgtcgc
 60

tgacagcggg tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg
 120
 ggtgctcagc tgttcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtagagctc
 180
 atggaccgtc aggggtctgtc ggcgatcacc gtcaccgacc cggccaacat cttctatctg
 240
 atcggttaca acgcctgggc gttctacacc ccgcagatgc tgttcgtgcc gatcgacgga
 300
 gagatgggtcc tctacgctcg cgagatggat cgcattgggc acatcngcac gacgtcgttg
 360
 cccgccgacc agatcgtcgg ttaccgggag agttatgtgc ac
 402

<210> 304

<211> 97

<212> PRT

<213> Homo sapiens

<400> 304

Met	Tyr	Leu	Gly	Ala	Gln	Leu	Phe	Ser	Asp	Ser	Glu	Tyr	Glu	Gln	Arg
1				5					10					15	
Leu	Arg	Arg	Val	Arg	Glu	Leu	Met	Asp	Arg	Gln	Gly	Leu	Ser	Ala	Ile
			20					25					30		
Ile	Val	Thr	Asp	Pro	Ala	Asn	Ile	Phe	Tyr	Leu	Ile	Gly	Tyr	Asn	Ala
		35				40					45				
Trp	Ser	Phe	Tyr	Thr	Pro	Gln	Met	Leu	Phe	Val	Pro	Ile	Asp	Gly	Glu
	50				55					60					
Met	Val	Leu	Tyr	Ala	Arg	Glu	Met	Asp	Arg	Met	Ala	His	Ile	Xaa	Thr
65				70				75					80		
Thr	Ser	Leu	Pro	Ala	Asp	Gln	Ile	Val	Gly	Tyr	Pro	Glu	Ser	Tyr	Val
			85				90						95		

His

<210> 305

<211> 375

<212> DNA

<213> Homo sapiens

<400> 305

nnacgcgtcg gttccgcatc gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc
 60
 gtgtcgtcct ggcgaatatg ggcgatcagc cgggtacagt cgggatcgtc gctcacctcg
 120
 gccgccatct cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc
 180
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggcccc
 240
 tcgccatgcg tcggaatcga catgcagcac cctcctgccg ggatcgatgg cgtaatacgt
 300
 gcgacgggtac acggcgcggtg ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat
 360
 acgtcacatc atatg
 375

<210> 306
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 306
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr
 1 5 10 15
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr
 20 25 30
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg
 35 40 45
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser
 50 55 60
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro
 65 70 75 80
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp
 85 90 95
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln
 100 105 110
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met
 115 120 125

<210> 307
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 307
 actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag
 60
 ggtaggaag gctattctct ttggccactc tcatcctaag acctatttgg agaacctctg
 120
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctcgcaca
 180
 tttgatgtct cttcttctca cccactcacc ccaccctggg ggttggggca aaaaagtggc
 240
 tcaaagctgc gggtcagagt tccttgtaaa caaggctcct ccctcactgt cctcaccctg
 300
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaacca
 360
 gcagaactgg acataatggg aacagggtct gaagacaatc aatccagggc tgcagtgggt
 420
 gctgagtctg gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttggaa
 480
 tggtcagcc tctggacatc accccaccca accagagccc tggtctctgc tggatgtcca
 540
 cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagagggtgat
 600
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaa
 660
 ttggtgctgc agcactggca cgcgt
 685

<210> 308
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 308
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser
 1 5 10 15
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala
 20 25 30
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu
 35 40 45
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly
 50 55 60
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly
 65 70 75 80
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro
 85 90 95
 Leu Ser Ser Ser
 100

<210> 309
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 309
 caggctcgta ctattcgtat ccctgtgcat atgggtcgagg tcatcaataa gctggctcgc
 60
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac
 120
 gaactcgata tgaccgcaga gaaggtcatt gaggtgcaga aatacggctc cgagccgatac
 180
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat
 240
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttgaggga gcagctgcat
 300
 gatgtcctcg atacctgtc cgagcgagag gccggtgtcg tgtcgatgcg attcggcttg
 360
 accgacggac agcccaagac cctggatgag atcggaag tctacggtgt tactcgggag
 420
 cgcacccgcc ag
 432

<210> 310
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 310
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn
 1 5 10 15
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

```

      20      25      30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
      35      40      45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
      50      55      60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
      65      70      75      80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
      85      90      95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
      100      105      110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
      115      120      125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
      130      135      140

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<210> 311

<211> 358

<212> DNA

<213> Homo sapiens

<400> 311

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acgcgtatcg aaaatatccc tcccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccc atgtgggtgt cattggtcct
120
ggactgggac aacaagcgtg gggcaaaaaa ggcgtacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccggcgag gccgcgcggc tgettagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

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<210> 312

<211> 116

<212> PRT

<213> Homo sapiens

<400> 312

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Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
1      5      10      15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
      20      25      30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
      35      40      45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
      50      55      60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
      65      70      75      80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
      85      90      95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg

```

100 105 110
 Leu Val Lys Arg
 115

<210> 313
 <211> 347
 <212> DNA
 <213> Homo sapiens

<400> 313
 ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac
 60
 acccctggtg gcgaaccgcg caccatccgc acctcgaacg cgcacatcat tgccgtcacc
 120
 agtggcgaag gcggcgtggg caagaccttt gtctccgcca acctggccgc cgcgctgacc
 180
 cgcctgggac tgcgctgct ggtactggac gccgacctgg gcctggccaa cttggacgtg
 240
 gtgctgaacc tctaccccaa ggtgacgctg cacgatgtgt tcaccggcaa ggctcgctg
 300
 caagacgcgg tggtcacggc ccccgccggc ttccatgtgc tgctagc
 347

<210> 314
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 314
 Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro
 1 5 10 15
 Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser
 20 25 30
 Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys
 35 40 45
 Thr Phe Val Ser Ala Asn Leu Ala Ala Leu Thr Arg Leu Gly Leu
 50 55 60
 Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val
 65 70 75 80
 Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly
 85 90 95
 Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His
 100 105 110
 Val Leu Leu
 115

<210> 315
 <211> 544
 <212> DNA
 <213> Homo sapiens

<400> 315
 nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggaggggaac catgcttgcc
 60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggctcgtccc ggggccatcc
 120
 aacaccttgc tgetcagcgc ccgtttccat ttcggctcgc tgcgggcggc gcccttcac
 180
 ctgcttgagg cggtgggcta ctgctatcc atttcggcat ggggctgggt attggcgcg
 240
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg
 300
 gcgcttctgg cggtgaagac ctggaatgcc ntcgatccgc agtgcggggc cggtaaattc
 360
 cgccatgggc ccctgccct gtctgtggca accctgtcga acccgaaggc gctgatcttc
 420
 gccagcgtga tctttcccg caaggcggtc ctgcacttct ggaacaacta cagcatctcg
 480
 ctgctggcct tcctggttgt gctggcgccc atcgggatgc tttgggtcgg gctggggggc
 540
 ggta
 544

<210> 316

<211> 159

<212> PRT

<213> Homo sapiens

<400> 316

Ile	Tyr	Ala	Ile	Met	Leu	Phe	Ser	Ser	Leu	Ile	Leu	Val	Val	Pro	Gly
1			5						10					15	
Pro	Ser	Asn	Thr	Leu	Leu	Leu	Ser	Ala	Arg	Phe	His	Phe	Gly	Ser	Leu
			20					25					30		
Arg	Ala	Ala	Pro	Phe	Ile	Leu	Leu	Glu	Ala	Leu	Gly	Tyr	Ser	Leu	Ser
		35					40					45			
Ile	Ser	Ala	Trp	Gly	Trp	Val	Leu	Ala	Arg	Leu	Ser	Glu	Ser	Asn	Pro
		50				55					60				
Trp	Ile	Ile	Ser	Leu	Thr	Lys	Ala	Leu	Cys	Ala	Leu	Tyr	Val	Ala	Leu
65					70				75					80	
Leu	Ala	Val	Lys	Thr	Trp	Asn	Ala	Xaa	Asp	Pro	Gln	Cys	Gly	Ala	Gly
			85					90					95		
Asn	Phe	Arg	His	Gly	Pro	Leu	Pro	Leu	Phe	Val	Ala	Thr	Leu	Ser	Asn
		100						105					110		
Pro	Lys	Ala	Leu	Ile	Phe	Ala	Ser	Val	Ile	Phe	Pro	Gly	Lys	Ala	Phe
		115					120					125			
Leu	Asp	Phe	Trp	Asn	Asn	Tyr	Thr	Ile	Ser	Leu	Leu	Ala	Phe	Leu	Val
	130					135					140				
Val	Leu	Ala	Pro	Ile	Gly	Met	Leu	Trp	Val	Gly	Leu	Gly	Ala	Gly	
145					150					155					

<210> 317

<211> 343

<212> DNA

<213> Homo sapiens

<400> 317

nggtcagcct ctcgcccagg caattctctt aagatacatg agctgctatg agtaccaaag
 60

ccagagggttt gtccactgag agaagcacat tggaaaagggg ggcgtgggcc tgggactgtg
 120
 tggcacttta tgcaacggggg gggcctaagg gggnggtcc accaaccatg cactgngggg
 180
 ggggtgtggg taacatgccg tgcattttgg ggggtgtgcca tgagtggcac accatggggg
 240
 tggcatgtgg ggcatttatg catgtggtgt tggcgagca aactcagctc ttacctggt
 300
 ggggccagcc tctaaaactt ctcacattgg gctcccttct gac
 343

<210> 318

<211> 98

<212> PRT

<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1				5				10						15	
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
		20					25					30			
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
		35					40					45			
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
	50					55				60					
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65					70					75				80	
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85					90						95	
Leu	Leu														

<210> 319

<211> 429

<212> DNA

<213> Homo sapiens

<400> 319

gaattctcga tgtacccct cccggcagtc ctattctcga gctgagcggg cacagtggcc
 60
 ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta
 120
 agggcatgat atgtacagga ggcgacgatg ctcagtgcct cgtatatgat ctgactagct
 180
 caactcttcg aacagcatct gctcaaggac ggcgtctctg aaacagtcca tataaacaaa
 240
 gccattcacc gggaatagac ggatggcgtg tcggcgagca agtgccggtg ctcgcttata
 300
 cggccccgtc tatgggtcaac aatgctagct ggctcggcat gcctgcgcca tcaaaacgca
 360
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagttag tggactgagt
 420
 atacgtccn
 429

<210> 320
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 320
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu
 1 5 10 15
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg
 20 25 30
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg
 35 40 45
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val
 50 55 60
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser
 65 70 75 80
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp
 85 90 95
 Thr Glu Tyr Thr Ser
 100

<210> 321
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 321
 ngtgacacgac gtgctcgcca agtccctcgg gtcctctaata gcatcaacg tggttcacgc
 60
 caccgtcgat gcgttcgagc agctcgagga gcccgaaagag gtcgcccgtc gccgcggcaa
 120
 gtccggttgag gagatcgccc cagcagccat gctgcgtgag cgcaaggagg ccgacgaggc
 180
 cgccgctgct gcccgcatgg aggaaaaggc ggggggtaac tgatgagcaa gctgaagatc
 240
 acccagatca agtctggcat cgctaccaag ccaaatcatc gtgagaccct gcgcagcctc
 300
 ggactgaagc gtattggtga caccgtcatc aaggaggacc gcccgaggtt ccgcggcatg
 360
 gtccggaccg ttcgtcacct cgtcaccatg gaagaggtgg actgacatgg ctattgagct
 420
 ccatgacctc aagcccgtc ctggtgcccc caaggccaag acccgcggtg gtcgtggtga
 480
 gggttccaag ggtaagaccg ctggtcgagg taccaagggc accggtgcac
 530

<210> 322
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

```

      10      15
1      5      10      15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly
      20      25      30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg
      35      40      45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp
      50      55      60

```

<210> 323
 <211> 468
 <212> DNA
 <213> Homo sapiens

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<400> 323
ntccggacccc gctgtggcca cgtattctgc cgttctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctgggt
180
tgcctcagtg aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
300
ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggagggcct
360
gtgttctgtc cactttgcca tttaataccc gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

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<210> 324
 <211> 156
 <212> PRT
 <213> Homo sapiens

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<400> 324
Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
1      5      10      15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
      20      25      30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
      35      40      45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
      50      55      60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
      65      70      75      80
Pro Leu Gln Glu Leu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
      85      90      95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
      100      105      110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
      115      120      125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His

```

130 135 140
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe
 145 150 155

<210> 325
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 325
 acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc
 60
 actggagccc cctaggaagc atctcacagg ctgtggcctt tggcacgggg atctggggcc
 120
 aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt
 180
 ggagctctgc tcccaggga tcccactcc cgcagatgac ttgcccgaga gagttctgct
 240
 ggtggatttt gatggaaatt ctatttgatc gcaccactt ggttcactgt gtgcttcggg
 300
 gtccccagggt tttagggtgct tcatgccctg ctgggaacga gacacgctcc tgccctcagt
 360
 gaatcttcag tcta
 374

<210> 326
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser
 1 5 10 15
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu
 20 25 30
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser
 35 40 45
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr
 50 55 60
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val
 65 70 75 80
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu
 85 90 95
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg
 100 105

<210> 327
 <211> 538
 <212> DNA
 <213> Homo sapiens

<400> 327
 cactataaaa tccagtttgg ggcccgtgtt ctttctatt ggtctgtcag gtgaaaaact
 60

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ccggctgggg gaaaagcgtc cgggtggtttg ttggtaaaaga ggggtgcgtga tgggctctgg
 120
 ggaatggagg atggcgacc ggctgtgggt ggactgtgga aacgggggggt ggcagtgccg
 180
 gggtagttgt cctgctggtc tgggttttggg atcctgggct ggagaaatgc gatccaaaag
 240
 agctcgggat gggctcagag cgaccacga aaataccagg ggccaagtaa aatgaaccca
 300
 ccctttaaca gtgcacaaag cgctggcaca cgggccacgt ctggtgacgc aggctgcccg
 360
 aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc
 420
 cgcccctgtc cactctggc cagccggagt ttttcaccta cagaccaata ggaaagaaca
 480
 cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgccc
 538

<210> 328

<211> 125

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5					10					15	
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20					25					30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
		35					40					45			
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50					55					60				
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
65					70				75					80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85					90						95	
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
			100					105					110		
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
		115					120					125			

<210> 329

<211> 407

<212> DNA

<213> Homo sapiens

<400> 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa
 60
 gctcttcagt ctttctgctc cactgagcag tgttttcttg atacccttgg tatectgcca
 120
 gcagcctcgt tatgactcct aactccattg ccctccatgg cccctgggag ctctctctct
 180
 ctttctctcc aggtagtaga gcaactgcttc tggcttcttg tgcacagaag ggtttccac
 240

agctgagagc tgggctccta ctgacatagt tatttccttt atatectgcc ccaccttctt
 300
 ctggttagcac acagcaacct tgcatactag ctggtatcat taccttccca atcaacagge
 360
 cttgatttct tataggactt tttctctcag atttacattg cttcttt
 407

<210> 330
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 330
 Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly
 1 5 10 15
 Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu
 20 25 30
 Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu
 35 40 45
 Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala
 50 55 60
 Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr
 65 70 75 80
 Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala
 85 90 95
 Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu
 100 105 110
 Arg

<210> 331
 <211> 523
 <212> DNA
 <213> Homo sapiens

<400> 331
 tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa
 60
 tccaccggcc cccatcccgg cgccactttc gctgaggcca tggagtcgat cggagccagc
 120
 tacgacggat cggccgggtt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg
 180
 ttcgacgcag cggctgaact cttcgtcgaa ttgttgaaca ccacgagcct ggttgaagag
 240
 gacatgccc gtcagatcga cgcggcgcca gcctccctgg cccagaccag ccagcgcgga
 300
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtggggtc acggctctcc
 360
 ctgcccacga tcggtaccct ctgctcggtg gaaaagctca acgccgcagc cgcacgagaa
 420
 ttctgggccc cgcactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc
 480
 gaggacctcg acttgtcaat attcaaggag tggacgacca gct
 523

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<210> 332
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 332
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg
 1 5 10 15
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu
 20 25 30
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala
 35 40 45
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala
 50 55 60
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu
 65 70 75 80
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr
 85 90 95
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Arg Ala Leu
 100 105 110
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser
 115 120 125
 Ser Val Glu Lys Leu Asn Ala Ala Ala Arg Glu Phe Trp Ala Ala
 130 135 140
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val
 145 150 155 160
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser
 165 170

<210> 333
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 333
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgaggca tgacggtgaa ggtgccaacc
 60
 gatccccatc accgcccggg agttccattg aagtctgcga aggaccgtat ggacatcatt
 120
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccaccac
 180
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccaccac cggtggcaag
 240
 gaacggggccc gcaactacga tgcgggtggcc cagctcgtcg cgcagcgagt cgcgcggtca
 300
 cacggccgga tcaactgcaa acggctgcta ccggtagcgc gagcggcagg atatgagggg
 360
 tcggcgcgga at
 372

<210> 334
 <211> 88
 <212> PRT

<213> Homo sapiens

<400> 334

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Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
          20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
          35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
          50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
          85

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<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

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gtgcacgcct tgctggggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtaccttt
60
ggcagggggag ggcattcgcg gctcatcctg cagcgggttg ggccgcaagg ccgcctgggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accagggggt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggctg gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

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<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

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Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
          20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
          35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
          50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
          85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100
Thr Thr Pro Met His Gly
115

105

110

<210> 337
<211> 447
<212> DNA
<213> Homo sapiens

<400> 337
cagcctctct cgcaccgcg cgggtgtgaag cacgggcatg ccggtgtgca agtggcacca
60
cagccaaaac agcgagctca cacttcaaac tccttcaaag acccaggcc tctgtaagaa
120
ccgctcatct ctgtgcccac agtcccccg ctccatgtg acccagaaat ggaaccacgc
180
agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa
240
acaggcgcca tcatgtcagc cggtgagcag gagcaacgtg cgtgggtcag ggggtggcca
300
cacgtccaac ttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca
360
gcagcaggca taggacttcc ggtggccctg cgtcttcac aacactgagt attgtcaggg
420
tttctgtact gtttttacag ccaattg
447

<210> 338
<211> 111
<212> PRT
<213> Homo sapiens

<400> 338
Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu
1 5 10 15
Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu
20 25 30
Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala
35 40 45
Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg
50 55 60
Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn
65 70 75 80
Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp
85 90 95
Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Ala
100 105 110

<210> 339
<211> 588
<212> DNA
<213> Homo sapiens

<400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgtca
 60
 gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaacca atggaagaca
 120
 ccgacctgca agcgctgatg gccagactcg aattgctaata tgatcgggtc gagcaactta
 180
 agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc
 240
 tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg
 300
 ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata
 360
 ttcgatcatc tgcccccagg aagaacgcag cacctggtga gtgctgcccg ctacctggaa
 420
 ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcacg ggtgccgacc gcacgcgcgt
 480
 gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca
 540
 ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt
 588

<210> 340

<211> 123

<212> PRT

<213> Homo sapiens

<400> 340

Met	Glu	Asp	Thr	Asp	Leu	Gln	Ala	Leu	Met	Ala	Arg	Leu	Glu	Leu	Leu
1				5					10					15	
Ile	Asp	Arg	Val	Glu	Gln	Leu	Lys	Ser	Gln	Asn	Gly	Leu	Leu	Leu	Ala
			20					25					30		
Gln	Glu	Lys	Thr	Trp	Ala	Arg	Xaa	Arg	Ala	His	Leu	Ile	Glu	Lys	Asn
		35				40					45				
Glu	Ile	Ala	Arg	Arg	Lys	Val	Glu	Ser	Met	Ile	Ser	Arg	Leu	Lys	Ala
	50				55				60						
Leu	Glu	Gln	Asp	Tyr	Glu	Leu	Ser	Asn	Ser	Val	Thr	Cys	Arg	Ser	Ser
65			70					75				80			
Thr	Lys	Asn	Ile	Arg	Ser	Ser	Ala	Pro	Arg	Lys	Asn	Ala	Ala	Pro	Gly
		85					90					95			
Glu	Cys	Cys	Pro	Leu	Pro	Gly	Arg	Pro	Lys	Gly	Val	Lys	Ser	Ala	Ala
		100				105									
Ala	Ala	Lys	Ser	Ser	Val	Pro	Thr	Ala	Ser	Pro					
		115				120									

<210> 341

<211> 401

<212> DNA

<213> Homo sapiens

<400> 341

ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtagaccg ctcggccttt
 60
 gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg
 120

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ctgaacattc ttaaccccaa gctgacaatt ttcttcctgg ccttcctgcc tcaattcgta
 180
 acgccaggcg gcaccgcgcc ggccttgag atgctggtac tgagcggcgt gttcatggcg
 240
 atgacgcttg cagtgtttgt gctgtatggc ctggtggcga atgtgtttcg tcgtgcagtg
 300
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg
 360
 ctgggggtga acctggcggt tgccgcagcg tgaggacgcg t
 401

<210> 342
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 342
 Xaa Arg Ala Ala Tyr Leu Leu Tyr Leu Ala Tyr Ala Thr Trp Arg Asp
 1 5 10 15
 Arg Ser Ala Phe Ala Met Asn Asp Thr Pro Thr Val Ala Thr Ala Arg
 20 25 30
 Ser Leu Ile Leu Arg Gly Phe Leu Leu Asn Ile Leu Asn Pro Lys Leu
 35 40 45
 Thr Ile Phe Phe Leu Ala Phe Leu Pro Gln Phe Val Thr Pro Gly Gly
 50 55 60
 Thr Ala Pro Ala Leu Gln Met Leu Val Leu Ser Gly Val Phe Met Ala
 65 70 75 80
 Met Thr Leu Ala Val Phe Val Leu Tyr Gly Leu Leu Ala Asn Val Phe
 85 90 95
 Arg Arg Ala Val Val Glu Ser Pro Arg Val Gln Asn Trp Leu Arg Arg
 100 105 110
 Ser Phe Ala Thr Ala Phe Ala Gly Leu Gly Leu Asn Leu Ala Phe Ala
 115 120 125
 Gln Arg
 130

<210> 343
 <211> 389
 <212> DNA
 <213> Homo sapiens

<400> 343
 gtgttgcgca actacatggc gtccctgccg ttcagcgtgg tcgagtcggc gcgcacgcac
 60
 ggggtgctcca acttccagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg
 120
 gcggcgcttcg cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc
 180
 ttctcacca acgacaacc caccggtgatc gtcaagctcc aacagctttc cnngggcccc
 240
 aaggcccagg gtgaggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg
 300
 atcgcttctc tcgtgctcca gaacttctcg gtgcgcggta tgacgtcggg tgccgtcaag
 360

gggtgaccgc tcaactgcag tggcccggg
389

<210> 344

<211> 121

<212> PRT

<213> Homo sapiens

<400> 344

Val	Leu	Arg	Asn	Tyr	Met	Ala	Ser	Leu	Pro	Phe	Ser	Val	Val	Glu	Ser
1				5					10					15	
Ala	Arg	Ile	Asp	Gly	Cys	Ser	Asn	Phe	Gln	Ile	Phe	Trp	Lys	Leu	Ile
		20					25						30		
Ala	Pro	Met	Ala	Met	Pro	Ala	Met	Ala	Ala	Phe	Ala	Thr	Leu	Gln	Phe
		35					40					45			
Leu	Trp	Val	Trp	Asn	Asp	Leu	Leu	Ile	Ala	Lys	Leu	Phe	Leu	Thr	Asn
	50				55						60				
Asp	Asn	Pro	Thr	Val	Ile	Val	Lys	Leu	Gln	Gln	Leu	Ser	Xaa	Gly	Pro
65				70					75					80	
Lys	Ala	Gln	Gly	Ala	Glu	Leu	Leu	Thr	Ala	Gly	Ala	Phe	Ile	Ser	Ile
			85					90						95	
Val	Leu	Pro	Met	Ile	Val	Phe	Phe	Val	Leu	Gln	Asn	Phe	Leu	Val	Arg
		100						105							
Gly	Met	Thr	Ser	Gly	Ala	Val	Lys	Gly						110	
		115					120								

<210> 345

<211> 360

<212> DNA

<213> Homo sapiens

<400> 345

ctagtacttt atgctgatgg tgaacgtcgt tacatccttg cccctaaagg catggttgct
60
ggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg
120
cgtaatatcc cagttggtac aacagttacac gctgtagaaa tgaaacctgc taaaggtgca
180
caaattgcac gttctgctgg ttcttacagc caaattatag ctctgatgg tgcttacggt
240
actctacggt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgtcg tgcaacaatc
300
ggtgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt
360

<210> 346

<211> 120

<212> PRT

<213> Homo sapiens

<400> 346

Leu	Val	Leu	Tyr	Ala	Asp	Gly	Glu	Arg	Arg	Tyr	Ile	Leu	Ala	Pro	Lys
1				5					10					15	
Gly	Met	Val	Ala	Gly	Asp	Val	Ile	Gln	Ser	Gly	Glu	Asp	Ala	Ser	Ile

```

          20          25          30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
          35          40          45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
          50          55          60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
65          70          75          80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
          85          90          95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
          100          105          110
Leu Gly Lys Ala Gly Ala Thr Arg
          115          120

```

<210> 347

<211> 565

<212> DNA

<213> Homo sapiens

<400> 347

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accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgtc gggatcctca cggatgcctt cttggtgcgg
180
atgaccctcg tcccggccgt gatggccctg ctaggtgaca aggcattggtg gttgcccggg
240
tggctggatc gacgcctacc ccgcctcgac atcgagggag aagggatcac ccacgaggaa
300
aagctggccg cctggccccc agcggatcac accgaggccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaa cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcgccgctc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctaccgc agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

```

<210> 348

<211> 188

<212> PRT

<213> Homo sapiens

<400> 348

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Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1          5          10          15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
          20          25          30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
          35          40          45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```

50 55 60
 Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
 65 70 75 80
 Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
 85 90 95
 Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
 100 105 110
 Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
 115 120 125
 Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
 130 135 140
 Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
 145 150 155 160
 Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
 165 170 175
 Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
 180 185

<210> 349
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 349
 ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
 60
 gagctcggtt cggctaccgc tcatacgttt gcggacaatt tgccgttcct tcttaaactg
 120
 ctgcggcag aagagccact atcgttgcag gctcatccca gtttggcgca agcacaggaa
 180
 ggggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
 240
 gatcccaacc ataaaccgga gcttattggtt gggctgacgc gattccacgc actagccggc
 300
 ttccgtgaac cacaacgcac acttgagctt tttgacgcg
 339

<210> 350
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 350
 Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
 1 5 10 15
 Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
 20 25 30
 Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
 35 40 45
 Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
 50 55 60
 Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
 65 70 75 80
 Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

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Ala Leu Ala Gly Phe Arg Glu Pro Gln Arg Thr Leu Glu Leu Phe Asp
 100 85 90 95
 105 110
 Ala

<210> 351
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 351
 gcgcgccccca gtgccgagac ccgggggcttc aggagccggc cccgggagag aagagtgcgg
 60
 cggcggacgg agaaaacaac tccaaagttg gcgaaaggca ccgcccctac tcccgggctg
 120
 ccgccccttc cccgccccca gccctggcat ccagagtacg ggctcgagccc gngggccatg
 180
 agcccccttg gggaggcggc accagggagc ctggggcccg gggctccgcc gcgaccccat
 240
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt
 300
 tggccaccen ntccctctcc tcctccttgg aggcgctctg gcccatccag accg
 354

<210> 352
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 352
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu
 1 5 10 15
 Arg Arg Val Arg Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys
 20 25 30
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Arg Pro Gln Pro
 35 40 45
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly
 50 55 60
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His
 65 70 75 80
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser
 85 90 95
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Pro Trp Arg Arg
 100 105 110
 Ser Gly Pro Ser Arg Pro
 115

<210> 353
 <211> 1469
 <212> DNA
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt
60
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatcctt
120
gaacccattt cagctgttgt cagcccacac ggcctcatgc tgttgctggt gaagcctcaa
180
tttgagggtg gttgcaaggc tttgggagcc catggcggtg tcacggaccc ggccctgcgc
240
ttgcaggcca tcgcgggtgt catggcagca gcggttagatt tgggttggcg tatgcgtgac
300
gagtgcgata gcccgttgcc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa
360
cgtacgggtc ggtgacagac gtccgggcat atcatgggcc gctactgtgg tcttgtgaac
420
gacacgagcc ctctgagata cgttgtcgtc gtcacccatg ccacgcggga cgacgctttt
480
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattggttg cgcggttccg
540
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttggga
600
gagttcggcc acgaggcgga ggtggtcgtc gtctttggcg gcgacggcac gatcttgcca
660
gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgtc
720
ggttttcttg ctgagctgga gcgtccgat atggcggtc tagtgaacaa ggtgtgttcg
780
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccga gcattccgga
840
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccggcgg
900
cgcatgctcg acgttctggc gtctgtcgac gagttgccg tgcaacgctg gagttgcgac
960
gggatccttg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcggcccc
1020
gtcatgtggc ccgatctcga cgccatgtc atggtgccgt tgagcgtca cgctctcttt
1080
gtcgcaccgc tggatcatgag ccagctgct cgagtggacc ttgacatcca gccagacggt
1140
tcagaatcgg cggttctgtg gtgcgacggg cgcgcgtcgt gcaccgtacg accgggggaa
1200
agaatcaccg tcgtccgcca tcccagcgt ctgcgcattg ctgctctggc cgcgcagccc
1260
ttcacatcgc gtctggtcaa gaagtttgag ctcccggta gcgggtggcg tcagggtcgt
1320
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg
1380
tcatcgatga gacggtcctc gaaccctcat ccgcgtgac ggcagtcacc ggcgagaccg
1440
gcgccggaaa gaccatggtg gtcaccggt
1469

<210> 354

<211> 318

<212> PRT

<213> Homo sapiens

<400> 354

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Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
      20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
      35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
 50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
      85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
      100           105           110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
      115           120           125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
      130           135           140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145           150           155           160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
      165           170           175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
      180           185           190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
      195           200           205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
      210           215           220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225           230           235           240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
      245           250           255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
      260           265           270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
      275           280           285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
      290           295           300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305           310           315

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<210> 355

<211> 558

<212> DNA

<213> Homo sapiens

<400> 355

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nggatccac ctcctggaat ggaaaccac ataccagttc tcttcctcga tttgaatgcg
60
gatgacctca gtgccaatga gcagcttggt ggcccccatg catccggcgt gaactccatc
120

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ctgccaagg agcatggcag ccagtttttc tacctgcca tcataaagca cagtgatgat
 180
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg
 240
 gtcacaccac agaatgaaag gatttaccta attgtgaaaa ccacagttca actcagccac
 300
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag
 360
 agtttcacgc agagtttgaa gaggagaata tccctgaaaa atatatttta ttcctgtggg
 420
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa
 480
 acgctggctc tcctggcagc aaggagtga aacgaaggca catcagatgg gaagacgtac
 540
 attgagaagt acactcga
 558

<210> 356

<211> 186

<212> PRT

<213> Homo sapiens

<400> 356

Xaa	Ile	Pro	Pro	Pro	Gly	Met	Glu	Thr	His	Ile	Pro	Val	Leu	Phe	Leu
1				5					10					15	
Asp	Leu	Asn	Ala	Asp	Asp	Leu	Ser	Ala	Asn	Glu	Gln	Leu	Val	Gly	Pro
			20					25					30		
His	Ala	Ser	Gly	Val	Asn	Ser	Ile	Leu	Pro	Lys	Glu	His	Gly	Ser	Gln
			35				40					45			
Phe	Phe	Tyr	Leu	Pro	Ile	Ile	Lys	His	Ser	Asp	Asp	Glu	Val	Ser	Ala
	50					55				60					
Thr	Ala	Ser	Trp	Asp	Ser	Ser	Val	His	Asp	Ser	Val	His	Leu	Asn	Gly
65					70				75					80	
Val	Thr	Pro	Gln	Asn	Glu	Arg	Ile	Tyr	Leu	Ile	Val	Lys	Thr	Thr	Val
				85					90					95	
Gln	Leu	Ser	His	Pro	Ala	Ala	Met	Glu	Leu	Val	Leu	Arg	Lys	Arg	Ile
			100					105					110		
Ala	Ala	Asn	Ile	Tyr	Asn	Lys	Gln	Ser	Phe	Thr	Gln	Ser	Leu	Lys	Arg
		115				120					125				
Arg	Ile	Ser	Leu	Lys	Asn	Ile	Phe	Tyr	Ser	Cys	Gly	Val	Thr	Tyr	Glu
	130					135				140					
Ile	Val	Ser	Asn	Ile	Pro	Lys	Ala	Thr	Glu	Glu	Ile	Glu	Asp	Arg	Glu
145				150					155					160	
Thr	Leu	Ala	Leu	Leu	Ala	Ala	Arg	Ser	Glu	Asn	Glu	Gly	Thr	Ser	Asp
			165					170						175	
Gly	Lys	Thr	Tyr	Ile	Glu	Lys	Tyr	Thr	Arg						
			180					185							

<210> 357

<211> 323

<212> DNA

<213> Homo sapiens

<400> 357

acgcgtgcgt gtgttggtgtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg
 60
 gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagc
 120
 cctggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg
 180
 cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggttga cagagtggat
 240
 ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg
 300
 gtcaccatgg gtcagcgagg atn
 323

<210> 358

<211> 102

<212> PRT

<213> Homo sapiens

<400> 358

Met	Val	Thr	Leu	Thr	His	Ala	Ser	Leu	Ile	Leu	Leu	Thr	Gly	Pro	Arg
1				5					10					15	
Arg	Cys	Phe	Arg	Arg	His	Pro	Ser	Thr	Leu	Ser	Ser	Pro	Ser	Arg	Gly
			20					25					30		
Leu	His	Ala	Leu	Pro	Ser	Val	Ala	Leu	Pro	Cys	Pro	Ala	Gly	Ala	Val
		35					40					45			
Leu	Thr	Pro	Ala	Val	Phe	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Pro	Gly	Leu
	50					55					60				
Glu	Pro	Gly	Leu	Ser	Pro	Arg	Ala	Leu	Cys	Leu	Ile	Ser	Leu	Gln	Pro
65					70					75				80	
Asp	Arg	Thr	Pro	Pro	Ala	Ala	His	Pro	His	Ala	Cys	Thr	His	Pro	Thr
				85					90					95	
His	Thr	Thr	His	Ala	Arg										
															100

<210> 359

<211> 265

<212> DNA

<213> Homo sapiens

<400> 359

acgcgtaccg acaagcgcgc ggtgatggcc gaccttcgcg aatcgggccc aatcgagcag
 60
 gatgcggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccc
 120
 gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc
 180
 aagctgaagt tcttcggcga gtacaccctg ttcgacaacc tggcccacaa ctcgggttgg
 240
 tcgttcgaat aacggatgat tccgg
 265

<210> 360

<211> 83

<212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1             5             10             15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
      20             25             30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
      35             40             45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
      50             55             60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
      65             70             75             80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

```

gctttgcagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catcccttc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtggttc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agcctttggt tccgtggggt atgaatatga atcctgcca
300
gatctaattc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgccctca acattcaaag tggcatcctg
420
cacaagggga atgngagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1             5             10             15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
      20             25             30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
      35             40             45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
      50             55             60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

```

65          70          75          80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
          85          90          95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
          100          105          110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
          115          120          125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
          130          135          140
Gly Glu Asn Gln Phe Val Ser
145          150

```

<210> 363
 <211> 502
 <212> DNA
 <213> Homo sapiens

```

<400> 363
ggtaccaaaa aagtttgcca cagtattcac actccaggtc tccataaacc ttccagatcc
60
gctcacacaa gctggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaag
120
cggtgatgcc tgaccggtgc tcaggggcag ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgagge ctcagctggg ttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc cttcccccta
300
gggggctctg ggcgccatgg ctttcctgat ctgaccacgc actctggggc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

<210> 364
 <211> 136
 <212> PRT
 <213> Homo sapiens

```

<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
          20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
          35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
          50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```

85 90 95
 Ala Phe Met Lys Val Leu Asn Ser Leu Gln Lys Lys Gln Met Asn Thr
 100 105 110
 Ser Leu Cys Glu Arg Ile Trp Lys Val Tyr Gly Asp Leu Glu Cys Glu
 115 120 125
 Tyr Cys Gly Lys Leu Phe Trp Tyr
 130 135

<210> 365

<211> 333

<212> DNA

<213> Homo sapiens

<400> 365

atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
 60
 ccactgatcg ttgggattct atttgggggt gagaccctct ctggagtcct tgctggtgcc
 120
 cttgtctctg gtgttcagat tgccatttct gcatccaaca ctggtggtgc ctgggacaaac
 180
 gccaaagaagt acattgaggc tggagtttca gagcatgccca ggacccttgg cccaaaaggt
 240
 tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
 300
 tctggccctt ccctcaacat cctcatcaag ctt
 333

<210> 366

<211> 111

<212> PRT

<213> Homo sapiens

<400> 366

Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro Pro Gly Ala Leu
 1 5 10 15
 Val Met Leu Thr Pro Leu Ile Val Gly Ile Leu Phe Gly Val Glu Thr
 20 25 30
 Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly Val Gln Ile Ala
 35 40 45
 Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn Ala Lys Lys Tyr
 50 55 60
 Ile Glu Ala Gly Val Ser Glu His Ala Arg Thr Leu Gly Pro Lys Gly
 65 70 75 80
 Ser Asp Pro His Lys Ala Ala Val Ile Gly Asp Thr Ile Gly Asp Pro
 85 90 95
 Leu Lys Asp Thr Ser Gly Pro Ser Leu Asn Ile Leu Ile Lys Leu
 100 105 110

<210> 367

<211> 381

<212> DNA

<213> Homo sapiens

<400> 367

gcgttcgctcg cactacccgg cggcggcgga acccttgacg agctactcga agcatggaca
 60
 tggcagcagc tcggtgtaca cagcaaaccg gtgngccttg tacgactcga cnncttctgg
 120
 gcaccgctga ccgcgctact caaccacatg accatcgaaa gcttcattcg ccctgaggac
 180
 cgcgcctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg
 240
 accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca
 300
 ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct
 360
 cngttcaggt ggcccgaat g
 381

<210> 368

<211> 89

<212> PRT

<213> Homo sapiens

<400> 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1			5					10					15		
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
		20					25					30			
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
		35				40					45				
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
	50					55				60					
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65					70				75					80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
					85										

<210> 369

<211> 313

<212> DNA

<213> Homo sapiens

<400> 369

gatacatgat cctctcatat cgcacacaca ccgctcccct ctgcgcgaat tcgcagacaa
 60
 acttgccgag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc
 120
 gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac
 180
 acattctacg agcagcaagc gaccagtctc cttcgccagc tgaacgacct cccacccgaa
 240
 gagcttcccg acgtcatcga ggacttcttc cgcctgtcca ctgatgtcct tctttaccat
 300
 ttccagcaag ctt
 313

<210> 370

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 370
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
 1 5 10 15
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
 20 25 30
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
 35 40 45
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
 50 55 60
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro
 65 70 75 80
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr
 85 90 95
 His Phe Gln Gln Ala
 100

<210> 371
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 371
 atgacgggtc acgtcatcct ggcgattcca cagggtggtga cgatcatggat cggcctcatc
 60
 tgcacgcgca ttggcacggg ctttatcaag ccgaacctct ccacgggtggt aggaggtctt
 120
 tacgatgacg gtgacccccg ccgcatcag ggtttcctgt acttctacat gtcgatcagt
 180
 attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac
 240
 gtaggtttca ttgccgtgc tatcggtatg gctctgggtc tgatcgctt cttccacggg
 300
 cgttccaaac tgcgtgagct cgccttcgac atccccaatc cgctggcccc cggcgagggt
 360
 cgccggatgg tgctccgagg
 380

<210> 372
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
 1 5 10 15
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
 20 25 30
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
 35 40 45
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```

      50              55              60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65              70              75              80
Val Gly Phe Ile Ala Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
      85              90              95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
      100              105              110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
      115              120              125

```

<210> 373

<211> 475

<212> DNA

<213> Homo sapiens

<400> 373

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acatgttgga aaaattgcct ccctactctgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
120
gcttctctct gggttcctaaa tcctttggcc aaacattttc cccacaaccc tccactccag
180
ttggctggtc actgcctctc agaaagaagt ccaggtccc tgtcagcccc agagcgctg
240
catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggacccctac
300
acctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaaggtcca atccactcag ttcttaaagt aaaaacagtt
420
gcccatgagt ccccccaaa gacgtccgca catatgccaa acattcgggtg tgcac
475

```

<210> 374

<211> 109

<212> PRT

<213> Homo sapiens

<400> 374

```

Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
1              5              10              15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
      20              25              30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
      35              40              45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
      50              55              60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65              70              75              80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
      85              90              95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
      100              105

```

<210> 375
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 375
 nnacgcgtcg cctccacctc gaaacccgcc gccgggtcggt ttttcaccat ggccgaccgc
 60
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga
 120
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg
 180
 gcggcatgct ccttcatagc gccagtggtt gcgaagctgg gctgcccga gcgcactatg
 240
 ggcacggcgc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg
 300
 ttacatgagg tggctttgac gtgtctcttc ac
 332

<210> 376
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 376
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr
 1 5 10 15
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr
 20 25 30
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp
 35 40 45
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser
 50 55 60
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met
 65 70 75 80
 Gly Thr Ala Gln Leu Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro
 85 90 95
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe
 100 105 110

<210> 377
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 377
 gcggtgccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg
 60
 aggctggaac gagggtgct gtgttcggtg tggactcagg gaactgccgc agacgccgag
 120
 aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcaggt actcgaagct
 180
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttggttcggg caaggtggct
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cgggtgaactt
 300
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccggctcg
 360
 gtctgattc
 369

<210> 378
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 378
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu
 1 5 10 15
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr
 20 25 30
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala
 35 40 45
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg
 50 55 60
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala
 65 70 75 80
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys
 85 90 95
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val
 100 105 110
 Lys Xaa Lys Val Val Asp Arg Ser Val
 115 120

<210> 379
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 379
 acgcgttact taaacttacc tgtaaataat aaattcatta tttctagttg gttagggtact
 60
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca
 120
 gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctggt
 180
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcattaaa
 240
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat
 300
 gctaaatttg ctgaagctgc tgggtggtaaa ggctatggtg tgagagatgt aagtcgtctt
 360
 gacgacatcg ttgaagaggc aatgggtcaa gatgttccaa caatcggt
 408

<210> 380
 <211> 136
 <212> PRT

<213> Homo sapiens

<400> 380

```

Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
      65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

```

nagcggtcat aggcggggccc agtgggaagac cagccaaca cagttggttg agatccgcgt
60
tgaggggcaag gtctcgcgcg tcccgcgaaa tctggtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcggtccag catgactgct caggctcatt
180
accaaaacgc gtcgatcccg taggggtgtc gtcgatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcggtgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgactac gtcggcggtg ccttaagcaa tggctgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccaggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggctg gtggacgacg caaactcgtc
480
atccccacc accttgctta cgggtccgcaa ggaatctccg gtgtgatcgc tggcggtgag
540
acgctggtct tcgtctgcga ccttgtaaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

```

<210> 382

<211> 137

<212> PRT

<213> Homo sapiens

<400> 382

```

Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
 20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
 35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
 50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
 65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
 85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
 100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
 115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
 130          135

```

<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

```

nggagcaaca cctggtcctt gggaaatgaag tgtaggaggt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctccccctt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgttttagaa cctaggattc tgtttttccc aaacaggatc an
352

```

<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

```

Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
 20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
 35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```

50 55 60
 Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser
 65 70 75 80
 Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile
 85 90

<210> 385
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 385
 gccggcgcca cgaaatgcaa aatgcgccct tcaccggacg ccaggttgat cgagccgcca
 60
 gcacctcggg caatgtcctg ggcctgactg gcacacgcaa tcaaagcgag caacaacaca
 120
 caaaaacgca tcatgaggca gacgccaggg aagtgcagaga agccgcagca ggcgcgcggc
 180
 gattggaaat atcggtgagg ctaatggtca ccagcgcttg caggttgat tcggtggcca
 240
 attcgcgga cgacagcacc gccagttcca gctcgccgcg cagcaccagg cgacgcaage
 300
 tgcggcgcaa ctccgggtgc accaacaaca ccgcactgtt ca
 342

<210> 386
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 386
 Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser
 1 5 10 15
 Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu
 20 25 30
 Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr
 35 40 45
 Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met
 50 55 60
 Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp
 65 70 75 80
 Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu
 85 90 95
 Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe
 100 105

<210> 387
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 387
 acgcgtgacg cgccggcatc ggaagcggtg actgcagaga agaccgcgca cgtggctgtg
 60

ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc
 120
 atgcaagagg agcttgacaa tgtgcgtgat ctgccccatg cgcggcagca agcgctcgat
 180
 gctgttcggt ccgagctgct cgaagcgcag caagcatgtg cctcgtgccca gctgcagctg
 240
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac
 300
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct
 360
 gagaatgcga gcctgcgcg
 379

<210> 388

<211> 114

<212> PRT

<213> Homo sapiens

<400> 388

Met	Arg	Leu	Val	Arg	Asp	Gln	Val	Leu	Ala	Ala	Cys	Lys	Gln	Arg	Pro
1			5					10					15		
His	Gly	Ala	Pro	Gly	Ile	Trp	Asp	Ala	Leu	Ala	His	Asp	His	Leu	Ala
			20					25					30		
His	Ala	Ala	Ala	Ala	Ala	Gly	Thr	Arg	His	Met	Leu	Ala	Ala	Leu	Arg
			35				40					45			
Ala	Ala	Arg	Asn	Glu	Gln	His	Arg	Ala	Leu	Ala	Ala	Ala	His	Gly	Arg
			50			55					60				
Asp	His	Ala	His	Cys	Gln	Ala	Pro	Leu	Ala	Trp	His	Ala	Gln	Ala	Lys
65					70					75				80	
Arg	Arg	Arg	Val	His	Ala	Pro	Cys	Gln	Thr	Cys	Gln	His	Val	Pro	Gln
			85						90					95	
Pro	Arg	Ala	Arg	Ser	Ser	Leu	Gln	Ser	Thr	Leu	Pro	Met	Pro	Ala	Arg
			100					105					110		
His	Ala														

<210> 389

<211> 382

<212> DNA

<213> Homo sapiens

<400> 389

ngatggccga ctgtcccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg
 60
 ggccctccac gtgctccgca accctccgaa gcgatgacct ggccccgggg cggcaacgag
 120
 gtattgcgtt tggagacgct tgggggtcaat tacggccagg tgcgcgccgt cgatgccctg
 180
 acgaccaccg tagagcgagg caccatcacc tgcctcatgg gtcgaaatgg atcaggcaag
 240
 tcgtctctga tgtggggcat ccaaggggca acaaagtctt cagggagggt actggtcaac
 300
 cacgagggtt cttgggctga cccccgaaa gccgacgccg cgaccgctcg acgaatgggtg
 360

agcttagtcc cgcagtcagc cn
382

<210> 390
<211> 127
<212> PRT
<213> Homo sapiens

<400> 390
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val
1 5 10 15
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met
20 25 30
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly
35 40 45
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val
50 55 60
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys
65 70 75 80
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg
85 90 95
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp
100 105 110
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala
115 120 125

<210> 391
<211> 456
<212> DNA
<213> Homo sapiens

<400> 391
nnacgcgttg ccgctctgtg aggcgcctat cacggtgaca ctctcggtgc tatgagcgtg
60
tgcgacccta tcggtggcat gcacgccttg ttcagcgact ctattcccca gcagatcttc
120
ctgcccgcg cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga
180
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc
240
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt
300
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggcgg
360
actggcaaac ttttcgcatg cgagtgggcc gatatcgctc ctgacatcat ggtggttggg
420
aatccatga ctggcggata cctgaccag tcggcc
456

<210> 392
<211> 55
<212> PRT
<213> Homo sapiens

<400> 392

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Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro
 1             5             10             15
Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile
      20             25             30
Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly
      35             40             45
Asp Val Val Gln Arg Gly Arg
      50             55

```

<210> 393

<211> 371

<212> DNA

<213> Homo sapiens

<400> 393

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nacgcgttgc tcgtcattgg tggtactcgc gcctacgaag gtatctacac catgatgact
60
gagcgggacc ggtaccgggc tttccgtatt ccgacgggtgt gcatcccggc ttctatcgac
120
aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgatcatcgtc
180
gaggcgatgg acaagattaa ggagtcgggt atcgcggtcca gacgctgctt cgtcgtcgag
240
acgatggggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcgagc tggcgctgag
300
cggatctata ccaacgagga cggatatctc ctggacgatc tagccaacga cgtccattgg
360
ttgcgggagt c
371

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<210> 394

<211> 123

<212> PRT

<213> Homo sapiens

<400> 394

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Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr
 1             5             10             15
Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr
      20             25             30
Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu
      35             40             45
Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp
      50             55             60
Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu
      65             70             75             80
Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala
      85             90             95
Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp
      100            105            110
Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu
      115            120

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<210> 395
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 395
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 gcgacaggtg gtcttgtgca tggtagaaag gcagtccaag cctatgtctc tgaaacctgc
 120
 tctcatttct gttttctact ttacgattta tgttatctca tactcccat gttgcctggt
 180
 ctccagtttt ttacttgtg ttatttccat tcttctattc ctgctcaatt tctgcctcag
 240
 ggcagaattg tgtccaacag ctcttaaag cagcgagaa actgtgatgt taaaaacatc
 300
 ttgttatccg gccccaaac atgttgcctc tggtaactct tactggttg t
 351

<210> 396
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 396
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile
 1 5 10 15
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys
 20 25 30
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu
 35 40 45
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys
 50 55 60
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys
 65 70 75 80
 His Val Val Leu Gly Asn Ser Tyr Trp Phe
 85 90

<210> 397
 <211> 483
 <212> DNA
 <213> Homo sapiens

<400> 397
 gccgtcatta aagagatcac ccctctctc caacctggtg atgtcctcgt cgacggtggt
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 aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac
 120
 tatgttggtg ctggcatctc cgggtgggga gtcggggccc tgagggtccc atcaattatg
 180
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgac
 240
 cacgtcgacg gtgaaccctg ctgcgcatgg atgggtactg acggcgccgg acacttcgtc
 300

aagatgggtcc ataatggcat cgagtacgcc gatatgcagt tcattggcga ggcgcccttc
 360
 ctttttgcgn tgccegcggg ttgaccaat gctgaggccg ccgatgcctt cgagtcgtgg
 420
 aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaaag
 480
 gat
 483

<210> 398

<211> 161

<212> PRT

<213> Homo sapiens

<400> 398

Ala	Val	Ile	Lys	Glu	Ile	Thr	Pro	Leu	Leu	Gln	Pro	Gly	Asp	Val	Leu
1				5					10					15	
Val	Asp	Gly	Gly	Asn	Ala	Tyr	Phe	Gly	Asp	Thr	Arg	Arg	Arg	Glu	Glu
		20						25					30		
Glu	Ile	Arg	Pro	Thr	Gly	Ile	His	Tyr	Val	Gly	Thr	Gly	Ile	Ser	Gly
		35				40						45			
Gly	Gly	Val	Gly	Ala	Leu	Arg	Val	Pro	Ser	Ile	Met	Pro	Gly	Gly	Val
	50					55					60				
Lys	Glu	Ser	Tyr	Glu	Ile	Ile	Gly	Pro	Val	Leu	Glu	Lys	Ile	Ser	Ala
65				70						75				80	
His	Val	Asp	Gly	Glu	Pro	Cys	Cys	Ala	Trp	Met	Gly	Thr	Asp	Gly	Ala
			85						90					95	
Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly	Ile	Glu	Tyr	Ala	Asp	Met
			100					105					110		
Gln	Phe	Ile	Gly	Glu	Ala	Pro	Phe	Leu	Phe	Ala	Xaa	Pro	Ala	Gly	Leu
	115					120						125			
Thr	Asn	Ala	Glu	Ala	Ala	Asp	Ala	Phe	Glu	Ser	Trp	Asn	His	Gly	Asp
	130					135						140			
Leu	Asn	Ser	Tyr	Leu	Val	Glu	Ile	Thr	Ser	Arg	Val	Leu	Arg	Ala	Lys
145					150					155					160
Asp															

<210> 399

<211> 314

<212> DNA

<213> Homo sapiens

<400> 399

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 ggctcatcca cccatccact cattcaccca tctatccate cactcatcca cccatccagt
 120
 cattcactca tttgtccate cactcatgta cccatccact cattcgccca tttatccate
 180
 cactcaacca tccatccate caccatcca nctcatcate cgtccagtca cccatctate
 240
 caccatgta tccatccact catccacca tccatccate tgtccatcca cttatccacc
 300

catctactca ccca
314

<210> 400
<211> 104
<212> PRT
<213> Homo sapiens

<400> 400
Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln
1 5 10 15
Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile
20 25 30
His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr
35 40 45
His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile
50 55 60
His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile
65 70 75 80
His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile
85 90 95
His Leu Ser Thr His Leu Leu Thr
100

<210> 401
<211> 2165
<212> DNA
<213> Homo sapiens

<400> 401
gagaaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgatata ggtagtttta
60
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatgggtg
120
caaaatgaaa gatctattga agtttactta tacattgcat tgattgaacc ttggagagtt
180
ttatgaaaaa gaggggcatc ccttgccatc tgtttgccag tcttccttgc cccttccttt
240
gaaatgcctg cctctttttt gccagattg tttcctgacc atccgaactc agatggggtc
300
ctctaagttc ttcctggata ttcacaaatc ccttcacaag gccacgtgc gaagtgaatg
360
atctggaggt gcctgggcat ctgtgttgga agggagtcaa gactcaccag ccagtcagtt
420
tgtgggctac agttgtccca caaaaatcag gcatgttcac ctcccctctg ggcccctaca
480
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag
540
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc
600
tgagcctaca gttttgtact ggggtgcacg gatgacagct ggggaagatg aaaggcagct
660
tgaggattta tagcagctaa agggtaaatg ctgttatgca aaaggcccc atatgaactt
720

cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatga
780
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc
840
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagttg
900
aggcccgagt tacacaggct cccggaatac agacctggga agatagggga ggagagggga
960
agcttgtggc cttttgatcc gccccggaa tgcccaccgt gcgctgcttt gctgccttca
1020
tctcctgctc agaggccttc tccttcccag agacctcctt ggatgggtct aaggagagaca
1080
ctgccccggc ctttttccct gcaatcaciaa ggtccaaatc ctccaggctg cgcttgatcg
1140
gccgcgccgc cccaatgttc tacgggctca ttttccggtg caggattggg tggaccatgc
1200
cttccatctt cctgaaattc tccagtctca catggtgagg ttttctgat cttgaaagcg
1260
attcagggta ttttttaggg cctgacatgg tcatgggtga taccgcacag gctttggggt
1320
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg
1380
gccctgtggt ggaatgagcc aggccagga ccttgccggt aggtttgtgc gggttcttgg
1440
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1500
cttgacagtg caggacagtg agataattta catggagctt ttcttggtgt ctgtgggaag
1560
gaaaagaact gttttccgat tccctgtaca tgtccctgga agggatattt gatgtctgtt
1620
cattatgaag atggtgctcg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga
1680
agtcagccag gaagctaggc atgtgggaat gggggagggc ctttttctct aagagtttat
1740
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaaggggg ttaaggatga
1800
gcttgagaaa gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt
1860
cattgatggt ctttctctct tccgagggtc tgcttctgaa actctggacg tgctgaatca
1920
ctgatggccg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac
1980
tggaacacaa gtcaccccta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc
2040
cataagggtg gctgctggag aggctggccc cactcacttg ggacaaaagc tttttcttgg
2100
ccagtgggga catcatgctt ggggttggccc tagagtagag caggggctg taattaagtc
2160
catgg
2165

<210> 402

<211> 87

<212> PRT

<213> Homo sapiens

<400> 402

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Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1             5             10             15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
      20             25             30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
      35             40             45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
      50             55             60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65             70             75             80
Pro Asn Pro Pro Gly Cys Ala
              85

```

<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

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cccatgggtg tgtcccagga cggcgtcatg aagcgtcagg taaatgacaa ggaaacggtc
60
gcgcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag
120
ccttcgcccc cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcattgcta
240
cagcccgaca tggtcgtctt ggtggacgtc ggcacgaagc ccggccacct cgccctatac
300
catctatggc aggcattcta tcaccgacct accttgggcg gtgcttgcg cgaaattcat
360
gctatgatc
369

```

<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

```

Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1             5             10             15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
      20             25             30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
      35             40             45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
      50             55             60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65             70             75             80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```

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<210> 405
<211> 840
<212> DNA
<213> Homo sapiens
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<210> 406
<211> 91
<212> PRT
<213> Homo sapiens
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634

50 55 60
 Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu
 65 70 75 80
 Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg
 85 90

<210> 407
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 407
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 60
 aggtcttact ttgtcttgcc tggcttcagg gtgtagggga tggagagctg gacttccagc
 120
 ctgtctcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca
 180
 caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaagg
 240
 agatgctcgc tcggagtggg tgctctggct ctgggattcc aaaccaagct gccttctctg
 300
 atgtggcctt agtgctctgg gcggatgtac cttggctctg cctggaccct ctctctcttc
 360
 caggcctctg tcccaccagg atgatgcta tccagagctc attgtcctct ccacttctct
 420
 ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtgtt
 480
 gcactgagga ccacagcagc cctcgcatc ccacgggcaa aggggtatgt gtagg
 535

<210> 408
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala
 1 5 10 15
 Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu
 20 25 30
 Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met
 35 40 45
 Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro
 50 55 60
 Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys
 65 70 75 80
 Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys
 85 90 95
 Val

<210> 409
 <211> 375

<212> DNA

<213> Homo sapiens

<400> 409

ngtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttggg
 60
 ggacttccga ttacgactaa tatttctctt gccaaacaact tcaatatgga tgaaatttct
 120
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct
 180
 agaaaattga ccgaaattgc tggctctcag caaggggagt atcaggtgtc agatgcgact
 240
 gcagccttcc aagaagtgc acaattgttc ggctttataa ctacgattat tagtgccatt
 300
 gcaggaattt ccttttttgt tggagggact ggtgttatga acatcatgct ggtttcggtg
 360
 acggagcgta cgcgt
 375

<210> 410

<211> 125

<212> PRT

<213> Homo sapiens

<400> 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1				5					10					15	
Phe	Gly	Ile	Gly	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn
			20					25					30		
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
		35					40					45			
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
	50					55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr	
65					70				75					80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85						90					95	
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
			100					105					110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
			115					120					125		

<210> 411

<211> 409

<212> DNA

<213> Homo sapiens

<400> 411

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 60
 ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca
 120
 gcacgcggtc ggggcccctt gagctcgaag gcgcggcgca tcgggcagtg ctgcgcggcc
 180

tgggtcgcagg gcacgtcgta ctggtgcgag acgcggaagc acttgtggcc gatgtaggcg
 240
 cgatcggctg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tgttgactc
 300
 ccggtccacc acgatcatgg gctgggactc gtgttccagg tggggggcca gggcttgggc
 360
 ctgcggtgag cgcgtggggg ggatggggca tagcgtcggg gaggagggtg
 409

<210> 412
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 412
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro
 1 5 10 15
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val
 20 25 30
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln
 35 40 45
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser
 50 55 60
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala
 65 70 75 80
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr
 85 90 95
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp
 100 105 110
 Gly Asp Cys Gln Val Val Glu
 115

<210> 413
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 413
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggt agggactcca
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 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag
 120
 gcaccacctc catatcccg cccacatcca gctggacccc ctgtcatata gcagccaaca
 180
 acacccatgt ttgtagctcc cccccaaaag acccagcggc ttcttctc agaggcctac
 240
 ctgaaatata ttgaaggact cagtgcggag tccaacagca ttagcaagt ggatcagaca
 300
 ctggcagctc ggagacgcga cgtccatttg tcgaaagaac aggagagccg cctaccc
 357

<210> 414
 <211> 119
 <212> PRT

<213> Homo sapiens

<400> 414

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Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1           5           10           15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
      20           25           30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
      35           40           45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
      50           55           60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
65           70           75           80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
      85           90           95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Arg Asp Val His Leu Ser Lys
      100          105          110
Glu Gln Glu Ser Arg Leu Pro
      115

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<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

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tctagagcca acttggttat cgtaatgaat agagagacta catctatatc aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg ggcacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

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<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1           5           10           15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
      20           25           30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
      35           40           45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
      50           55           60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```


130	135	140
Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro		
145	150	155
Arg		160

<210> 419
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 419
 atttcacccc aggaaaacca gtaaggacca atgattaagc ccaaggttgg gtaccgagtt
 60
 cggatccata agtaccggcc gcccagggtg ctggaatttg ggctcccccc ggtgaaaata
 120
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtgggtg ggctgagctc
 180
 aagccccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc
 240
 gaacttctag taagcgcgcc ccgctgcaag cgaaagcact cccctgccaa gaaacagatc
 300
 ttttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta
 360
 catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg
 420
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa
 480
 tttcagtgtg gcagtgcacg cagattcttc attggtgtta gtgtatttcc atacggtatg
 540
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt
 600
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat
 660
 aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaaattttg
 720
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct
 780
 tgaatgatgg ctggcca
 797

<210> 420
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu
 1 5 10 15
 Arg Cys Leu Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys
 20 25 30
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn
 35 40 45
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg

```

      50              55              60
Thr Leu Ser His Thr Asn Val Leu Ser Pro Glu Asn Val Lys Asp Phe
65              70              75              80
His Gln Pro Leu Pro Asp Ser Pro Asn Leu Glu Asn Val Met Ser Thr
      85              90              95
Leu Gln Ile Met Tyr Thr Leu Phe Val Gln
      100              105

```

<210> 421
 <211> 406
 <212> DNA
 <213> Homo sapiens

```

<400> 421
ggatccacca tgatggagcc caccaccca tctcagtc acctgctgca gcttctccat
60
aaccaaacac aggtcaatct tgtctcccta aacacaccat gtgctctcat gctgccatgg
120
tttgccctggg gccctctcta cctcctctgc tttctggaga acccttgac tcctcccaag
180
ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgctgga
240
ttcatgaaga ttggttctact gtcagccct gaccagaacg tgtgttttag gaaagcagga
300
accaagtctt accaatgtct gtagtccag cctccaccct ggcatacagt aggtgctcat
360
tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
406

```

<210> 422
 <211> 104
 <212> PRT
 <213> Homo sapiens

```

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
1              5              10              15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
      20              25              30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
      35              40              45
Leu Glu Asn Pro Cys Thr Pro Lys Pro Ser Ser Trp Lys Val Asn
      50              55              60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65              70              75              80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
      85              90              95
Gly Thr Lys Ser Tyr Gln Cys Leu
      100

```

<210> 423
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 423

ngccacccta cgcctcgcct gcaatggcaa cttcagatcc ccggtggcac cgtagtctta
 60
 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agagggagaa
 120
 ggagatgggg atttgctgac gcagacccaa gcccaaacgc cgactccagc acccgcttgg
 180
 ccggcgcccc cagccacacc gcgttctctg gccctcgcaa atggctccct gttggtgccc
 240
 ctcttgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcggc
 300
 aactctacgt caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc
 360
 gccgggggag aaccgacgg acaggccccg acctctgagc gcaagtccac agccaagggc
 420
 cggggcaaca gcgtcctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc
 480
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgagggagag
 540
 gaggccgaag accagatcct cgcggaccgc gcggaggagc agcgtgtgtg caacggggac
 600
 ccctctcggc acgtttctaa ccacgcgt
 628

<210> 424

<211> 209

<212> PRT

<213> Homo sapiens

<400> 424

Xaa His Pro Thr Pro Arg Leu Gln Trp Gln Leu Gln Ile Pro Gly Gly
 1 5 10 15
 Thr Val Val Leu Glu Pro Pro Val Leu Ser Gly Glu Asp Asp Gly Val
 20 25 30
 Gly Ala Glu Glu Gly Glu Gly Glu Gly Asp Gly Asp Leu Leu Thr Gln
 35 40 45
 Thr Gln Ala Gln Thr Pro Thr Pro Ala Pro Ala Trp Pro Ala Pro Pro
 50 55 60
 Ala Thr Pro Arg Phe Leu Ala Leu Ala Asn Gly Ser Leu Leu Val Pro
 65 70 75 80
 Leu Leu Ser Ala Lys Glu Ala Gly Val Tyr Thr Cys Arg Ala His Asn
 85 90 95
 Glu Leu Gly Ala Asn Ser Thr Ser Ile Arg Val Ala Val Ala Ala Thr
 100 105 110
 Gly Pro Pro Lys His Ala Pro Gly Ala Gly Gly Glu Pro Asp Gly Gln
 115 120 125
 Ala Pro Thr Ser Glu Arg Lys Ser Thr Ala Lys Gly Arg Gly Asn Ser
 130 135 140
 Val Leu Pro Ser Lys Pro Glu Gly Lys Ile Lys Gly Gln Gly Leu Ala
 145 150 155 160
 Lys Val Ser Ile Leu Gly Glu Thr Glu Thr Glu Pro Glu Glu Asp Thr
 165 170 175
 Ser Glu Gly Glu Glu Ala Glu Asp Gln Ile Leu Ala Asp Pro Ala Glu

180 185 190
 Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser Asn His
 195 200 205
 Ala

<210> 425
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 425
 ccggccgctcg aagactttga ggacgatgta gctcgcagcg cagcggttacg agccctggag
 60
 tacgtggatt tgacccagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta
 120
 ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgaggttcc caaaggacga
 180
 catatcgag cgggcacccg gatgctcgtc gccctggat ctgctcgtgt ccgtctgcag
 240
 gctatggagg aaggcctcga cgagatcggg tcccggtttg ctgacatctt tcgcaataac
 300
 tctgcgaaca atggcttggt actggctcag gttgacccg aggtcgtcga agagttgtgg
 360
 gactttgccg agcagcatcc tggtagagcag ctacccgtct ccctcgagaa tcggacgatc
 420
 aaccttcggg gtcgcacgac ctaccggttc catattgatg acgtcacgcg t
 471

<210> 426
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 426
 Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu
 1 5 10 15
 Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val
 20 25 30
 Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu
 35 40 45
 Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala
 50 55 60
 Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln
 65 70 75 80
 Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile
 85 90 95
 Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp
 100 105 110
 Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly
 115 120 125
 Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly
 130 135 140
 Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg

145

150

155

<210> 427

<211> 546

<212> DNA

<213> Homo sapiens

<400> 427

ctagcggtag tagaaggat gcagttgat cgcggctact tgtctccgta tttcatcaac
60
aatcaagaaa caatgaatgc agagctagaa aacccattta ttcttcttgt tgataagaaa
120
atttctaata tccgtgactt gctaccaatt ttggaagggtg ttgctaaagc atcgcgccca
180
ttgttgatca ttgcggaaga cgttgaaggc gaagcgttgg caaccttggg ttgtaacact
240
atgcgcggca tcgtaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa
300
gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc
360
attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcgt tacattgaca
420
aaagaaagta caacgattgt tgatgggtgcg ggtgttcgag ctaatattac tggtcgtgtt
480
gagcaaattc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa
540
gaacgc
546

<210> 428

<211> 182

<212> PRT

<213> Homo sapiens

<400> 428

Leu Ala Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro
1 5 10 15
Tyr Phe Ile Asn Asn Gln Glu Thr Met Asn Ala Glu Leu Glu Asn Pro
20 25 30
Phe Ile Leu Leu Val Asp Lys Lys Ile Ser Asn Ile Arg Asp Leu Leu
35 40 45
Pro Ile Leu Glu Gly Val Ala Lys Ala Ser Arg Pro Leu Leu Ile Ile
50 55 60
Ala Glu Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr
65 70 75 80
Met Arg Gly Ile Val Lys Val Ala Ala Lys Ala Pro Gly Phe Gly
85 90 95
Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Val Leu Thr Gly Ser
100 105 110
Thr Val Ile Ser Glu Glu Ile Gly Ile Lys Leu Glu Glu Ala Thr Ile
115 120 125
Glu Gln Leu Gly Thr Ala Lys Arg Val Thr Leu Thr Lys Glu Ser Thr
130 135 140
Thr Ile Val Asp Gly Ala Gly Val Ala Ala Asn Ile Thr Gly Arg Val

145 150 155 160
Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys
 165 170 175
Glu Lys Leu Gln Glu Arg
 180

```
<210> 429
<211> 425
<212> DNA
<213> Homo sapiens
```

```
<400> 429
gctagcagcc cttacaggag acgggctaataataatgcag cagtgggtcc gacaacttgc
60
ccgttgccgc cggtcacgga tccatttgc tttagtagac aggcgtcca aagtacacca
120
ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcagggttt
180
tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc
240
ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg
300
tgcatcgaca ccttcagcac ctctggggc tgagatgaac aggagtgcag aggtcggtcc
360
cagttcagag cctgaagttc agactctgcc atatcttct cactacattc caggagtggg
420
tcctg
425
```

```
<210> 430
<211> 130
<212> PRT
<213> Homo sapiens
```

```

<400> 430
Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile
  1              5              10              15
His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val
      20              25              30
Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly
      35              40              45
Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn
  50              55              60
Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro
65              70              75              80
Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro
      85              90              95
Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu
      100             105             110
Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val
      115             120             125
Asp Pro
      130

```

<210> 431
 <211> 192
 <212> DNA
 <213> Homo sapiens

<400> 431
 ctagccatcc accagcgtag acacacggga gagaggccct acactggcct cgggtgcaac
 60
 cgccgcttcc gccagcgtag ggcctctgtc atccaccagc gcatccacac gggcgagaag
 120
 cctnaccogt gcccggtactg cgagcggcgc ttctctctct cctctcgctt ggtcagtcac
 180
 cggcgtgtgc ac
 192

<210> 432
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 432
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly
 1 5 10 15
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His
 20 25 30
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu
 35 40 45
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His
 50 55 60

<210> 433
 <211> 635
 <212> DNA
 <213> Homo sapiens

<400> 433
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac
 60
 ctcatggagg agcgtggcgc gtatgcggag gccgccgcgc tcatgccgct gctgctccgg
 120
 accgaccgag gcgcgtggga cacgtttgtg tgctgctacc tcgagcggca ccaaagggat
 180
 gccgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc
 240
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg
 300
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc
 360
 agccgcacgc tgctcgagtg cctgcacag ctgtacatgg ccgcacatca gcccggaag
 420
 gctctgacat actacatgag cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtag
 480
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc
 540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac
 600
 tcgattccca tccagcgcgc catggcgcag ctcga
 635

<210> 434
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 434
 Xaa Pro Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu
 1 5 10 15
 Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala
 20 25 30
 Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr
 35 40 45
 Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro
 50 55 60
 His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu
 65 70 75 80
 Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr
 85 90 95
 Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala
 100 105 110
 Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu
 115 120 125
 Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr
 130 135 140
 Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr
 145 150 155 160
 Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu
 165 170 175
 Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met
 180 185 190
 Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met
 195 200 205
 Ala Gln Leu
 210

<210> 435
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 435
 nncgtacgtt cgcgtatattt ccgcgcccgg gaagctatcg ataataaagt tcaaccgctg
 60
 atccagcgtt agcaatggcg ggcacaggaa gggtagcttag gcatgcagaa agaaaagctt
 120
 tccgctctga tggatgggtga atcggttcgac agcgagctgt tgagttctct gtcgcaagat
 180
 cgaacgcttc aacaaaagctg gcagggctat cacctgatac gtgacacact gcgaggtgat
 240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa
 300
 cccgcccggc tggcgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag
 360
 aaaatgccgt tctgggacaa agtgcgcccc tgggcgagcc agattacgca aatcggatatg
 420
 gcggcctgcg tgcgctggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg
 480
 ccatcgaacg cgt
 493

<210> 436

<211> 130

<212> PRT

<213> Homo sapiens

<400> 436

Met	Gln	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Met	Asp	Gly	Glu	Ser	Phe	Asp
1				5					10					15	
Ser	Glu	Leu	Leu	Ser	Ser	Leu	Ser	Gln	Asp	Arg	Thr	Leu	Gln	Gln	Ser
			20					25					30		
Trp	Gln	Gly	Tyr	His	Leu	Ile	Arg	Asp	Thr	Leu	Arg	Gly	Asp	Val	Gly
		35				40					45				
Gln	Val	Met	His	Leu	Asp	Ile	Ala	Asp	Arg	Val	Ala	Ala	Ala	Leu	Glu
	50				55					60					
Lys	Glu	Pro	Ala	Arg	Leu	Val	Pro	Ser	Ala	Val	Gln	Glu	Ser	Gln	Pro
65					70					75				80	
Gln	Pro	His	Thr	Trp	Gln	Lys	Met	Pro	Phe	Trp	Asp	Lys	Val	Arg	Pro
				85					90					95	
Trp	Ala	Ser	Gln	Ile	Thr	Gln	Ile	Gly	Met	Ala	Ala	Cys	Val	Ser	Leu
			100					105					110		
Ala	Val	Ile	Val	Gly	Val	Gln	Gln	Tyr	Asn	Gln	Pro	Ser	Ala	Pro	Ser
		115					120						125		
Asn	Ala														
	130														

<210> 437

<211> 447

<212> DNA

<213> Homo sapiens

<400> 437

ntggtaaccg gtgtccctga tatggaccct gctgtgtag agcgtaaatt atttatttta
 60
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caactttttc
 120
 attaatacat tctcatataa aacaatcggt tataaagggtc agttaaccac tgaacaagtg
 180
 ccacaatatt tcttagattt acaaaatcca agtatggtaa cggcattagc gcttgttcat
 240
 tcacgtttct caacaaatac atttcctcgt tggcgtttag cacaaccatt ccgttacatc
 300
 gtcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa
 360

gcgttacttg aagctgaatt ttctactcgc tcagaattag atatgttaat gccaatctgt
 420
 acggatggta tgtctgactc ggcaagg
 447

<210> 438
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 438
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys
 1 5 10 15
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val
 20 25 30
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr
 35 40 45
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe
 50 55 60
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His
 65 70 75 80
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro
 85 90 95
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn
 100 105 110
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe
 115 120 125
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met
 130 135 140
 Ser Asp Ser Ala Arg
 145

<210> 439
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 439
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag
 60
 cttcccaggg gccggctgga cctggccacg caaagcctga cggaggagac ctgcagggcc
 120
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggctcctgag tgactgcatg
 180
 ctcagcgagg aagggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc
 240
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc
 300
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg
 360
 gacgatgcct tcgccacctt ctgcgggggc ctggc
 395

<210> 440

<211> 128
 <212> PRT
 <213> Homo sapiens

<400> 440
 Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
 1 5 10 15
 Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
 20 25 30
 Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
 35 40 45
 Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
 50 55 60
 Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
 65 70 75 80
 Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
 85 90 95
 Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
 100 105 110
 Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
 115 120 125

<210> 441
 <211> 364
 <212> DNA
 <213> Homo sapiens

<400> 441
 gccagtgact acgtgaacat gttcgatgcc gagcagggct tcttcgacag gcgcagcccg
 60
 ggctggcgagt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc
 120
 gacggttgga acttcgcctt ccacgtcca caggacggcc gggggctggc cgcgctctac
 180
 ggctgtccga aaggcttgga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcg
 240
 gacaagccgg cgtacggcgg aatccacgaa atggctgagg ccagagcggc cgggatgggc
 300
 caattgggca tgtccaacga gccctcgac catattccct acatctacaa ctatgccggc
 360
 gcgc
 364

<210> 442
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 442
 Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
 1 5 10 15
 Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
 20 25 30
 Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His


```

      35              40              45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
      50              55              60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
      65              70              75              80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
      85              90              95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
      100             105             110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
      115             120

```

<210> 443
 <211> 430
 <212> DNA
 <213> Homo sapiens

```

<400> 443
accggttacg gctcagtgc acaagagatg ttccgccaaca acctcgtgcg gatgccgctg
60
ctcatggtgc tggcaatccc cttcgccaag atcctctcga cgaccctgtc catcggtatcg
120
ggcgggtccgg cggcgtcttc cggccctggc atggtcatcg gcggagccac tggcgcgga
180
ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag tttcgtcatt
240
gtcggcatga tcgcctgctt cgggtcggtt gcccatgccc cactcggcgt gctgctcatg
300
gttggcgaga tgaccggaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtcgccgtc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agtcaagga tcgcctggag
420
ggcgacgcgt
430

```

<210> 444
 <211> 143
 <212> PRT
 <213> Homo sapiens

```

<400> 444
Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
1      5      10      15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
20     25     30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
35     40     45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
50     55     60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65     70     75     80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
85     90     95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

```

	100		105		110										
Pro	Gly	Met	Ile	Ala	Val	Ala	Val	Ala	Gly	Arg	Val	Val	Gly	Asp	Thr
	115		120		125										
Ser	Ile	Tyr	Thr	Ser	Gln	Leu	Lys	Asp	Arg	Leu	Glu	Gly	Asp	Ala	
	130				135						140				

<210> 445
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 445
 ccattggggct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt
 60
 tcttgcttta ttgctcacc tgtccagggt tccctctgtt tgtgaggag ctgctgccac
 120
 cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtggagg acttttcctt
 180
 agttttcttt gctcttctgc tctgagtcca gccctggctg gacctttgat cccttctctc
 240
 tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc
 300
 caagtgggaa caagccatga aggagctgca ccccggaag tctgagggtg ggacacgcgt
 360

<210> 446
 <211> 101
 <212> PRT
 <213> Homo sapiens

	1		5		10		15		20		25		30		35		40		45		50		55		60		65		70		75		80		85		90		95		100	
Met	Ala	Cys	Ser	His	Leu	Glu	Met	Ala	Ser	Gln	Ile	Leu	Lys	Arg	Gln																											
Lys	Lys	Lys	Val	Arg	Lys	Phe	Pro	Asp	Lys	Glu	Arg	Arg	Asp	Gln	Arg																											
Ser	Ser	Gln	Gly	Trp	Thr	Gln	Ser	Arg	Arg	Ala	Lys	Lys	Thr	Lys	Glu																											
Lys	Ser	Ser	His	Gln	Glu	Ala	Asp	Leu	Arg	Ser	Phe	Met	Leu	Pro	Gly																											
Pro	Lys	Val	Ala	Ala	Ala	Pro	Ser	Gln	Thr	Glu	Gly	Thr	Leu	Asp	Arg																											
Val	Ser	Asn	Lys	Ala	Arg	Asn	Leu	Pro	Cys	Trp	Cys	His	Gln	Leu	Arg																											
Gly	Leu	Pro	Arg	Gly																																						

<210> 447
 <211> 487
 <212> DNA
 <213> Homo sapiens

<400> 447
 acgcgtgaag ggggaaattg ctcgtgccac ctgaggatta atcattaccc tggaaccctt
 60

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc
 120
 gagtgaggct gaggtcatgg agaagggaat ggggggcccc catggccagc tggacctgat
 180
 cactgcctcc ccactcagcc acagccctca gggccctgtg ccagtccaga agccattca
 240
 gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttcccca gtgccccaac
 300
 catagcgttt tccccaaac accctcagga aggagggacc actacctgtg cagggggggc
 360
 caggagcctc ctgagagcct catatgggga ggaagtggta ccatctcacc cccattgcct
 420
 ttctctcta cttccacctg gccagcttcc ctgagtccc ctctgcctc agtgccctt
 480
 cacgcgt
 487

<210> 448
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 448
 Met Glu Lys Gly Met Gly Gly Pro His Gly Gln Leu Asp Leu Ile Thr
 1 5 10 15
 Ala Ser Pro Leu Ser His Ser Pro Gln Gly Pro Val Pro Val Gln Lys
 20 25 30
 Pro Ile Gln Gly His Leu Trp Pro Met Phe Cys Phe Ile Cys Glu Ala
 35 40 45
 Thr Phe Pro Ser Ala Pro Thr Ile Ala Phe Ser Pro Lys His Pro Gln
 50 55 60
 Glu Gly Gly Thr Thr Thr Cys Ala Gly Gly Ala Arg Ser Leu Leu Arg
 65 70 75 80
 Ala Ser Tyr Gly Glu Glu Val Val Pro Ser His Pro His Cys Leu Ser
 85 90 95
 Leu Leu Leu Pro Pro Gly Gln Leu Pro Ser Val Pro Leu Leu Pro Gln
 100 105 110
 Cys Pro Phe Thr Arg
 115

<210> 449
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 449
 gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttggga gcaggccaag
 60
 gagaaggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac
 120
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg
 180
 gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc
 240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca
 300
 gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt
 353

<210> 450

<211> 117

<212> PRT

<213> Homo sapiens

<400> 450

Glu	Leu	Ser	Gln	Leu	Glu	Phe	Glu	Lys	Arg	Gln	Leu	His	Arg	Asp	Leu
1			5					10					15		
Glu	Gln	Ala	Lys	Glu	Lys	Gly	Glu	Arg	Ala	Glu	Lys	Leu	Glu	Arg	Glu
		20					25					30			
Leu	Gln	Arg	Leu	Gln	Glu	Glu	Asn	Gly	Arg	Leu	Ala	Arg	Lys	Val	Thr
	35					40					45				
Ser	Leu	Glu	Thr	Ala	Thr	Glu	Lys	Val	Glu	Ala	Leu	Glu	His	Glu	Ser
	50				55					60					
Gln	Gly	Leu	Gln	Leu	Glu	Asn	Arg	Thr	Leu	Arg	Lys	Ser	Leu	Asp	Thr
65				70				75					80		
Leu	Gln	Asn	Val	Ser	Leu	Gln	Leu	Glu	Gly	Leu	Glu	Arg	Asp	Asn	Lys
		85						90					95		
Gln	Leu	Asp	Ala	Glu	Asn	Leu	Glu	Leu	Arg	Arg	Leu	Val	Glu	Thr	Met
	100						105					110			
Arg	Arg	Arg	Gln	Arg											
	115														

<210> 451

<211> 444

<212> DNA

<213> Homo sapiens

<400> 451

gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa
 60
 gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cgtaaatggt
 120
 gcagaagttt taatgttggg agaaatgctg actttaccac agaattttgg gaatatattt
 180
 ttgggagaga ccttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa
 240
 gacatattag taaaagctga tcttcagaca agttctcagc gtttaaactt ttcagcctcc
 300
 aatgctgcag tggctgaact taaaccggat tgttgattg atgatgtcat acatcatgaa
 360
 gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga
 420
 gaaaaaatgt atttcagaaa attt
 444

<210> 452

<211> 148

<212> PRT

<213> Homo sapiens

<400> 452

```

Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
      20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
      35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
      50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
      85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
      100          105          110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
      115          120          125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
      130          135          140
Phe Arg Lys Phe
145

```

<210> 453

<211> 373

<212> DNA

<213> Homo sapiens

<400> 453

```

gctagctctg accccacctt tgccaagtgg cactaggggtg gccaatgggg actaggggtg
60
tataattgga aaatacagtc tcccctgttg tccaagaaag gcccagatg acctggggct
120
tgaaaggcac tcccgctggg tgcttctctg gagcaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttctctg gagacaccct ggccatcatt
360
tctgacaacg cgt
373

```

<210> 454

<211> 108

<212> PRT

<213> Homo sapiens

<400> 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

```

      20      25      30
Gln Ala Ser Pro Ser Gln Asn Ala Pro Val Gly Leu Arg Ala Gln His
      35      40      45
Leu Pro Trp Ser Trp Gly Cys Ser Ala Gln Thr Gly Pro Ala Ala Pro
      50      55      60
Leu Pro Pro Thr Cys Ser Gln Glu Ala Pro Ser Gly Ser Ala Phe Gln
      65      70      75      80
Ala Pro Gly His Leu Gly Pro Phe Leu Asp Asn Arg Gly Asp Cys Ile
      85      90      95
Phe Gln Leu Tyr Asn Pro Ser Pro His Trp Pro Pro
      100      105

```

<210> 455
 <211> 602
 <212> DNA
 <213> Homo sapiens

```

<400> 455
cctaggcaaa gcatgcccac cctacctccc cttaccctta cccttcattt tcccctaagc
60
acccatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccaccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagctttgta ggggtgtggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtctt ttttctctcg cccctctca ctgacctggt tttgatgcca
360
gacagcacag atgggctagg gaggcagggtg ggggaagcaga gatctgcgtc tcttggaagt
420
ggagctgggtg ggtggggctc cttcctgggtg ctgcggaggc tcattgggga ggtggcagcg
480
accccctcag gagcctctgt cgctgcact cagatctgtg cctttccaca gcgcccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

```

<210> 456
 <211> 100
 <212> PRT
 <213> Homo sapiens

```

<400> 456
Met Pro Thr Leu Pro Pro Leu Thr Leu Thr Leu His Phe Pro Leu Ser
1      5      10      15
Thr His His His Arg Cys Tyr Cys Met Cys Leu Leu Thr Leu Thr Ala
20      25      30
His His Pro His Trp Asn Val Arg Thr Thr Lys Ala Gly Leu Leu Ala
35      40      45
Ala Leu Ala Thr Ala Gly Ser Pro Glu Leu Cys Arg Val Leu Gly Thr

```

```

      50              55              60
Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
65              70              75              80
Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
      85              90              95
Leu Ala Thr Tyr
      100

```

<210> 457
 <211> 324
 <212> DNA
 <213> Homo sapiens

```

<400> 457
acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gcccccgacc
60
agaggtcagg gaacttttct tattattctg cacgtgccca gggatagtca aaccaggtct
120
tcccccttctg ctggccgcaa cacgccagcc gccgccacga ccgcacgctg aattcatgac
180
ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
240
tcgttttctg tccactggcc agcgccacta tgatcaggtg gggatatccgc ccggcggcgg
300
gagcaccggg acgccggggc gccg
324

```

<210> 458
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 458
Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
1              5              10              15
Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
      20              25              30
Ile Val Lys Pro Gly Leu Pro Leu Leu Leu Ala Ala Thr Arg Gln Pro
      35              40              45
Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
      50              55              60
Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
65              70              75              80
Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
      85              90              95
Gly Gly Ser Thr Gly Thr Pro Gly Arg
      100              105

```

<210> 459
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 459

acgcgttcat tcggcatctg cttccatgga tttcctgcgg ggaggcgcg cccagagtg
 60
 ggggtgtcgaa cacgacactt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg
 120
 ctggggttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccgggtggtt
 180
 tatgctgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg
 240
 agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa tcttcctcgc
 300
 ctccctcaaag ccgatcatcg gcatgccagg tttgtgggtg aatgcttcga tcaacacact
 360
 aggatcggtg ggggtccacca catacaccga gcggcaatcg agcggatacg acctc
 415

<210> 460

<211> 105

<212> PRT

<213> Homo sapiens

<400> 460

Met	Pro	Met	Ile	Gly	Phe	Glu	Glu	Ala	Arg	Lys	Ile	Arg	Arg	Gly	Leu
1				5					10					15	
Arg	Lys	Ser	Asp	Ala	Gln	Leu	Ser	Gly	Glu	Ala	Ser	Pro	Phe	Lys	His
			20					25					30		
Val	Gln	Ile	Pro	Arg	Glu	Gly	Arg	Ala	Gln	Ser	Ser	Ala	Gly	Ser	Ile
		35				40					45				
Asn	His	Arg	Asn	Arg	Ala	Ala	Arg	Asp	Gln	Glu	Arg	Glu	Arg	Lys	Arg
	50				55					60					
Leu	Glu	Ala	Gln	Arg	Gln	Asp	Pro	Ser	Arg	Pro	Val	Val	Glu	Thr	Ile
65				70					75					80	
Thr	Glu	Val	Ser	Cys	Ser	Thr	Pro	Ala	Leu	Ser	Ala	Ala	Pro	Pro	Arg
			85					90						95	
Arg	Lys	Ser	Met	Glu	Ala	Asp	Ala	Glu							
			100					105							

<210> 461

<211> 357

<212> DNA

<213> Homo sapiens

<400> 461

acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt ggctcacaac
 60
 cgggtcacat gcatgatgac aaaaactggc agaataagagt tgatgtcatc ccgtctacca
 120
 gctcctagaa ccagctcaga gagtcccggg gtcgggtaccg tcgagactca gtacacaact
 180
 gtcgagatac cggacgaccc tcttcatctg gttgcagatg ggcgtctcaa tcacgtcact
 240
 gtcgcttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt
 300
 catgcgctta ctgggtgatg ccatgcagcc ggatttcacc ccggtgtagt ccgtccg
 357

<210> 462
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 462
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val
 1 5 10 15
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile
 20 25 30
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser
 35 40 45
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro
 50 55 60
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr
 65 70 75 80
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala
 85 90 95
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe
 100 105 110
 His Pro Gly Val Val Arg Pro
 115

<210> 463
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 463
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac
 60
 gaggcagctg gtgacgatga agtgggtgcga tgcgaggaat gcgatcgtat cctgggtgcgt
 120
 accggagagt ccatctgagc ccttcttctg gcggtgatgc cgggatatcc gtagaattag
 180
 cggtcggacg agccatccgg gtgatcgcgg cagcgggtgag ttgtcgagga aagtcggggc
 240
 tccatagagc aggggtggtgg gtaacgcccc cccgggggtga cccgcgggaa agtgccacag
 300
 agaacagact gccggtttcg agccgggtgag ggtgaaacgg tggagtaagt gccaccgcg
 360
 tcatcggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga
 420
 ggtcgcggac gcgt
 434

<210> 464
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1           5           10           15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20           25           30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35           40           45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50           55           60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65           70           75           80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85           90           95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100          105          110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115          120          125

```

<210> 465
 <211> 438
 <212> DNA
 <213> Homo sapiens

```

<400> 465
gatcatttag aatttatgga agaagctgat gtgaaagcta tggtaaatac tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcggttat cattacgggt aatgatgaat atggcatgta ccttggttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaaag cggtggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattgggt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

<210> 466
 <211> 143
 <212> PRT
 <213> Homo sapiens

```

<400> 466
Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
1           5           10           15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20           25           30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35           40           45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50           55           60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

65 70 75 80
 Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
 85 90 95
 Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
 100 105 110
 Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
 115 120 125
 Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
 130 135 140

<210> 467
 <211> 460
 <212> DNA
 <213> Homo sapiens

<400> 467
 ntctccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcggttaagc
 60
 tgcattccctg caccttcttc tcccaccgct tcaaagccac agtgaggaac ttcggagctt
 120
 ctgcagtga agatggcggt ggaggaatgg atgccctggc tagaagaggc ggaatatctg
 180
 ttgatttgtt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
 240
 tccaggcaag caagaagggc ccagctgttt acctggttcc acttttccct ctctaccgg
 300
 ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggcccc
 360
 ttcctccagg cttgcctgtc acccggggtc ccgtcaaacc ctggccttcg tgcgacaaca
 420
 ctcttggtgc cttctatggt tctgtatgtt gccgcaattg
 460

<210> 468
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 468
 Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
 1 5 10 15
 Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
 20 25 30
 Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
 35 40 45
 Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
 50 55 60
 Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
 65 70 75 80
 Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
 85 90 95
 Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
 100 105 110
 Leu Tyr Val Ala Ala Ile

115

<210> 469
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 469
 cttgtgcaca cggtattttt ccaatacaaa tagtttaaaa agtaaaactcc aaatacctat
 60
 aagccccctc aaagcacctt ccaaatatga accttgtaa tgcccaagggt ccagaggggt
 120
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcgggggtccc catgctgact
 180
 ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct
 240
 tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag
 300
 ccctgagttc ctggctagct gtggttaacc acaaaaaatg cgggggggtga tgattttcga
 360
 agtccatcgg caaagaaaga c
 381

<210> 470
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 470
 Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr
 1 5 10 15
 Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu
 20 25 30
 Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln
 35 40 45
 Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser
 50 55 60
 Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe
 65 70 75 80
 Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly
 85 90 95
 Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe
 100 105 110

<210> 471
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 471
 accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgcc
 60
 gaggtcttcc tgggttaactg gttccgccgc ggcgacgatg gccgcttcct gtggccgngg
 120

cttggcgaaa acttcccggg cctanagtgg atcatcgacc gcattgaagg caacgtagag
 180
 gccgaggaca cgggtggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt
 240
 gacttcgatg tcgacgacgt tcgcgccgca ctgcgcgttg acccgaagga atgggaaggc
 300
 gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg
 360
 tggaaccagt tccgcgcc
 378

<210> 472

<211> 126

<212> PRT

<213> Homo sapiens

<400> 472

Thr	Gly	Asp	Tyr	Leu	Gln	His	Trp	Ile	Asp	Met	Gly	Lys	Lys	Gly	Gly
1				5				10						15	
Asp	Arg	Met	Pro	Glu	Val	Phe	Leu	Val	Asn	Trp	Phe	Arg	Arg	Gly	Asp
			20					25					30		
Asp	Gly	Arg	Phe	Leu	Trp	Pro	Xaa	Leu	Gly	Glu	Asn	Phe	Pro	Val	Leu
		35					40					45			
Xaa	Trp	Ile	Ile	Asp	Arg	Ile	Glu	Gly	Asn	Val	Glu	Ala	Glu	Asp	Thr
	50					55				60					
Val	Val	Gly	Arg	Thr	Ala	Arg	Ala	Glu	Asp	Ile	Asp	Leu	Gln	Gly	Leu
65					70					75				80	
Asp	Phe	Asp	Val	Asp	Asp	Val	Arg	Ala	Ala	Leu	Ala	Val	Asp	Pro	Lys
			85					90					95		
Glu	Trp	Glu	Gly	Asp	Met	Gln	Asp	Asn	Ala	Glu	Tyr	Leu	Asn	Phe	Leu
		100						105					110		
Gly	Ser	Arg	Val	Pro	Glu	Glu	Val	Trp	Asn	Gln	Phe	Arg	Ala		
		115					120					125			

<210> 473

<211> 339

<212> DNA

<213> Homo sapiens

<400> 473

accggttggt gggggaaggg acccatccca tgccacctgt cctagaaaat gtttcccctt
 60
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa
 120
 aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctcccacc
 180
 ctgcttccat ttccctctcc agggaacagg tgtacctccc ctctccctg tctctctcag
 240
 atgccccagg ggctctctac ttcatctctg ccgaccctgc caggagtggc ctcaggggta
 300
 gaggtccta gttggagaat ttgcttgacg gaaggtgaa
 339

<210> 474

<211> 97
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu
 1 5 10 15
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly
 20 25 30
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe
 35 40 45
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln
 50 55 60
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val
 65 70 75 80
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly
 85 90 95
 Glu

<210> 475
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 475
 acgcgtgaag ggtccctccc aaactctgag cctccttcca agccttgctg ggagctcccc
 60
 agcgccctgcc ggagaggcct ctctccagg cgggcttccc gcgccgatgt gaaggagagg
 120
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtcccacagc cataatccccg
 180
 aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa
 240
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc
 300
 ctttgatgga tcttggttaga agtgggttgt tcatcttggg gtttt
 345

<210> 476
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro
 1 5 10 15
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu
 20 25 30
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu
 35 40 45
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr
 50 55 60
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

```

65              70              75              80
Pro Ala Trp Arg Arg Gly Leu Ser Gly Arg Arg Trp Gly Ala Pro Ser
              85              90              95
Lys Ala Trp Lys Glu Ala Gln Ser Leu Glu Gly Thr Leu His Ala
              100              105              110

```

<210> 477
 <211> 422
 <212> DNA
 <213> Homo sapiens

```

<400> 477
acgcgtggcc gagccagcgt gctcaaggaa atgggtcaacg gcactcttat taacggctgg
60
gactctcccg aggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgcccga
120
gattgccccca ccggaatcga catggccagc taccgcagca cggttcttga cgaaaaatac
180
cgtcaccgtc tccgccctcg ctccacctg acgatggggc tgctgcccac gtgggaacgt
240
ttgctcaatc ggaccccagg agcgccgtcg ctggctaacg cagtgccttc gatgccggtc
300
ttcgcacgtc ttgctagatg gacagccggg gtggatcagc gtcgtcccct cccccgattc
360
cagccctcgg ccagattggc cagtccgcag gccgccccgg ttaaggagat tgtggcggat
420
cc
422

```

<210> 478
 <211> 140
 <212> PRT
 <213> Homo sapiens

```

<400> 478
Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
1      5      10      15
Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
      20      25      30
Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
      35      40      45
Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
      50      55      60
Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
65      70      75      80
Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
      85      90      95
Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
      100      105      110
Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
      115      120      125
Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
      130      135      140

```

<210> 479
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 479
 cgcggtggcca ttggccgggc gctggtgctg caccgcgac tgggtgattgc cgatgagccg
 60
 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag
 120
 gcgcagtacg gctttgcctg cctgttcac tcccacgacc tggcagcggg ggaacgcac
 180
 gccccaccggg tggcgggtgat gagcgagggc aggggtggtgg aaatgggtgc ccgcgacgag
 240
 atcttcgacc gcccgagca cccctacacc cgcaagctgc tggccgcccgc cagccccttg
 300
 gagaaacttg aaaacggtgg ctaccgcac cgccagggcc ccgtaccg
 348

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile
 1 5 10 15
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile
 20 25 30
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu
 35 40 45
 Phe Ile Ser His Asp Leu Ala Val Glu Arg Ile Ala His Arg Val
 50 55 60
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu
 65 70 75 80
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala
 85 90 95
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln
 100 105 110
 Gly Pro Val Pro
 115

<210> 481
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 481
 aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg
 60
 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tgggtgccttc
 120
 cctgccctgc cggcttgccg tggcttcctc agtggttagga ttaccatcac attgcatcat
 180

gagagcagaa gaccatctcc atgtgactgc tgccctgct cccagcaggg cccacaan
 240
 cccagtccag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct
 300
 gctctttctc ctgcaggacc aggaaaccgc tgccctgtcc ctgccccagg aaacctcag
 360
 taaatcccca gtcatttgag tttccctca gcgcagaga ccaataacac atctccacca
 420
 acctgaaaaa ccttcacgcg t
 441

<210> 482

<211> 120

<212> PRT

<213> Homo sapiens

<400> 482

Lys	Leu	Leu	Thr	Val	Ala	Phe	Ser	Leu	Leu	Asn	Met	Ser	Ser	Ile	Ser
1				5					10					15	
Pro	Thr	Tyr	Trp	Ala	Lys	Ser	Cys	Leu	Cys	Phe	Gly	Thr	Ser	Ser	Lys
			20					25					30		
Thr	Thr	Pro	Leu	Asp	Gly	Ala	Phe	Pro	Ala	Leu	Pro	Ala	Cys	Ala	Gly
			35				40						45		
Phe	Leu	Ser	Val	Arg	Ile	Thr	Ile	Thr	Leu	His	His	Glu	Ser	Arg	Arg
	50					55					60				
Pro	Ser	Pro	Cys	Asp	Cys	Cys	Pro	Cys	Ser	Gln	Gln	Gly	Pro	Gln	Xaa
65					70					75				80	
Pro	Ser	Pro	Gly	Pro	Gly	Ser	Arg	Trp	Val	Ala	Asp	Ala	Gln	Glu	Trp
			85						90					95	
Gly	Ser	Gly	Ser	Ala	Ser	Ser	Pro	Ala	Gly	Pro	Gly	Asn	Arg	Cys	Pro
			100					105					110		
Val	Pro	Ala	Pro	Gly	Asn	Pro	Gln								
			115				120								

<210> 483

<211> 330

<212> DNA

<213> Homo sapiens

<400> 483

acgcgttcat tccctgatgg ccacgcacga gctaacggag ggatggggcg aaggaagggc
 60
 caagggtgcc tcgaagacca aggagtgtgc agggcaggac ctcgttttaa aggaatatcc
 120
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg
 180
 agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag
 240
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc
 300
 tcccgggacc ctgcagcgtg ggctggggcc
 330

<210> 484

<211> 96
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
 1 5 10 15
 Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
 20 25 30
 Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
 35 40 45
 Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
 50 55 60
 Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
 65 70 75 80
 His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
 85 90 95

<210> 485
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 485
 acgcgtgctc gcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtgcc
 60
 gcccgattcg gcgatcgccg cattcggccg gccggaatcg agaaggaatg cgtggacgta
 120
 cgggggatac caaaggaatc ttgtcgaggg cttcgcggcc ctcgacgtgg atcacctgta
 180
 cccgacggac gtggggaagc cgtcccgcaa gctcacggga ctccgcgaca tcgatgtgcg
 240
 atacgatttg caccgtcgtc ggctgcgtgc gcgacacatg ctccgcgata gcctcagcgg
 300
 tggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg
 360
 cattcccatt cctcggg
 377

<210> 486
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 486
 Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
 1 5 10 15
 Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
 20 25 30
 Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
 35 40 45
 Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
 50 55 60
 Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

```

65              70              75              80
Pro Arg Ser Pro Gln Arg Trp Phe Pro Thr Ser Ala Gly Thr Trp Arg
              85              90              95
Arg Val Ala Trp Arg Ser Pro Leu Cys Arg His Ser His Ser Ser
              100              105              110

```

<210> 487
 <211> 459
 <212> DNA
 <213> Homo sapiens

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<400> 487
nnacgcgtaa gatcgattgt ggatcagcac cgatgctggt ccccccgcac ttgttgttgg
60
cgggtgttgt tgtaaggagt gtgtgtgatg cgtgttggtg ttcctactga ggttaagaat
120
agtgaagttc gtgtggctgt gacgccggcg ggtgttcattg cgttggttgg tcgtgggtcat
180
gaggtgttgg ttcaggctgg tgctgggtgtg ggttcgggta ttccggattc ggattttgtg
240
ggtgctgggtg cgcgggttgt gggtgatgtg gagtcggtgt ggggtgatgc tgatttggtg
300
ttgaaggtga aggagcctgt tgcggaggag tatgggagggt tgcattgaggg tttggttctt
360
tttacgtatc ttcatttggc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
420
gtgacgtcga ttgcgtatga gacggtggag ttggccgat
459

```

<210> 488
 <211> 124
 <212> PRT
 <213> Homo sapiens

```

<400> 488
Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
1              5              10              15
Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
              20              25              30
Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
              35              40              45
Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
              50              55              60
Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
65              70              75              80
Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
              85              90              95
Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
              100              105              110
Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
              115              120

```

<210> 489
 <211> 542

<212> DNA

<213> Homo sapiens

<400> 489

nacgcgtttg gcgtactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc
 60
 aaccagcacg gttgctacaa agtgcgcttt ccatttacct gcgatcaaaa gccagcact
 120
 cgggggttcg catggctgcg caggggtgctg ttgtctgccg gttccagcca tggcatgcac
 180
 tttccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg
 240
 ccgattatcg ttggctgcgt accaaactcg gaaaccccg aatgggtcgt tgagcgtaac
 300
 gccacccaga gcggcttctc cacggccgga gggcacttcc tggcgatgga agaccacccc
 360
 ggggctgccc atctgaagct ggggtgcgctt ggcggcaaca gcgtcttcac actgggcaat
 420
 ggcaaagtcg ccggcgcgca actgcgcacc aacgccccac atgcaattga catcgtcttc
 480
 gctcaaacac gaagtgcccc gcgtgtactc attgtcgatg ggcaccgggg acccgggggg
 540
 cg
 542

<210> 490

<211> 180

<212> PRT

<213> Homo sapiens

<400> 490

Xaa Ala Phe Gly Val Leu Ser Ala Val Val Asp Gly Asp Asp Ser Gly
 1 5 10 15
 Lys Pro Leu Leu Asn Gln His Gly Cys Tyr Lys Val Arg Phe Pro Phe
 20 25 30
 Thr Arg Asp Gln Lys Pro Ser Thr Arg Gly Ser Ala Trp Leu Arg Arg
 35 40 45
 Val Ser Leu Ser Ala Gly Ser Ser His Gly Met His Phe Pro Leu Leu
 50 55 60
 Lys Gly Ser Glu Val Leu Val Ser Phe Leu Gly Gly Asp Pro Asp Arg
 65 70 75 80
 Pro Ile Ile Val Gly Cys Val Pro Asn Ser Glu Thr Pro Ser Met Val
 85 90 95
 Val Glu Arg Asn Ala Thr Gln Ser Gly Phe Ser Thr Ala Gly Gly His
 100 105 110
 Phe Leu Ala Met Glu Asp His Pro Gly Ala Ala His Leu Lys Leu Gly
 115 120 125
 Ala Pro Gly Gly Asn Ser Val Phe Thr Leu Gly Asn Gly Lys Val Ala
 130 135 140
 Gly Ala Gln Leu Arg Thr Asn Ala Pro His Ala Ile Asp Ile Val Phe
 145 150 155 160
 Ala Gln Thr Arg Ser Ala Arg Arg Val Leu Ile Val Asp Gly His Arg
 165 170 175
 Gly Pro Gly Gly

180

<210> 491
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 491
 nacgcgtcga ggcgacggtc ggcgccgtca tggcgactgt tctcgagggc acatgggaac
 60
 gcatcggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg
 120
 tgggcgggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg
 180
 aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggaggggtca atcgaattgg
 240
 tcgacgtgtc ggtcgggtgac gaagagcgca gactcgacgt caccatgaag ggagcatgcc
 300
 gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcg
 360
 nattgcgcga gccggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg
 420
 acgagcacct ccacgacgag gccaaagccac tcgtagacgc attcctctctc ggcattccaat
 480
 tcctcccggg ccgcccggagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg
 540
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgctg catcacaggg
 600
 ttcatggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg
 660
 tcttcccagc gcgcccgcgac atcctcggcg tcatggtcga catggaattg cgcgtcagct
 720
 gactcgtcgt cagcataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg
 780
 agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc
 825

<210> 492
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 492
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg
 1 5 10 15
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg
 20 25 30
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser
 35 40 45
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro
 50 55

<210> 493
 <211> 863

<212> DNA

<213> Homo sapiens

<400> 493

nacgcgttcc aacctcgtca aaacggctat cgcaggaaat gaccccaact ggggtcgc
 60
 cctcgcggcg atcgatgtg ttctgagaa tatagctccc ttcgatcccg accaggtgga
 120
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct
 180
 cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga
 240
 agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata gcgcgtatac
 300
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa
 360
 tctgagggcc tggtagaagc gctgccttgg atcaggcggt ttcagggccg cactgtcgtc
 420
 gtgaaatatg gcggcaacgc gatggttgat cccggtctgc agcaggcctt cgccgacgac
 480
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacggtgg tggccctcag
 540
 atcaatgcca tgcttcttga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg
 600
 acatctccgg aggtcatgga ggttgtccgg atggtgctcg tcgggcagggt gggccgtcag
 660
 ctcgtaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt
 720
 ggcctttttt cggcccgga gtcgcgggta attgttgatg gcgagcaa at agacatgggt
 780
 ttagtgggag acatcgttga cgtcaacatc gatctcgta tctctatgct tgatcgcggt
 840
 cagattccgg tcattgcacc ggt
 863

<210> 494

<211> 186

<212> PRT

<213> Homo sapiens

<400> 494

Met	Thr	Leu	Ala	Leu	Asp	Ile	Pro	Leu	Asn	Asp	Ser	Gln	Phe	Ser	Ala
1				5					10					15	
Gln	Arg	Lys	Ser	Glu	Val	Leu	Val	Glu	Ala	Leu	Pro	Trp	Ile	Arg	Arg
		20						25					30		
Phe	Gln	Gly	Arg	Thr	Val	Val	Val	Lys	Tyr	Gly	Gly	Asn	Ala	Met	Val
		35					40					45			
Asp	Pro	Gly	Leu	Gln	Gln	Ala	Phe	Ala	Asp	Asp	Ile	Val	Phe	Met	Ala
		50				55					60				
Ser	Val	Gly	Ile	Arg	Pro	Ile	Val	Val	His	Gly	Gly	Gly	Pro	Gln	Ile
65					70					75				80	
Asn	Ala	Met	Leu	Ala	Glu	Ser	Ala	Thr	Pro	Val	Glu	Phe	Arg	Asn	Gly
			85						90					95	
Leu	Arg	Val	Thr	Ser	Pro	Glu	Val	Met	Glu	Val	Val	Arg	Met	Val	Leu

```

      100      105      110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala
      115      120      125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala
      130      135      140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu
      145      150      155      160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu
      165      170      175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro
      180      185

```

<210> 495
 <211> 514
 <212> DNA
 <213> Homo sapiens

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<400> 495
gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttggccga tccaccggga tccccgggcc ttcgatgacc ttgagcccgga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcgggtt ttcgccggtg tcggtgagcg taccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcggccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggtaactg ctgtgggacc ttgg
514

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<210> 496
 <211> 171
 <212> PRT
 <213> Homo sapiens

```

<400> 496
Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
1      5      10      15
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
      20      25      30
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
      35      40      45
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
      50      55      60
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
65      70      75      80
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu

```

```

      85              90              95
Met Ile Tyr Arg Ile Ala His Asn Phe Gly Gly Thr Ser Val Phe Ala
      100              105              110
Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Leu Ile Asn Glu Met
      115              120              125
Asp Glu Ala Gly Val Leu Lys Asp Thr Ala Leu Val Phe Gly Gln Met
      130              135              140
Asp Glu Pro Pro Gly Thr Arg Tyr Glu Leu Ser Arg Trp Gln Pro Cys
      145              150              155              160
Gly Pro Cys Leu Val Asn Cys Cys Gly Thr Leu
      165              170

```

<210> 497

<211> 662

<212> DNA

<213> Homo sapiens

<400> 497

```

acgcgtcctg ggatctcaac cccagcagtc tggcttggtt ctcattccca caatttcctg
60
ggttcacca agcagcgaaa actgccagga tgaatgagga aaaaaccag cccacaaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgctcagc acaggcctgg gacctcccc ggcaggcacc tgtgggggggt gcagcccccg
360
ggaaggaggc aactgcctca cttaacatcc tccgctgcaa ggtggtggcg ccgagaggcg
420
tgtctgtgaa gacaggtacc aggatggcag gaccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc toccaggaca agccagtctg
540
cctcttcctc ctacttctgc tgtagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagctc tcgtcctgcc gtggcccccg cgatggcttg gggtgcaagc
660
tt
662

```

<210> 498

<211> 191

<212> PRT

<213> Homo sapiens

<400> 498

```

Met Asn Glu Glu Lys Thr Gln Pro His Lys Arg Asp Thr Arg Trp Arg
1          5          10          15
Gly Glu Thr Gln Gln Ser Ser Phe Leu Ser Val Asp Ser Glu Gln Arg
20          25          30
Arg Gly Ala Pro Ser Phe Val Phe Ser Ser Ser Gly Glu Arg Met Asp

```



```

      35      40      45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
  50      55      60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
  65      70      75      80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
      85      90      95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
      100      105      110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
      115      120      125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
      130      135      140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
      145      150      155      160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
      165      170      175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
      180      185      190

```

<210> 499
 <211> 444
 <212> DNA
 <213> Homo sapiens

```

<400> 499
acgcgtgaag ggtgggcagt gttgagctga gtgagccctc ctccctgcaa tgctggagcc
60
ctgccttctg cctgaccctc tggcttccta agcagtctat acgtgagaag ccctttcttc
120
aagtgaagc ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
180
tcctcaactg gggggttgga ggaggttact tcacttctca aaacctcaat ttccttatct
240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaatgc ctggcacagt
300
agggcagtta ccgtcatgga gaacagaaag gccccgagct atcctggatg tggtgagaat
360
gggtcctgga tcctgcctgc tcggcctttt cattctcttc ttcacctaca ggctcccaca
420
aagggcctct gaaaacacag ggtg
444

```

<210> 500
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 500
Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
  1      5      10      15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20      25      30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

```

      35              40              45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
      50              55              60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
      65              70              75              80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
      85              90              95
Gln Leu Asn Thr Ala His Pro Ser Arg
      100              105

```

<210> 501

<211> 800

<212> DNA

<213> Homo sapiens

<400> 501

```

agatctgata cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
60
gggtactcctt attcaatgag aggctgagg tgagaccgcg catgcggcgc gtggatcgca
120
tggtgttagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
180
gaccttgtagc tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
240
gaagtttatt ctcccatgga tgatgctggc ttcccgggtca aagctgagga gtttgtgggtg
300
ctttctcagg aaccttctgt cacggaaacc attgcaccca aaattgcaag acctttcata
360
gaggccctca agagtattga gtatctggag gaggatgccc agaagtccgc acaggagggg
420
gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
480
gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
540
tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgccgtact
600
tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
660
tgcagttcga ctcaggtatg cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
720
cctggatgat gaggcgctct tgatgtgatt cgtttccag ggaagttgga agcttttagct
780
atcttgcttc agaaactgaa
800

```

<210> 502

<211> 103

<212> PRT

<213> Homo sapiens

<400> 502

```

Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
1          5          10          15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

```

      20      25      30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
      35      40      45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
      50      55      60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
65      70      75      80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
      85      90      95
Ala Leu Asn Tyr Leu Glu Ser
      100

```

<210> 503
 <211> 538
 <212> DNA
 <213> Homo sapiens

```

<400> 503
nnacgcgttg tcgtctctcc gatcattgat tttgttgtat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcataggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttcagact attggaaggg gaaggtcccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
agggaagcga aactgggtcat ccggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacgggtcca gtgagcattt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggccct tcacgcgt
538

```

<210> 504
 <211> 179
 <212> PRT
 <213> Homo sapiens

```

<400> 504
Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
1      5      10      15
Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
      20      25      30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
      35      40      45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
      50      55      60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
65      70      75      80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

```

      85              90              95
Lys Asn Ala Pro Leu Leu Leu Pro Asp Val Ile Lys Val Ser Thr Arg
      100              105              110
Ser Ser Glu His Phe Phe Ser Val Phe Leu Asn Ile Asn Glu Thr Phe
      115              120              125
Lys Leu Met Glu Gln Leu Ala Asn Ile Ala Met Arg Gln Leu Leu Asp
      130              135              140
Asn Glu Gly Phe Glu Gln Asp Arg Ser Leu Pro Lys Leu Lys Arg Lys
      145              150              155              160
Ser Pro Lys Lys Val Ser Ala Leu Lys Arg Asp Leu Asp Ala Trp Ala
      165              170              175
Leu His Ala

```

<210> 505
 <211> 381
 <212> DNA
 <213> Homo sapiens

```

<400> 505
gtgcacgaca ccgaacggta cgaacgtatc tcccaggcac gtcgcgagga acagcaggcc
60
atgctcggct acgacngctc aagaacctgt cgcattgacct tgctcaccgg gcagctggac
120
gacccctcca cgactccttg cggacgctgc gacgtctgtg ctggcccgtg gtactcagtc
180
gaggtcgatc agtcagccgc tgtgagagcc gtccaatccc tcaaccgggt gggagttccg
240
gtggaaccac gcgcgcctg gcccgagggt atggacgccc tccaggttgc gctcaagggt
300
cgcattcagtg ccgaggagat cgctgcagag ggccgcgtca tcgccagact ctccgatctg
360
ggttggggag gggcgctgcg c
381

```

<210> 506
 <211> 127
 <212> PRT
 <213> Homo sapiens

```

<400> 506
Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
1      5      10      15
Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
20     25     30
Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
35     40     45
Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
50     55     60
Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65     70     75     80
Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
85     90     95
Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg

```

100 105 110
 Val Ile Ala Arg Leu Ser Asp Leu Gly Trp Gly Gly Ala Leu Arg
 115 120 125

<210> 507
 <211> 499
 <212> DNA
 <213> Homo sapiens

<400> 507
 gccggcgtgt tcaacctcat ggtgtgggcc ttcatcaccg acgtcatcga tgcccaggag
 60
 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgcaaa
 120
 cttgcccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag
 180
 tcctcctccc aaggtggtgc cgttcagtcg gagtccgtcg tcaatcacct gtacacgctc
 240
 gccaccgcca tcccagcgat ctgctgcctc ggcgctgccc tgctcatgct gggctaccgg
 300
 ctaccccgcg acaaggtggt cgccaacgcc gacgagttgg ctgctcgcca cgagtagacg
 360
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac
 420
 cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc
 480
 cgtcacattt gtgacgcgt
 499

<210> 508
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 508
 Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile
 1 5 10 15
 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr
 20 25 30
 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly
 35 40 45
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln
 50 55 60
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu
 65 70 75 80
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met
 85 90 95
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu
 100 105 110
 Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser
 115 120 125

<210> 509
 <211> 360

<212> DNA

<213> Homo sapiens

<400> 509

ttggccatgg atttggtcgc caagttcagt cccaaagatg tcacgtctta tctaattggac
 60
 ttcgggacca atggtgtggc accactaggc caattaccac aggtggccga caccttgctt
 120
 ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg
 180
 cgtaagaagc tcttgtccga ctacggtgtt ggtacactag agctctaccg tcaggctagc
 240
 ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag
 300
 gcctatgaag cggagctctt cacgctcttg gtgcggatct cccgggaagg tctcagcatc
 360

<210> 510

<211> 120

<212> PRT

<213> Homo sapiens

<400> 510

Leu Ala Met Asp Leu Ala Arg Lys Phe Ser Pro Lys Asp Val Thr Leu
 1 5 10 15
 Tyr Leu Met Asp Phe Gly Thr Asn Gly Val Ala Pro Leu Gly Gln Leu
 20 25 30
 Pro Gln Val Ala Asp Thr Leu Leu Asp His Thr Glu Lys Ile Ala
 35 40 45
 Lys Phe Val Arg Ile Met Glu Arg Glu Leu Asn Arg Arg Lys Lys Leu
 50 55 60
 Leu Ser Asp Tyr Gly Val Gly Thr Leu Glu Leu Tyr Arg Gln Ala Ser
 65 70 75 80
 Gly Gln Gln Glu Pro Ala Ile Val Ile Leu Leu Asp Ser Tyr Glu Ser
 85 90 95
 Met Lys Glu Glu Ala Tyr Glu Ala Glu Leu Phe Thr Leu Leu Val Arg
 100 105 110
 Ile Ser Arg Glu Gly Leu Ser Ile
 115 120

<210> 511

<211> 361

<212> DNA

<213> Homo sapiens

<400> 511

ntcgcgaacc gcggctatgc ggtgctccag cccaatttcc gcggatcggg cggttatggc
 60
 actgcgttcg gcgatgccgg catcggccag atcggggcgca agatgcagga cgatctcgac
 120
 gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc
 180
 ggggcctcct atggcgggcta tgccgcgatg tggggcgcgca tccgcaatcc cgaacgctat
 240

cgctgcgcgg cgagcctggc gggggttgcc gattaaggcc atgctcaaat ataaccggcg
 300
 ctatctcgac aaggaggcgg gcaagcgctg gccgccccgn tcaaccggcg aaccggaatt
 360
 c
 361

<210> 512
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 512
 Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser
 1 5 10 15
 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly
 20 25 30
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys
 35 40 45
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr
 50 55 60
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr
 65 70 75 80
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp
 85 90

<210> 513
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 513
 nnatgcagac tagaagatgg catgacgggt ttggctggcg gtttcgggct atgcggcatt
 60
 ccagaaaatc tgattcaaga gatcaaacga cgccagactt gtgatttgac catagtgtca
 120
 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc
 180
 aaaatggtgt cttcttatgt gggtgaaaat gactgtttg agaagcaatt attacaaggt
 240
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc
 300
 gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa
 360
 gacacgcgt
 369

<210> 514
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 514
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

```

      1             5             10             15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
      20             25             30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
      35             40             45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
      50             55             60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
      65             70             75             80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
      85             90             95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
      100            105            110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
      115            120

```

<210> 515
 <211> 387
 <212> DNA
 <213> Homo sapiens

```

<400> 515
gcgtgggacg agaaggccgc cggcaactgc gcgatcgact acgggttcca ccagatcctc
60
tccgacgtgc aggactcgtc gctgaccgcg atggacgagc tgatcaccga gggcgtgaca
120
tccttcaagc tcttcgtggc ctacaagggc gtcttctctc cggacgacgg gcagatcctg
180
cgggcgttcc agaaggccgc cgacaacggc gcgatgatga tgatgcacgc cgagaacggc
240
gcgatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
300
cacggcatca gccggccgtg gcaggccgag gaggaggcca cccaccgcgc gatcatgac
360
gccgacctga ccggtgcgcc gttgtac
387

```

<210> 516
 <211> 129
 <212> PRT
 <213> Homo sapiens

```

<400> 516
Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
1             5             10             15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
      20             25             30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
      35             40             45
Lys Gly Val Phe Leu Ser Asp Gly Gln Ile Leu Arg Ala Phe Gln
      50             55             60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
      65             70             75             80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

```



```

      85              90              95
Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu
      100              105              110
Ala Thr His Arg Ala Ile Met Ile Ala Asp Leu Thr Gly Ala Pro Leu
      115              120              125
Tyr

```

<210> 517
 <211> 377
 <212> DNA
 <213> Homo sapiens

```

<400> 517
acgcgtgaag ggctggtggg caggccttgc gccccctctg gggacagctc tcctccaccc
60
agacccttc gggccaacag tggggagggg ctgccgtctg agccactgtt ccgacagggg
120
attcgcgagt tccgggggag ctggggactg agctgcgggc ctctctgggct ggggctcttc
180
tccgaggttg gaggcagctt tagaaacttg agacccttag ctggagaggg cagaaggggt
240
ccctgagctt ccccaggaga agggggggcca atttgagct tgcttttcac ctgagatgag
300
gaatgggggt ggccaggccg agagcccagt ggggcatccc cagcacccat gaacatgcta
360
aggaagggga ggggccc
377

```

<210> 518
 <211> 118
 <212> PRT
 <213> Homo sapiens

```

<400> 518
Met Phe Met Gly Ala Gly Asp Ala Pro Leu Gly Ser Arg Pro Gly His
1              5              10              15
Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro
      20              25              30
Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
      35              40              45
Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro
      50              55              60
Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
65              70              75              80
Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
      85              90              95
Arg Gly Leu Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
      100              105              110
Pro Thr Ser Pro Ser Arg
      115

```

<210> 519
 <211> 311

<212> DNA

<213> Homo sapiens

<400> 519

gcgcgccagg gggaaggag agaaaacaca gaaaaatgag ggggaaatac cagatactga
 60
 agaatttaaa ttattataaa ggaacctttt ctgcaactct gaaaaatgtt agaatatcca
 120
 aagaaattga taatttttcta ggaaaacatg acttaccaaa attaactcta gaaaagaatc
 180
 gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgcc aacctggaat
 240
 tcatgattga attctttgag atctactgtg agtacatact ctgcctctgt tcagctgttc
 300
 cagaacttaa g
 311

<210> 520

<211> 92

<212> PRT

<213> Homo sapiens

<400> 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
1				5				10						15	
Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
			20					25					30		
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
			35				40					45			
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50					55					60				
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65					70					75				80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85					90							

<210> 521

<211> 352

<212> DNA

<213> Homo sapiens

<400> 521

nnngatgcc a cgcggtcta cggaatctcc accggcttcg gcgcgcttgc ccgcgccac
 60
 attccagaag agatgcgcgc gcagctgcag ctgtccctgg tgcgctccca cgcggccggc
 120
 accggccctg aggtggaaga agaagtaatt cgcgcgctca tgctgctgcg cctatccacc
 180
 ctgtgtaccg gccgtaccgg cgtgcgcccc gtggtggtag aaacttatgc caagggcgtc
 240
 aacgccggca tcgtgccggg ggtgcgcgaa tacgggtcgc tgggctgctc cggcgacttg
 300
 gccccgctgg ctactgcgc cctagcgtg ttgggtgagg gtgaggtacg cn
 352

<210> 522
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 522
 Xaa Asp Ala Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly Ala Leu
 1 5 10 15
 Ala Arg Arg His Ile Pro Glu Glu Met Arg Ala Gln Leu Gln Leu Ser
 20 25 30
 Leu Val Arg Ser His Ala Ala Gly Thr Gly Pro Glu Val Glu Glu
 35 40 45
 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly
 50 55 60
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu
 65 70 75 80
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys
 85 90 95
 Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly
 100 105 110
 Glu Gly Glu Val Arg
 115

<210> 523
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 523
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<212> PRT

<213> Homo sapiens

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Glu Glu Trp Gln Gln Cys Ser Arg Thr Cys Gly Gly Gly Thr Gln Asn		175
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<211> 4566

<212> DNA

<213> Homo sapiens

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<210> 530

<211> 802

<212> PRT

<213> Homo sapiens

<400> 530

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Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro Glu Gly Cys
 35          40          45
Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly Ala Arg Gly Asp
 50          55          60
Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser Asp Pro Asp Gly Gly
 65          70          75          80
Pro Arg Asp Arg Asn Phe Leu Phe Val Gly Val Met Thr Ala Gln Lys
 85          90          95
Tyr Leu Gln Thr Arg Ala Val Ala Ala Tyr Arg Thr Trp Ser Lys Thr
100          105          110
Ile Pro Gly Lys Val Gln Phe Phe Ser Ser Glu Gly Ser Asp Thr Ser
115          120          125
Val Pro Ile Pro Val Val Pro Leu Arg Gly Val Asp Asp Ser Tyr Pro
130          135          140
Pro Gln Lys Lys Ser Phe Met Met Leu Lys Tyr Met His Asp His Tyr
145          150          155          160
Leu Asp Lys Tyr Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile
165          170          175
Lys Gly Asp Arg Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu
180          185          190
Pro Leu Phe Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly
195          200          205
Lys Leu Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly
210          215          220
Val Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
225          230          235          240
Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly
245          250          255
Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser Tyr Glu
260          265          270
Met Gln Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys Lys Gly Tyr
275          280          285
Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala Ile Thr Leu His
290          295          300
Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu His Ser Tyr Met Leu
305          310          315          320
Ser Arg Lys Ile Ser Glu Leu Arg His Arg Thr Ile Gln Leu His Arg
325          330          335
Glu Ile Val Leu Met Ser Lys Tyr Ser Asn Thr Glu Ile His Lys Glu
340          345          350
Asp Leu Gln Leu Gly Ile Pro Pro Ser Phe Met Arg Phe Gln Pro Arg
355          360          365
Gln Arg Glu Glu Ile Leu Glu Trp Glu Phe Leu Thr Gly Lys Tyr Leu
370          375          380
Tyr Ser Ala Val Asp Gly Gln Pro Pro Arg Arg Gly Met Asp Ser Ala
385          390          395          400
Gln Arg Glu Ala Leu Asp Asp Ile Val Met Gln Val Met Glu Met Ile

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405 410 415
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 Val Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
 465 470 475 480
 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys Arg
 485 490 495
 Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser Leu Lys
 500 505 510
 Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu His Lys Glu
 515 520 525
 Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu Ser Gly Arg Phe
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 Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu Lys Thr Cys Leu Ile
 545 550 555 560
 Pro Asn Gln Asn Val Lys Leu Val Val Leu Leu Phe Asn Ser Asp Ser
 565 570 575
 Asn Pro Asp Lys Ala Lys Gln Val Glu Leu Met Thr Asp Tyr Arg Ile
 580 585 590
 Lys Tyr Pro Lys Ala Asp Met Gln Ile Leu Pro Val Ser Gly Glu Phe
 595 600 605
 Ser Arg Ala Leu Ala Leu Glu Val Gly Ser Ser Gln Phe Asn Asn Glu
 610 615 620
 Ser Leu Leu Phe Phe Cys Asp Val Asp Leu Val Phe Thr Thr Glu Phe
 625 630 635 640
 Leu Gln Arg Cys Arg Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe
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 Pro Ile Ile Phe Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys
 660 665 670
 Val Pro Ser Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp
 675 680 685
 Arg Asn Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val
 690 695 700
 Arg Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
 705 710 715 720
 Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe Arg
 725 730 735
 Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp
 740 745 750
 Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala
 755 760 765
 Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys
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<210> 531

<211> 321

<212> DNA

<213> Homo sapiens

<400> 531

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<210> 532

<211> 96

<212> PRT

<213> Homo sapiens

<400> 532

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			20					25					30		
Ser	Val	Lys	Arg	Cys	Arg	Thr	Ser	Val	Ser	Asn	Ala	Pro	Glu	Val	Asn
		35				40					45				
Pro	Arg	Gly	Arg	Leu	Asn	Gln	Ala	Ser	Trp	Ala	Trp	Asp	Asp	Ser	Gly
	50				55					60					
Cys	Ser	Gly	Ser	Asn	Gly	Ala	Cys	Gly	Ser	Ala	Leu	Ile	Asp	Ser	Arg
65				70					75					80	
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<210> 533

<211> 335

<212> DNA

<213> Homo sapiens

<400> 533

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 180
 accaacattg acaacgtcct caacaaagat cacctgcgtt ggctacactt tcttttggag
 240
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<210> 534
 <211> 103
 <212> PRT
 <213> Homo sapiens

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 Glu Thr Trp Ser Ser Gln Val Arg His Phe Ile Ser Leu Leu His Pro
 35 40 45
 Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu
 50 55 60
 Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg
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 Leu Ile Val Gln Gly Tyr Cys Ser Pro Gly Lys Leu Tyr Arg Lys Leu
 85 90 95
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<210> 535
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 535
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 <211> 114
 <212> PRT
 <213> Homo sapiens

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 Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

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      35              40              45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
      50              55              60
Met Thr Arg Pro Arg Arg Leu Leu Leu Gly Ser Ile Val Val Leu Gly
65              70              75              80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
      85              90              95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
      100             105             110
Thr Arg

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<210> 537
 <211> 404
 <212> DNA
 <213> Homo sapiens

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<400> 537
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<210> 538
 <211> 118
 <212> PRT
 <213> Homo sapiens

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<400> 538
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20     25     30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
35     40     45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
50     55     60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
65     70     75     80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
85     90     95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
100    105    110
Asp Asn Leu Leu Glu Arg

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115

<210> 539
 <211> 534
 <212> DNA
 <213> Homo sapiens

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 420
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<210> 540
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 540
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 20 25 30
 Ile Leu Lys Lys Asp His Gln Leu Leu Leu Ala Ile Tyr Gly Lys Lys
 35 40 45
 Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr
 50 55 60
 Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu
 65 70 75 80
 Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly
 85 90 95
 Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu
 100 105 110
 Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys
 115 120 125
 Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile
 130 135 140

<210> 541
 <211> 551

<212> DNA

<213> Homo sapiens

<400> 541

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 gagtcggagc ccagccagt ggcgtgtaaa gtgtgttctg ccaccttctt ggagctgcag
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 360
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 420
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<210> 542

<211> 168

<212> PRT

<213> Homo sapiens

<400> 542

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 Ala Cys Lys Val Cys Ser Ala Thr Phe Leu Glu Leu Gln Leu Leu Asn
 35 40 45
 Gly Lys Glu Asp Val Trp Gly Ala Pro Val Val Lys Leu Leu Cys Arg
 50 55 60
 Phe Leu Ser Asp Leu Arg Cys His Leu Ser Ala Ala Val Gly Gly Val
 65 70 75 80
 Pro Asp Phe Val Leu Ser Ala Pro Leu Pro His Asn Val Val Ala Arg
 85 90 95
 Thr Lys Ala Phe Ser Gly Phe Lys Ala Ser Gly Gln Ser Arg Phe Pro
 100 105 110
 Pro Pro Thr Pro Ala Gly Leu Thr Pro His Ser Ser Trp Leu Gly Ser
 115 120 125
 Cys Ile Ser Ala Gly Arg Leu Asp Ser Gly Ala Leu Ala Gly Ala Arg
 130 135 140
 Gly Gln Glu Pro Ala Val Ala Cys Val Val His Ser Cys Leu Cys Cys
 145 150 155 160
 Leu Tyr Leu Thr Ala Pro Ser Arg
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<210> 543
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 543
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<210> 544
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 544
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 20 25 30
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile
 35 40 45
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp
 50 55 60
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly
 65 70 75 80
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met
 85 90 95
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly
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 Asn Ala His Ala
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<210> 545
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 545
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 120
 ccaaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca
 180

atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca
 240
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<210> 546

<211> 130

<212> PRT

<213> Homo sapiens

<400> 546

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			20					25					30		
Pro	Gly	Gly	Ser	Ala	Asn	Arg	Ile	Pro	Asn	Lys	Ala	Gly	Ser	Asn	Pro
			35				40					45			
Glu	Gly	Ser	Ile	Ala	Thr	Arg	Phe	Ile	Ala	Glu	Thr	Met	Tyr	Asn	Glu
			50			55				60					
Leu	Lys	Thr	Val	Asp	Leu	Thr	Ile	Gln	Asn	Ala	Gly	Gly	Val	Arg	Ala
65					70				75					80	
Asp	Ile	Leu	Pro	Gly	Asn	Val	Thr	Phe	Asn	Asp	Ala	Tyr	Thr	Phe	Leu
				85					90					95	
Pro	Phe	Gly	Asn	Thr	Leu	Tyr	Thr	Tyr	Lys	Met	Glu	Ser	Ser	Leu	Val
			100				105						110		
Lys	Gln	Val	Leu	Glu	Asp	Ala	Met	Leu	Phe	Ala	Leu	Gly	Pro	Pro	Pro
		115					120					125			
Pro	Pro														
															130

<210> 547

<211> 306

<212> DNA

<213> Homo sapiens

<400> 547

aagcttggtt ttctgatttt tattcaaata tctatcatgg atgaagcatg cagtttcaga
 60
 atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcac
 120
 gaagcctcca acatattttg tgggatacca tctttgtcag gcattgtgct aggcactgtc
 180
 cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc
 240
 tcaaactttc atgtttgtgt atacaaatca gctgaggcct tcactaaact cnnnnncnn
 300
 nncnn
 306

<210> 548

<211> 90
 <212> PRT
 <213> Homo sapiens

<400> 548
 Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr
 1 5 10 15
 Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn
 20 25 30
 Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val
 35 40 45
 Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser
 50 55 60
 Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu
 65 70 75 80
 Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa
 85 90

<210> 549
 <211> 780
 <212> DNA
 <213> Homo sapiens

<400> 549
 nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttgtaaat
 60
 gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcatatca gaaatatttc
 120
 aattcagcga tttgaaatgt ttactttctg tttattgaaa atttttgttc tttttcacca
 180
 tgttattttt ttctcctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg
 240
 gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgt
 300
 tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt
 360
 aagattttcta aggatgcagg gatgcccac cagggccagc catgcttctg caaatatgca
 420
 cagggggcag acagcgtaga gcccatgttc cggcatctca agaacacata ttctggccta
 480
 cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta
 540
 ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaaca
 600
 tctcctcaaa ctctgtcaaa cttgtgccta aagataaatg ttaaactcgg agggatcaat
 660
 aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga
 720
 gccgatgtca ctcatccacc tgctggtgat ggaaagaagc cttctattgc tgctgttgta
 780

<210> 550
 <211> 192
 <212> PRT

<213> Homo sapiens

<400> 550

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Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1           5           10           15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
          20           25           30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
        35           40           45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
        50           55           60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
65           70           75           80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
          85           90           95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
        100          105          110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
        115          120          125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
        130          135          140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
145          150          155          160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
          165          170          175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
        180          185          190

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<210> 551

<211> 291

<212> DNA

<213> Homo sapiens

<400> 551

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nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gctcgttgcc
60
gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttcgag
120
gaaccgtcct cgtcgtcaat cgcaccggtc cgcgcggccc cgacgactgc agtaccacg
180
actagttcgt cgtcgggccc ctgaccgatg cgcccatcgg cgggctcatc tggtggcgc
240
tagcgggggc ttcgatgtcc ccataccaca gcgtccgcta aattgccnc c
291

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<210> 552

<211> 67

<212> PRT

<213> Homo sapiens

<400> 552

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Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1           5           10           15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

```

```

      20      25      30
Pro Thr Asn Ser Ala Pro Ser Glu Glu Pro Ser Ser Ser Ser Ile Ala
      35      40      45
Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser
      50      55      60
Ser Gly Arg
65

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<210> 553
 <211> 471
 <212> DNA
 <213> Homo sapiens

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<400> 553
ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
60
gtatctaaag ccaaaccgaa aattggtgca tatcatttca ctacaattaa acctaactta
120
ggtgttgttt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt
180
gaagggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
240
aaagttattg ttcacatgat tgatatgagc ggttctgaag gtagagaacc tattgaagat
300
tataaagtca ttaatcaaga attagctgcy tacgagcaac gtttagaaga tagacctcaa
360
atcgtagtag ctaacaagat ggatttacct gaatcacaag ataatttaaa cttgttttaa
420
gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcy t
471

```

<210> 554
 <211> 157
 <212> PRT
 <213> Homo sapiens

```

<400> 554
Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
1      5      10      15
Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
20      25      30
Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
35      40      45
Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
50      55      60
Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
65      70      75      80
Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
85      90      95
Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
100      105      110
Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
115      120      125
Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

```

130 135 140
 Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg
 145 150 155

<210> 555
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 555
 tctagagatt gagaacaatt atggatacag aaatggttga ttccgtcaaa tatattcgag
 60
 attcgggaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg
 120
 tgcagatctt gcggtggcgac ggcttaatta acgaagacca gagattagtc agattatggc
 180
 ttaataaaagt acctagaatt gttcgcctgc ttctccggct tagtgtgttc gtcgctgcgg
 240
 caataggtgc ccgtgcggta tgggcggcgg cttccggtaa tcccgatctt gttcacgcgt
 300

<210> 556
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 556
 Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu
 1 5 10 15
 Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met
 20 25 30
 Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg
 35 40 45
 Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu
 50 55 60
 Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val
 65 70 75 80
 Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala
 85 90

<210> 557
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 557
 atcttcccggt tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag
 60
 gccctcacga cgatgcaccc gtcaccggg gaggtcatca gcgaggacga gcaggtctac
 120
 gtgttcccggt ctaccacta tgctgccggc ccggaacgta tggagcgggc catagcgctc
 180
 atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttggag
 240

gccaacgggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggctcgtgcc
 300
 tgtgctggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccg ctcagccccg
 360
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atcccacgtg
 420
 accgtccccg agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta
 480
 gaacatgggt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc
 540
 acccagcggg tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa
 600
 cgagctcacg gcgtcgtcga acaaatcatt cgtccgacag gtctgggtgga tccggagatt
 660
 atcgtcaagc ctacgcgt
 678

<210> 558

<211> 226

<212> PRT

<213> Homo sapiens

<400> 558

Ile	Phe	Pro	Val	Tyr	Glu	Glu	Asn	Ala	Leu	Arg	Val	Glu	Phe	Phe	Gly
1				5					10					15	
Asp	Glu	Ile	Glu	Ala	Leu	Thr	Thr	Met	His	Pro	Leu	Thr	Gly	Glu	Val
			20					25					30		
Ile	Ser	Glu	Asp	Glu	Gln	Val	Tyr	Val	Phe	Pro	Ala	Thr	His	Tyr	Val
		35				40						45			
Ala	Gly	Pro	Glu	Arg	Met	Glu	Arg	Ala	Ile	Ala	Ser	Ile	Gln	Gln	Glu
	50				55					60					
Leu	Glu	Glu	Arg	Leu	Ala	Val	Leu	Glu	Arg	Asp	Gly	Lys	Leu	Leu	Glu
65				70					75					80	
Ala	Gln	Arg	Leu	Arg	Met	Arg	Thr	Thr	Tyr	Asp	Ile	Glu	Met	Met	Gln
			85						90					95	
Gln	Val	Gly	Ala	Cys	Ala	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp
		100						105					110		
Gly	Arg	Ala	Pro	Gly	Ser	Ala	Pro	Asn	Cys	Leu	Leu	Asp	Tyr	Phe	Pro
	115					120						125			
Glu	Asp	Phe	Val	Leu	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln
	130				135						140				
Ile	Gly	Gly	Met	Tyr	Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Thr	Leu	Val
145				150						155				160	
Glu	His	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Lys
			165					170						175	
Phe	Asp	Glu	Phe	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Val	Tyr	Leu	Ser	Ala
		180						185					190		
Thr	Pro	Gly	Ser	Tyr	Glu	Thr	Glu	Arg	Ala	His	Gly	Val	Val	Glu	Gln
	195					200						205			
Ile	Ile	Arg	Pro	Thr	Gly	Leu	Val	Asp	Pro	Glu	Ile	Ile	Val	Lys	Pro
	210					215					220				
Thr	Arg														
225															

<210> 559
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 559
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa
 60
 tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag
 120
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg
 180
 tatgggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa
 240
 ctaaagtgtg tccaggagct gaagccctta atcagctagg gctcacacag agtcaaggta
 300
 ggggtcaaaaa cattcagtct gggaccatat ctaga
 335

<210> 560
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 560
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met
 1 5 10 15
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp
 20 25 30
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe
 35 40 45
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr
 50 55 60
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly
 65 70 75 80
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg
 85 90

<210> 561
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 561
 ngcgcgcccc ctctccgat ggcggcggag atccagccca agcctctgac ccgcaagccg
 60
 atcctgctgc agcggatgga ggggtcccag gaggtggtga atatggccgt gatcgtgccc
 120
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga
 180
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga
 240
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgcagat
 300

gacccctgttt gtcctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc
 360
 ctggcactgc tctgagagtg ggcagcgcct gggagggttat cggaccagtg ctgtggcctc
 420
 aggcctgcaa tttgatgttg aaacccggca tgtgtttatc ggtgaccact caggcca
 477

<210> 562
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 562
 Xaa Ala Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu
 1 5 10 15
 Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val
 20 25 30
 Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val
 35 40 45
 Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln
 50 55 60
 Tyr Trp Pro Ser Val Tyr His Ala Met Pro
 65 70

<210> 563
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 563
 ccatggcaga cagggagctg agcggcctgc ggaccaggt gcaccagagc atggtgcccc
 60
 tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccceaaga
 120
 aaaggaaggg aaaaggcctc aaccttggtc agggctggaa cccacaggag gccagggtac
 180
 ggggcagacg gatggcagca gcaactgcctg agagttgggg gagctccac ggggcagcaa
 240
 gtggcgggca gagggctctg ccatctgcac tggtttctgt gaccacagtt ggctgccccg
 300
 ctccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa
 360
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat
 403

<210> 564
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 564
 Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser
 1 5 10 15
 Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala

```

                20                25                30
Thr Gly Asn Ala His Pro Lys Lys Arg Lys Gly Lys Gly Leu Asn Leu
                35                40                45
Gly Gln Gly Trp Asn Pro Gln Glu Ala Arg Val Arg Gly Arg Arg Met
                50                55                60
Ala Ala Ala Leu Pro Glu Ser Trp Gly Ser Ser His Gly Ala Ala Ser
65                70                75                80
Gly Gly Gln Arg Val Trp Pro Ser Ala Leu Val Ser Val Thr Thr Val
                85                90                95
Gly Leu Pro Ala Pro Pro Leu His His
                100                105

```

<210> 565
 <211> 311
 <212> DNA
 <213> Homo sapiens

```

<400> 565
ncctctccat ggagcagccc catcttcaact cttcacctgg ggccaggcct tccacagcag
60
ccaccaccca gcgaccacag agaggctgcg cggaggacac aggagagagg gagcccacgg
120
gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctctctctc
180
tctcccatat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240
gcttggggccg cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
300
aggaggcccc n
311

```

<210> 566
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 566
Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
1                5                10                15
Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
20                25                30
Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
35                40                45
Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
50                55                60
Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
65                70                75                80
Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
85                90                95
Ala Gln Glu Ala Pro
                100

```

<210> 567
 <211> 929

<212> DNA

<213> Homo sapiens

<400> 567

atcacatcgg tcgctgaacc ccgacgagcc tcacctgtgc gaaatattca tccttgagat
 60
 cagcccacgt gccgtcgacc tctacctcgg tgagggtcgc gggcggttac caacagccga
 120
 cctcgtcctc ggctccactc atggcgga gttccgctgc cagtccgggg atcgtcgggg
 180
 catgggcat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgcgcagca
 240
 cggatatcagt gccgcagtaa tagagggtc gcataaattc gaccggacaa tccagttgga
 300
 ggcagtccca ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc
 360
 gcagtcctaa acgctgccc acctcacggg cctgacggcg cccacgtcg gtgagcggac
 420
 gctcccgatc ccgcccga gcattgggat cgggctgtgc atgtctcatg aggaacagag
 480
 tgtgcatgga tccatcgttg cacttcgcgg tcgcccgggt tctacgatgt tggcatgccg
 540
 ttgacggatt tgggcattga tgaggcgcgt acctaccgcc cgaacgtccc tgaacccgat
 600
 ggtttcgact ctttttgggc cgagaccctc gatgagtatt ccggcgttcc ccaagatctg
 660
 acggcgggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg
 720
 gggatatcaca actctcgggt gagcgggtga ttacatgccc cagccgctgt gaacggccca
 780
 ttcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca
 840
 gtcttcgctg ctgctggcta tgcacatc gtcgtcgatc cactgggtca ggggtggggc
 900
 caccacacct tgacggaaaa ctgtccgga
 929

<210> 568

<211> 71

<212> PRT

<213> Homo sapiens

<400> 568

Met Pro Leu Thr Asp Leu Gly Ile Asp Glu Ala Arg Thr Tyr Arg Pro
 1 5 10 15
 Asn Val Pro Glu Pro Asp Gly Phe Asp Ser Phe Trp Ala Glu Thr Leu
 20 25 30
 Asp Glu Tyr Ser Gly Val Pro Gln Asp Leu Thr Ala Val Pro Phe Asp
 35 40 45
 Asn Arg Gln Ala Leu Ile Asp Thr Trp Asp Leu Ser Trp Val Gly Tyr
 50 55 60
 His Asn Ser Arg Val Ser Gly
 65 70

<210> 569
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 569
 ncgcaaacctt caacgggtgcc atctgccata ttccagggat gccagatttg gatggaaaat
 60
 accatatcac tctcgattca gaattcgtac ttgatttagt ggcttttaac aaaacgctac
 120
 ctgtcgatta cttaatggtc gaaggaacgg aacttggtga ttcaaactg gaagaactac
 180
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaaac
 240
 tcaaggaaca accaacagcc gttgctctct tctcgatgt tgataaacgg ccagagatta
 300
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcggtactt
 360
 cccatgtcta n
 371

<210> 570
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 570
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe
 1 5 10 15
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu
 20 25 30
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro
 35 40 45
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys
 50 55 60
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp
 65 70 75 80
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp
 85 90 95
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa
 100 105 110

<210> 571
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 571
 nacgcgtatc ttcgctggtc cacaccagac gtggcattaa acgacgtcac aagaacgaca
 60
 ccgggccttg acgggcccac gcacgaagag gccaaagacac tgaccgagac tactgtttcc
 120
 gttcccacct ccttcgccga cctcggcgtc cgagaagata tctgccaggc gctggaaggg
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tcccgattgc cgtcgagggc
 240
 acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgcctt cggcatcacc
 300
 atcttgacgc gcatcaccct gcccggtgac gaagggtggg aagaactcac caccaaaggg
 360
 aagcccccaa gcactcgtga tgtgcccta cccgggagct aggtcgg
 407

<210> 572
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 572
 Leu Thr Glu Thr Thr Val Ser Val Pro Thr Ser Phe Ala Asp Leu Gly
 1 5 10 15
 Val Arg Glu Asp Ile Cys Gln Ala Leu Glu Gly Val Gly Ile Val Ser
 20 25 30
 Pro Phe Pro Ile Gln Ala Met Ser Ile Pro Ile Ala Val Glu Gly Thr
 35 40 45
 Asp Leu Ile Gly Gln Ala Arg Thr Gly Thr Gly Lys Thr Leu Ala Phe
 50 55 60
 Gly Ile Thr Ile Leu Gln Arg Ile Thr Leu Pro Gly Asp Glu Gly Trp
 65 70 75 80
 Glu Glu Leu Thr Thr Lys Gly Lys Pro Pro Ser Thr Arg Asp Val Pro
 85 90 95
 Leu Pro Gly Ser
 100

<210> 573
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 573
 acggtcttac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg
 60
 actacgaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg
 120
 tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc
 180
 ccaccccgca ggcagccgag gactttggcc gccgactggc tcacaccac gcagccgggg
 240
 cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcggccgtg
 300
 ctccccctgcc actgccgtcc gaaccaatct cctcctgggg agagttttac gctcagtgcc
 360
 gcatcgaacc atatatggac agtctcgacg ctg
 393

<210> 574
 <211> 124
 <212> PRT

<213> Homo sapiens

<400> 574

```

Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10          15
Val Ala Gly Leu Met Trp Leu Ala Ala Ala Arg Pro Asp Gly Ala Gly
          20          25          30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
          35          40          45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
          50          55          60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
          65          70          75          80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
          85          90          95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
          100         105         110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
          115         120

```

<210> 575

<211> 372

<212> DNA

<213> Homo sapiens

<400> 575

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nntatccatg cagacatggg accaggggtct ctgagggcag gaagcaaagt gggtagggg
60
gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttcagg gcctcagggg
240
actgggggtca gaacagccta tggagaaagg tcaaggggcc ttgggcctag gagtacaggg
300
ccaggggggtg aggcaggctt tagagatggg tcaggaggcc tccaaggaat gggatcagca
360
gatggggcccgt
372

```

<210> 576

<211> 124

<212> PRT

<213> Homo sapiens

<400> 576

```

Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10          15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
          20          25          30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
          35          40          45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50              55              60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65              70              75              80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85              90              95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100              105              110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115              120

```

<210> 577

<211> 432

<212> DNA

<213> Homo sapiens

<400> 577

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nagcgcgaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcggc gggcgcggtat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgcctct tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaaccctg catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccaccta caagattccc tcaacgccgc catgaccgcg
300
ccaaagcaag gcccgaaacg caccctggag tcagcggtag tggccctgct ggactacatc
360
gacgaccgtc cagacgggtt tcggatcacc tcgcgagact cctcggtcgg ttcagccacc
420
ggttcgtacg cg
432

```

<210> 578

<211> 118

<212> PRT

<213> Homo sapiens

<400> 578

```

Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1              5              10              15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20              25              30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35              40              45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
      50              55              60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65              70              75              80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85              90              95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100              105              110
Ala Thr Gly Ser Tyr Ala

```

115

<210> 579
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 579
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 60
 ctgctcccag ggatcaccac cttaccacagc gggccacctg ctcccccggt ccccgcgggc
 120
 cccggcccct ggctgcgagc acccctcttc agcctgaagc tgtccgacac agaggacgtc
 180
 tttcctcgcc gcgcggggcc gctcgaggtc ccggccgaca gccgcgtggt cgtgcaggcg
 240
 gccttggtccc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg
 300
 tcttcacgcc cggccccggg
 320

<210> 580
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 580
 Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr
 1 5 10 15
 Leu Pro Ser Gly Pro Pro Ala Pro Phe Pro Ala Ala Pro Gly Pro
 20 25 30
 Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp
 35 40 45
 Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg
 50 55 60
 Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu
 65 70 75 80
 Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro
 85 90 95

<210> 581
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 581
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 cacgtcggca tgggcttcaa gacgccagta cgcattgaca gcgtcgaccc caagaccgc
 120
 gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacggtggac
 180
 accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgcggaa
 240

ctggatcgcc atgacgtgct gtcgtttctc ggccgagtt acttccgtgc ggtggacgca
 300
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc
 360
 gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt
 419

<210> 582

<211> 139

<212> PRT

<213> Homo sapiens

<400> 582

Xaa	Asp	Gly	Asn	His	Ser	Leu	Trp	Lys	Glu	Leu	Asn	Gly	Gln	Leu	Asp
1				5					10					15	
Val	Gln	Phe	Phe	His	Val	Gly	Met	Gly	Phe	Lys	Thr	Pro	Val	Arg	Met
			20					25					30		
His	Ser	Val	Asp	Pro	Lys	Thr	Arg	Glu	Ala	Arg	Glu	Val	His	Phe	Arg
		35				40					45				
Pro	Ser	Leu	Phe	Asn	Tyr	Ala	Lys	Thr	Thr	Val	Asp	Thr	Lys	Gln	Leu
		50				55					60				
Thr	Gly	Asp	Leu	Gly	Phe	Ser	Gly	Phe	Lys	Leu	Phe	Lys	Ala	Pro	Glu
65				70					75					80	
Leu	Asp	Arg	His	Asp	Val	Leu	Ser	Phe	Leu	Gly	Ala	Ser	Tyr	Phe	Arg
			85						90					95	
Ala	Val	Asp	Ala	Thr	Arg	Gln	Tyr	Gly	Leu	Ser	Ala	Arg	Gly	Leu	Ala
		100						105					110		
Ile	Asp	Thr	Tyr	Ala	Lys	Lys	Arg	Glu	Glu	Phe	Pro	Asp	Phe	Thr	Gln
		115				120						125			
Phe	Trp	Phe	Glu	Thr	Pro	Ser	Lys	Asp	Pro	Arg					
		130				135									

<210> 583

<211> 407

<212> DNA

<213> Homo sapiens

<400> 583

cttttgatca atgctgatgg cacgaagcta tcgaaaaggc cgggtgatgt ccgcgtagct
 60
 gattatatgg agcagggatg ggagccggag acgctggtga acctagttgc cctcacgggc
 120
 tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc
 180
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt
 240
 gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag
 300
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat
 360
 tcagatgatt atatcctgcg cgtcgtaaca ctgggacccc aacgcgt
 407

<210> 584

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 584
 Leu Leu Ile Asn Ala Asp Gly Thr Lys Leu Ser Lys Arg Ser Gly Asp
 1 5 10 15
 Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu
 20 25 30
 Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His
 35 40 45
 Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu
 50 55 60
 Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu
 65 70 75 80
 Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr
 85 90 95
 Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile
 100 105 110
 Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val
 115 120 125
 Val Thr Leu Gly Pro Gln Arg
 130 135

<210> 585
 <211> 502
 <212> DNA
 <213> Homo sapiens

<400> 585
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 60
 gatattttgt tgtgcgcggt gggattgttg gttcagcacc gtgacatcac tgaggagatt
 120
 cgggctcggg accgacattt cggtgtcgac gaataccagg acgtttctcc gctgcagcat
 180
 aggttgcttg aactgtgggt tggcgatcga aatgatgtat gcgtcgtggg agatccgcac
 240
 caggccattc actcttatgc aggcgcacga gctgactacc tcctcgactt cgttgccgat
 300
 catcctggcg ctaaaccgat cgatttggtt cgcaactacc gctccactcc cgagatcggt
 360
 cagttggcca atgaagtctt tgtcaaccgt atgactccag aggaggcttt ggaacatggc
 420
 aggggagtca cattggtttc gcggggtcga tccggtcccg agcccatcta tcaggctctc
 480
 ggggacgatg cctccgaagc tt
 502

<210> 586
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 586

Xaa Arg Val Leu Ala Gly Tyr Glu Ala Val Lys Arg Glu Arg Cys Val
 1 5 10 15
 Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln
 20 25 30
 His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val
 35 40 45
 Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu
 50 55 60
 Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His
 65 70 75 80
 Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp
 85 90 95
 Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn
 100 105 110
 Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val
 115 120 125
 Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr
 130 135 140
 Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu
 145 150 155 160
 Gly Asp Asp Ala Ser Glu Ala
 165

<210> 587

<211> 746

<212> DNA

<213> Homo sapiens

<400> 587

gcgtcctgcc tcgagggcct cgggagcttc cgctgcctct gttggccagg ctacagcggc
 60
 gagctgtgcg aggtggacga ggacgagtgt gcatcgagcc cctgccagca tgggggcccga
 120
 tgcttcgacg gctctgaccc ggccctctac ggggggtgtcc aggccgcctt ccctggcgcc
 180
 ttcagcttcc gccatgctgc ggggttctctg tgccactgcc ctctgggctt tgagggagcc
 240
 gactgcggtg tggaggtgga cgagtgtgcc tcacggccat gcctcaatgg aggccactgc
 300
 caggacctgc ccaatggctt ccagtgtcac tgcccagatg gctacgcagg gccgacatgt
 360
 gaggaagatg tggatgaatg cctgtccgat ccctgcctgc acggcggaac ctgcagtgc
 420
 actgtggcag gctatatctg caggtgcccga gagacctggg gtgggcgcga ctgttctgtg
 480
 cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcat ccctatcttc
 540
 gagtctgggg tccacagtta cgtctgccac tgcccacctg gtacccatgg accgttctgt
 600
 ggccagaata ccaccttctc tgtgatggct gggagcccca ttcaggcatc agtgccagct
 660
 ggtggccccc tgggtctggc actgaggttt cgcaccacac tgcccgctgg gaccttggcc
 720

actcgcaatg acaccaagga aagctt

746

<210> 588

<211> 248

<212> PRT

<213> Homo sapiens

<400> 588

Ala Ser Cys Leu Glu Gly Leu Gly Ser Phe Arg Cys Leu Cys Trp Pro
 1 5 10 15
 Gly Tyr Ser Gly Glu Leu Cys Glu Val Asp Glu Asp Glu Cys Ala Ser
 20 25 30
 Ser Pro Cys Gln His Gly Gly Arg Cys Leu Gln Arg Ser Asp Pro Ala
 35 40 45
 Leu Tyr Gly Gly Val Gln Ala Ala Phe Pro Gly Ala Phe Ser Phe Arg
 50 55 60
 His Ala Ala Gly Phe Leu Cys His Cys Pro Pro Gly Phe Glu Gly Ala
 65 70 75 80
 Asp Cys Gly Val Glu Val Asp Glu Cys Ala Ser Arg Pro Cys Leu Asn
 85 90 95
 Gly Gly His Cys Gln Asp Leu Pro Asn Gly Phe Gln Cys His Cys Pro
 100 105 110
 Asp Gly Tyr Ala Gly Pro Thr Cys Glu Glu Asp Val Asp Glu Cys Leu
 115 120 125
 Ser Asp Pro Cys Leu His Gly Gly Thr Cys Ser Asp Thr Val Ala Gly
 130 135 140
 Tyr Ile Cys Arg Cys Pro Glu Thr Trp Gly Gly Arg Asp Cys Ser Val
 145 150 155 160
 Gln Leu Thr Gly Cys Gln Gly His Thr Cys Pro Leu Ala Ala Thr Cys
 165 170 175
 Ile Pro Ile Phe Glu Ser Gly Val His Ser Tyr Val Cys His Cys Pro
 180 185 190
 Pro Gly Thr His Gly Pro Phe Cys Gly Gln Asn Thr Thr Phe Ser Val
 195 200 205
 Met Ala Gly Ser Pro Ile Gln Ala Ser Val Pro Ala Gly Gly Pro Leu
 210 215 220
 Gly Leu Ala Leu Arg Phe Arg Thr Thr Leu Pro Ala Gly Thr Leu Ala
 225 230 235 240
 Thr Arg Asn Asp Thr Lys Glu Ser
 245

<210> 589

<211> 381

<212> DNA

<213> Homo sapiens

<400> 589

atctcacaag tacaattaca gtctcaagaa ctgagctatc agcaaaagca aggtcttcag
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 ccagtacctc tgcaagccac tatgagtgtc gcaactggta tccagccatc gcctgtaaat
 120
 gtgggttggtg taacttcagc tttagggtcag cagccttcca tttccagttt ggctcaacc
 180

cagctaccat attctcaggc ggctcctcca gtgcaaactc cccttccagg ggcaccacca
 240
 ccccaacagt tacagtatgg acaacagcaa ccaatgggtt ctacacagat ggccccaggc
 300
 catgtcaaat cagtgactca aaatcctgct tcagagtatg tacaacagca gccatttctt
 360
 caaacagcaa tgtcctccgg a
 381

<210> 590

<211> 127

<212> PRT

<213> Homo sapiens

<400> 590

Ile	Ser	Gln	Val	Gln	Leu	Gln	Ser	Gln	Glu	Leu	Ser	Tyr	Gln	Gln	Lys
1				5					10					15	
Gln	Gly	Leu	Gln	Pro	Val	Pro	Leu	Gln	Ala	Thr	Met	Ser	Ala	Ala	Thr
		20						25					30		
Gly	Ile	Gln	Pro	Ser	Pro	Val	Asn	Val	Val	Gly	Val	Thr	Ser	Ala	Leu
	35						40					45			
Gly	Gln	Gln	Pro	Ser	Ile	Ser	Ser	Leu	Ala	Gln	Pro	Gln	Leu	Pro	Tyr
	50					55					60				
Ser	Gln	Ala	Ala	Pro	Pro	Val	Gln	Thr	Pro	Leu	Pro	Gly	Ala	Pro	Pro
65					70					75				80	
Pro	Gln	Gln	Leu	Gln	Tyr	Gly	Gln	Gln	Gln	Pro	Met	Val	Ser	Thr	Gln
			85					90						95	
Met	Ala	Pro	Gly	His	Val	Lys	Ser	Val	Thr	Gln	Asn	Pro	Ala	Ser	Glu
		100						105					110		
Tyr	Val	Gln	Gln	Gln	Pro	Ile	Leu	Gln	Thr	Ala	Met	Ser	Ser	Gly	
		115					120						125		

<210> 591

<211> 684

<212> DNA

<213> Homo sapiens

<400> 591

tcgaccatgg atcatctgcg ccacggcatc cacctgctgt gttatgctga gaagaacccg
 60
 aagcaggaat acaagcgga gtcgttcacc ctgttctccg agctgctgga ctgatcaag
 120
 cgcgattcga ttcgggtcct cttccacgtc caggggcccgg gggaaaaatc cgtatcgaaa
 180
 naaaaagcgc gcctgcgtca ggaagccgaa gccctggccc agcgcattgca gttcgagcac
 240
 gctgaagccc caggcctgga cgcgccgga atcctcggtg aagaagtcga tgcgcacctg
 300
 gccaccgcgc cggtagcga cgagcagaag ctgggcccgt acgaactgtg ctactgcggt
 360
 tcgggcaaga agtacaagca ctgccacggt cagatcagct aagggtctta ccggatactg
 420
 aaatacctgc gccgcgaccg gcattagccg tcgcggcggt tttccatttg aaacactgcc
 480

cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcattgggtg ttgggttctgg
 540
 gtccttggcc tacgttgacac ccggttgccg gttttgaact cggatcgcgc tcggccggta
 600
 tcaagcgcgc tgggcgcaag gatgtggtgg cgatgcgctg cgccgaaggt tccacggtgg
 660
 cgggggtggt taccctcaac gcgt
 684

<210> 592

<211> 133

<212> PRT

<213> Homo sapiens

<400> 592

Ser	Thr	Met	Asp	His	Leu	Arg	His	Gly	Ile	His	Leu	Arg	Gly	Tyr	Ala
1				5					10					15	
Gln	Lys	Asn	Pro	Lys	Gln	Glu	Tyr	Lys	Arg	Glu	Ser	Phe	Thr	Leu	Phe
			20					25					30		
Ser	Glu	Leu	Leu	Asp	Ser	Ile	Lys	Arg	Asp	Ser	Ile	Arg	Val	Leu	Phe
		35					40					45			
His	Val	Gln	Gly	Pro	Gly	Glu	Lys	Ser	Val	Ser	Lys	Xaa	Lys	Ala	Arg
		50				55					60				
Leu	Arg	Gln	Glu	Ala	Glu	Ala	Leu	Ala	Gln	Arg	Met	Gln	Phe	Glu	His
65					70					75				80	
Ala	Glu	Ala	Pro	Gly	Leu	Asp	Ala	Pro	Glu	Ile	Leu	Gly	Glu	Glu	Val
				85					90					95	
Asp	Val	Ala	Leu	Ala	Thr	Ala	Pro	Val	Arg	Asn	Glu	Gln	Lys	Leu	Gly
			100					105					110		
Arg	Asn	Glu	Leu	Cys	Tyr	Cys	Gly	Ser	Gly	Lys	Lys	Tyr	Lys	His	Cys
		115					120					125			
His	Gly	Gln	Ile	Ser											
			130												

<210> 593

<211> 615

<212> DNA

<213> Homo sapiens

<400> 593

nnacgcgtgc agaccgcgcg gaggctcgcct ccggtgcgga tagcgttagg ctcccaaacc
 60
 tgtgaaaccg tcacggtaga gcgtcgtggc gggctaccac ttagagcggc ccgattcacc
 120
 gataccatcc ccgcgccgct aggccagcca cgatgggtcga cggccaccat ccagacccca
 180
 gtcataccta ctacacgtgg tcgattcgtg atcgcccccg tcatgatgcg caccatcgac
 240
 ccgtttggca tggcccgcca tcacaccgat ctcggtcagg ttgccgaagt cattgtcacg
 300
 ccaaggatcg tcgatttggg cgccctccggg gagctcgggg gtcagggatt cgacacaagg
 360
 tcctcagcga tccatgccgg acgacgtggt cccgacgatg ccatggtgcg cgattggcac
 420

accggagact cgggtgcgacg cattcactgg cgctccaccg ctcaccgcgg ggacctcatg
 480
 gtccgatgcg aggagcaggc ctggaaccca tccgtcgtca tcgtgttga ttctcgggct
 540
 cggcgctacg ctggaactgg ccccgacgca tcctttgaat gggccgtcaa cgcggtggca
 600
 tccatctcga cgcgt
 615

<210> 594

<211> 205

<212> PRT

<213> Homo sapiens

<400> 594

Xaa	Arg	Val	Gln	Thr	Ala	Arg	Ser	Leu	Ala	Pro	Val	Arg	Ile	Ala	Leu
1				5					10					15	
Gly	Ser	Gln	Thr	Cys	Glu	Thr	Val	Thr	Val	Glu	Arg	Arg	Gly	Gly	Leu
		20						25					30		
Pro	Leu	Arg	Ala	Ala	Arg	Phe	Thr	Asp	Thr	Ile	Pro	Ala	Pro	Leu	Gly
	35					40						45			
Gln	Pro	Arg	Trp	Ser	Thr	Ala	Thr	Ile	Gln	Thr	Pro	Val	Ile	Pro	Thr
	50					55					60				
Thr	Arg	Gly	Arg	Phe	Val	Ile	Gly	Pro	Val	Met	Met	Arg	Thr	Ile	Asp
65					70					75				80	
Pro	Phe	Gly	Met	Ala	Arg	His	His	Thr	Asp	Leu	Gly	Gln	Val	Ala	Glu
				85					90					95	
Val	Ile	Val	Thr	Pro	Arg	Ile	Val	Asp	Leu	Gly	Ala	Ser	Gly	Glu	Leu
		100						105					110		
Gly	Gly	Gln	Gly	Phe	Asp	Thr	Arg	Ser	Ser	Ala	Ile	His	Ala	Gly	Arg
		115					120					125			
Arg	Gly	Pro	Asp	Asp	Ala	Met	Val	Arg	Asp	Trp	His	Thr	Gly	Asp	Ser
	130					135					140				
Val	Arg	Arg	Ile	His	Trp	Arg	Ser	Thr	Ala	His	Arg	Gly	Asp	Leu	Met
					150					155				160	
Val	Arg	Cys	Glu	Glu	Gln	Ala	Trp	Asn	Pro	Ser	Val	Val	Ile	Val	Leu
			165					170						175	
Asp	Ser	Arg	Ala	Arg	Arg	His	Ala	Gly	Thr	Gly	Pro	Asp	Ala	Ser	Phe
		180						185				190			
Glu	Trp	Ala	Val	Asn	Ala	Val	Ala	Ser	Ile	Ser	Thr	Arg			
	195					200						205			

<210> 595

<211> 303

<212> DNA

<213> Homo sapiens

<400> 595

acgcgtccta gccgcagtga atgttgctga accccggtga cctcacagtg gaggggcggc
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 cccatggggc catcggaccg cgccgcgcgg gggcggttcgc cagggcctcc gcagaagccc
 120
 gcctgtgccc gcaaccgccc cgaaattctc tccctggcac cgtgtccgct ttacggagcc
 180

cggagcaagg ctcagaaaaa tgtcccagcc aaaaacatgg tacatgcctg tcatcaggca
 240
 agtcttcaaa gagcggctgg gaccaggggc cgagggacct cgtttagagg cggcttaggg
 300
 gga
 303

<210> 596

<211> 88

<212> PRT

<213> Homo sapiens

<400> 596

Met	Leu	Leu	Asn	Pro	Gly	Asp	Leu	Thr	Val	Glu	Gly	Arg	Pro	His	Gly
1			5					10					15		
Ala	Ile	Gly	Pro	Arg	Arg	Ala	Gly	Ala	Phe	Ala	Arg	Ala	Ser	Ala	Glu
		20				25							30		
Ala	Arg	Leu	Cys	Pro	Gln	Pro	Pro	Arg	Asn	Ser	Leu	Pro	Gly	Thr	Val
	35				40						45				
Ser	Ala	Leu	Arg	Ser	Pro	Glu	Gln	Gly	Ser	Glu	Lys	Cys	Pro	Ser	Gln
	50				55					60					
Lys	His	Gly	Thr	Cys	Leu	Ser	Ser	Gly	Lys	Ser	Ser	Lys	Ser	Gly	Trp
65				70					75					80	
Asp	Gln	Gly	Pro	Arg	Asp	Leu	Val								
				85											

<210> 597

<211> 2709

<212> DNA

<213> Homo sapiens

<400> 597

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<210> 598

<211> 240

<212> PRT

<213> Homo sapiens

<400> 598

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 20 25 30
 Glu Cys Gly Lys Ser Phe Gly Asp Leu Val Ser Arg Arg Lys His Met
 35 40 45
 Arg Ile His Ile Val Lys Lys Pro Val Glu Cys Arg Gln Cys Gly Lys
 50 55 60
 Thr Phe Arg Asn Gln Ser Ile Leu Lys Thr His Met Asn Ser His Thr
 65 70 75 80
 Gly Glu Lys Pro Tyr Gly Cys Asp Leu Cys Gly Lys Ala Phe Ser Ala
 85 90 95
 Ser Ser Asn Leu Thr Ala His Arg Lys Ile His Thr Gln Glu Arg Arg
 100 105 110
 Tyr Glu Cys Ala Ala Cys Gly Lys Val Phe Gly Asp Tyr Leu Ser Arg
 115 120 125
 Arg Arg His Met Ser Val His Leu Val Lys Lys Arg Val Glu Cys Arg
 130 135 140
 His Cys Gly Lys Ala Phe Arg Asn Gln Ser Thr Leu Lys Thr His Met
 145 150 155 160
 Arg Ser His Thr Gly Glu Lys Pro Tyr Glu Cys Asp His Cys Gly Lys
 165 170 175
 Ala Phe Ser Ile Gly Ser Asn Leu Asn Val His Arg Arg Ile His Thr
 180 185 190
 Gly Glu Lys Pro Tyr Glu Cys Leu Val Cys Gly Lys Ala Phe Ser Asp
 195 200 205
 His Ser Ser Leu Arg Ser His Val Lys Thr His Arg Gly Glu Lys Leu
 210 215 220
 Phe Xaa Cys His Pro Cys Gly Lys Gly Ser Ser Glu Arg Ala Xaa Leu
 225 230 235 240

<210> 599
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 599
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 caggcatgtt tgccggggcg catcccttgc acttgacgtc cgtggcctat cggccgaggg
 180
 gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgcg aggagcgtgt tggcagacta
 240
 tggggctcgt cggaggacga ggatgtgagt ggcgatggct ttgcgcgact gggcgtattc
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<210> 600
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 600
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 20 25 30
 Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn
 35 40 45
 Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly
 50 55 60
 Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys
 65 70 75 80
 Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp
 85 90 95
 Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg
 100 105 110

<210> 601
 <211> 421
 <212> DNA
 <213> Homo sapiens

<400> 601
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 120
 cagctgtcga tggccccgct gtctatcgggt aatctgcaat cgggtggacgt ggtgcgcggc
 180
 ggcggcgcg tgcgctacgg gccgcagaac gtcggcgcg tgatcaactt cgttaccgga
 240

gacattccca aaacgtttgg cggtgccgcc agcgtacaaa cccaggggtgc cagccacggc
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 ggccctgaaga ccctgaccag cgcctccgtg ggcggcacccg cagacaacgg cctcggcgcc
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 421

<210> 602
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 602
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 20 25 30
 Ala Val Ala Pro Tyr Gly Gln Pro Gln Leu Ser Met Ala Pro Leu Ser
 35 40 45
 Ile Gly Asn Leu Gln Ser Val Asp Val Val Arg Gly Gly Gly Ala Val
 50 55 60
 Arg Tyr Gly Pro Gln Asn Val Gly Gly Val Ile Asn Phe Val Thr Arg
 65 70 75 80
 Asp Ile Pro Lys Thr Phe Gly Gly Ala Ala Ser Val Gln Thr Gln Gly
 85 90 95
 Ala Ser His Gly Gly Leu Lys Thr Leu Thr Ser Ala Ser Val Gly Gly
 100 105 110
 Thr Ala Asp Asn Gly Leu Gly Ala Glu Leu Leu Tyr Ser Gly Leu His
 115 120 125
 Gly Gln Gly Tyr Arg Asp Asn Asn Asp Asn Thr Asp
 130 135 140

<210> 603
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 603
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 180
 ggcaaaccgg aagacctcgt agagggtgtg cgccgcggtg tggacatgtt cgattgcgtg
 240
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 300
 cgtaacgag
 309

<210> 604

<211> 103
 <212> PRT
 <213> Homo sapiens

<400> 604
 Xaa Gly Gly Met His Glu Ser Leu Arg Lys Arg Ser Leu Glu Gly Leu
 1 5 10 15
 Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly
 20 25 30
 Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu
 35 40 45
 Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu
 50 55 60
 Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val
 65 70 75 80
 Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly
 85 90 95
 Val Leu Lys Ile Arg Asn Ala
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<210> 605
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 605
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 120
 caccacatc acatttcagt accttggtta tcttcaatcg gaaaaaaga ttggagtaaa
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 tggttgagttt tggtaatggc aacgccgttt gactggaaga gttttggaag gtaatgaccg
 240
 attcccagtg caaagggtccc catgctacat cctgcgacaa tgaggccggt agcacgttta
 300
 ttgcttcgct gctttgccga acgccaacct ctgtaccgat acgctgatac tgattgttga
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 tggatataggc ttgcgccagg taggtataat tgggtcaattc gtccatggca atgcgcagtg
 420
 aagtcttg
 428

<210> 606
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 606
 Met Asp Glu Leu Thr Asn Tyr Thr Tyr Leu Ala Gln Ala Tyr Thr Ile
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 Asn Asn Gln Tyr Gln Arg Ile Gly Thr Glu Val Gly Val Arg Gln Ser
 20 25 30
 Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

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      35              40              45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
      50              55              60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
65              70              75              80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85              90              95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100             105             110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
      115             120             125
Asn Tyr Pro Ile Val Asn Ala
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<210> 607
 <211> 366
 <212> DNA
 <213> Homo sapiens

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<400> 607
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120
gttttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
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ttgggcacca cgttgccgca gacattcaag aagcccaccg acgaaaagta tttgcccgag
360
gacgcg
366

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<210> 608
 <211> 122
 <212> PRT
 <213> Homo sapiens

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<400> 608
Asp His Asp Glu Leu Trp Ala Tyr Thr Tyr Glu Asn Val Met Ala Leu
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      20              25              30
Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
      35              40              45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
      50              55              60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
65              70              75              80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
      85              90              95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

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100 105 110
 Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala
 115 120

<210> 609
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 609
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 180
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 240
 cctggaccat ctggggcgggg ggcgccgccg tgggtggtggc ggggtggagcc g
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<210> 610
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 610
 Met Ser Pro Val Ala Met Asp Asp Ser Ser Ser Pro Tyr Pro Ala Trp
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 Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro
 20 25 30
 Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys
 35 40 45
 Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp
 50 55 60
 Trp Arg Val Glu Pro
 65

<210> 611
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 611
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 120
 acgcgcacatc ggcgcacatcagggtc ggcactcttg agcaagcgcct tgatgcagggt
 180
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 240
 atggcaacgg ttctggagag ctatctgcgg gaagagtttc ccagtagcga aatcaggagc
 300

gattcgcaga acaagtccat tgacgagacc atctctatcg tccgctccta tctgcggtag
 360
 aggcaccagg gtgtcctcgg tgagggcaaa ttt
 393

<210> 612
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 612
 Xaa Ile Leu Cys Arg Phe Ser Val Ala Tyr Thr Met Gly Glu Tyr Cys
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 Ile Met Arg Arg Cys Thr Gln Val Glu Arg Cys Ser Met Pro His Ser
 20 25 30
 Pro Glu Glu Lys Lys Gln Ala Leu Thr Arg Ile Arg Arg Ile Lys Gly
 35 40 45
 Gln Val Ala Thr Leu Glu Gln Ala Leu Asp Ala Gly Ala Lys Cys Pro
 50 55 60
 Ala Ile Leu Gln Gln Leu Ala Ala Val Arg Gly Ala Val Asn Gly Leu
 65 70 75 80
 Met Ala Thr Val Leu Glu Ser Tyr Leu Arg Glu Glu Phe Pro Ser Ser
 85 90 95
 Glu Ile Arg Ser Asp Ser Gln Asn Lys Ser Ile Asp Glu Thr Ile Ser
 100 105 110
 Ile Val Arg Ser Tyr Leu Arg
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<210> 613
 <211> 567
 <212> DNA
 <213> Homo sapiens

<400> 613
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 120
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 180
 tagaaattca gatttaccta gaagtccttg gggccaaatc acagatttga aaacatctga
 240
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 300
 agacacccaaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt
 360
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 420
 tttatgtggc tatttggagg aagaagagga agtaccacc gttcaaaaat ttatagacca
 480
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 540
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 567

<210> 614
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 614
 Met Leu Leu Ala Pro Gln Gly Arg Ser Phe Ser Lys Lys Arg Met Gly
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 Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr
 20 25 30
 Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala
 35 40 45
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu
 50 55 60
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln
 65 70 75 80
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn
 85 90 95
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu
 100 105 110
 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala
 115 120 125
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu
 130 135 140
 Glu Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu
 145 150 155 160
 Leu His Lys Asn Val Val Asp Ser Ala Met Met Glu Asp Leu Gly Arg
 165 170 175
 Lys Glu Asn Gln Asp Lys Lys Gln Gln Lys Asp
 180 185

<210> 615
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 615
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 gggcggggcg cgtgtgcagg gccattggta gccgcagctg tcattcttga tgatcgaga
 180
 tccggcagga ttgcggggct agcagattcc aagacactat ctgcggccaa gagagaggcc
 240
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 300
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 360
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 480

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 540
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 cattcatcat gagtgccgaa gatct
 685

<210> 616
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 616
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 20 25 30
 Gly Ala Cys Ala Gly Pro Leu Val Ala Ala Val Ile Leu Asp Asp
 35 40 45
 Arg Arg Ser Gly Arg Ile Ala Gly Leu Ala Asp Ser Lys Thr Leu Ser
 50 55 60
 Ala Ala Lys Arg Glu Ala Leu Phe Asn Val Ile Met Asp Lys Ala Leu
 65 70 75 80
 Ala Val Ser Trp Val Arg Val Glu Ala Asp Glu Cys Asp Arg Leu Gly
 85 90 95
 Met Gln Glu Ala Asp Ile Ser Gly Leu Arg Arg Ala Val Val Arg Leu
 100 105 110
 Gly Val Glu Pro Gly Tyr Val Leu Ser Asp Gly Phe Pro Val Asp Gly
 115 120 125
 Leu Thr Val Pro Asp Leu Gly Met Trp Lys Gly Asp Ser Val Cys Ala
 130 135 140
 Cys Val Ala Ala Ala Ser Ile Val Ala Lys Val Ala Arg Asp Arg Ile
 145 150 155 160
 Met Ile Ala Met Asp Ala Glu Ile Pro Gly Tyr Asp Phe Ala Val His
 165 170 175
 Lys Gly Tyr Ala Thr Ala Leu His Gln Arg Arg Leu Lys Glu Leu Gly
 180 185 190
 Pro Ser Arg Gln His Arg Met Ser Tyr Ala Asn Val Arg Arg Ala Ala
 195 200 205
 Arg Leu His Ser Ser
 210

<210> 617
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 617
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 120

tcggcgccaa cggccagcgc caggccatgt tectcgaaaa cgtttcgggc cttcccgag
 180
 cgaatcctcc gaaacttcga cctgtcccaa caagactctg cactcgtgat ttcacaaagc
 240
 gctgcaacgt cgtgccaatc gagatggccg aggagttcca gcgtcgcggc gtccgcgtcg
 300
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 337

<210> 618

<211> 112

<212> PRT

<213> Homo sapiens

<400> 618

Xaa	Thr	Cys	Leu	Ala	Arg	Gly	Thr	Arg	Gly	Ser	Trp	Ser	Arg	Lys	Cys
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			20					25					30		
Arg	Cys	Arg	Ser	Thr	Thr	Ser	Ser	Ala	Pro	Thr	Ala	Ser	Ala	Arg	
		35				40					45				
Pro	Cys	Ser	Ser	Lys	Thr	Phe	Pro	Ala	Phe	Pro	Glu	Arg	Ile	Leu	Arg
	50					55				60					
Asn	Phe	Asp	Leu	Ser	Gln	Gln	Asp	Ser	Ala	Leu	Val	Ile	Ser	Ser	Ser
65					70					75				80	
Ala	Ala	Thr	Ser	Cys	Gln	Ser	Arg	Trp	Pro	Arg	Ser	Ser	Ser	Val	Ala
			85						90					95	
Ala	Ser	Ala	Ser	Ser	Arg	Ser	Ser	Arg	Trp	Arg	Thr	Arg	Arg	Arg	Arg
			100					105						110	

<210> 619

<211> 425

<212> DNA

<213> Homo sapiens

<400> 619

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 gttttatagc atctttgtca gaaggcaaacc ctgccaaacc agatgaatcg atgccactct
 180
 caaacttgct caaatgttca attaaatcat ccaagttgtg gccatgetta ccgcttccag
 240
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Leu Gln Asn Gly Ser Arg Leu Glu Glu Pro Ile Phe Thr Pro Ala Ile
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Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
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Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
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<211> 1294

<212> PRT

<213> Homo sapiens

<400> 628

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	1155	1160
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	1250	1255
Cys Thr Asp Lys Tyr Asp Phe Thr Thr His Ile Gln Arg Gly Leu His		1260
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 <212> DNA
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Leu Val Ala Trp Gly Lys Leu Ser Gly Lys Val Ala Ser Lys Pro Leu
      35           40           45
Thr Leu Pro Gly Arg Asn Trp Ile Asn Leu Gly Leu Leu Val Val Ile
      50           55           60
Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp
      65           70           75           80
Leu Pro Leu Ala Leu Leu Thr Leu Ala Ser Leu Phe Leu Gly Phe His
      85           90           95
Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met
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Leu Asn Ser Tyr Ser Gly Trp Ala Ala Ala Phe Ser Gly Phe Ser Leu
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His Ile Pro Val Leu Ile Val Thr Gly
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<210> 631

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Glu Arg Asp Gln Tyr Lys Leu Met Ala Asn Gln Leu Arg Glu Arg His
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 Val Asp Ala Val Val Asn Ala Val Glu His Tyr Ser Glu Leu Thr Pro
 35 40 45
 Gln Leu Leu Thr Thr Gly Gly Thr Ser Asp Gly Arg Phe Ile Ala Gln
 50 55 60
 Met Gly Xaa Gln Val Val Glu Leu Gly Pro Val Asn Ala Thr Ile His
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<210> 636

<211> 619

<212> PRT

<213> Homo sapiens

<400> 636

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Val	Val	Leu	Asp	Phe	Ser	Ala	Asp	Ala	Thr	Glu	Gly	Pro	Ile	Arg	Ala
			20					25					30		
Tyr	Leu	Leu	Asp	Val	Val	Asp	Ser	Glu	Glu	Gln	Asp	Met	Ala	Leu	Asn
			35				40					45			
Ile	His	Ala	Phe	Ser	Ala	Gly	Leu	Gly	Gly	Ala	Ile	Gly	Tyr	Val	Leu
	50					55					60				
Gly	Gly	Leu	Asp	Trp	Thr	Gln	Thr	Phe	Leu	Gly	Ser	Trp	Phe	Arg	Thr
65					70					75				80	
Gln	Asn	Gln	Val	Leu	Phe	Phe	Phe	Ala	Ala	Ile	Ile	Phe	Thr	Val	Ser
				85					90					95	
Val	Ala	Leu	His	Leu	Phe	Ser	Ile	Asp	Glu	Glu	Gln	Tyr	Ser	Pro	Gln
			100					105					110		
Gln	Glu	Arg	Ser	Ala	Glu	Glu	Pro	Gly	Ala	Leu	Asp	Gly	Gly	Glu	Pro
		115					120					125			
His	Gly	Val	Pro	Ala	Phe	Pro	Asp	Glu	Val	Gln	Ser	Glu	His	Glu	Leu
	130					135					140				
Ala	Leu	Asp	Tyr	Pro	Asp	Val	Asp	Ile	Met	Arg	Ser	Lys	Ser	Asp	Ser
145					150					155				160	
Ala	Leu	His	Val	Pro	Asp	Thr	Ala	Leu	Asp	Leu	Glu	Pro	Glu	Leu	Leu
				165					170					175	
Phe	Leu	His	Asp	Ile	Glu	Pro	Ser	Ile	Phe	His	Asp	Ala	Ser	Tyr	Pro
			180					185					190		
Ala	Thr	Pro	Arg	Ser	Thr	Ser	Gln	Glu	Leu	Ala	Lys	Thr	Lys	Leu	Pro
		195					200						205		
Arg	Leu	Ala	Thr	Phe	Leu	Lys	Glu	Ala	Ala	Lys	Glu	Asp	Glu	Thr	Leu
	210					215					220				
Leu	Asp	Asn	His	Leu	Asn	Glu	Ala	Lys	Val	Pro	Asn	Gly	Ser	Gly	Ser
225				230						235				240	
Pro	Thr	Lys	Asp	Ala	Leu	Gly	Gly	Tyr	Thr	Arg	Val	Asp	Thr	Lys	Pro
				245					250					255	
Ser	Ala	Thr	Ser	Ser	Ser	Met	Arg	Arg	Arg	His	Ala	Phe	Arg	Arg	
			260				265					270			
Gln	Ala	Ser	Ser	Thr	Phe	Ser	Tyr	Tyr	Gly	Lys	Leu	Gly	Ser	His	Cys
		275					280					285			
Tyr	Arg	Tyr	Arg	Arg	Ala	Asn	Ala	Val	Val	Leu	Ile	Lys	Pro	Ser	Arg

290	295	300
Ser Met Ser Asp Leu Tyr Asp Met Gln Lys Arg Gln Arg Gln His Arg		
305	310	315
His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser		320
	325	330
Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met		335
	340	345
Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu		350
	355	360
Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Tyr Thr Asp Phe Met		365
	370	375
Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr		380
385	390	395
Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu		400
	405	410
Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys		415
	420	425
Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly		430
	435	440
Thr Leu Gly Phe Ser Val Gly Thr Ala Val Met Ala Met Phe Pro Asn		445
	450	455
Val Tyr Val Ala Met Val Thr Ile Ser Thr Met Gly Ile Val Ser Met		460
465	470	475
Ser Ile Ser Tyr Cys Pro Tyr Ala Leu Leu Gly Gln Tyr His Asp Ile		480
	485	490
Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly		495
	500	505
Ile Asp Cys Ala Ile Leu Ser Cys Gln Val Tyr Ile Ser Gln Ile Leu		510
	515	520
Val Ala Ser Ala Leu Gly Gly Val Val Asp Ala Val Gly Thr Val Arg		525
	530	535
Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr		540
545	550	555
Ala Thr Phe Leu Val Ile Tyr Pro Asp Val Ser Glu Glu Ala Lys Glu		560
	565	570
Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly		575
	580	585
Gly Asn Ser Glu Lys Pro Thr Val Leu Lys Leu Thr Arg Lys Glu Gly		590
	595	600
Leu Gln Gly Pro Val Glu Thr Glu Ser Val Val		605
610	615	

<210> 637

<211> 370

<212> DNA

<213> Homo sapiens

<400> 637

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tctcgatcgg tgatgatctg gaaaggaaaa atcatcgtga ctactacatc acccgctact

120

acgcaaagac cgtcagttgg caggaaagtt ggttcctggt cccttaatcc atggtgtttt

180

tgtagggccct tattatTTTT cggaaTgggt cggtttattg cgattccagt attcctcact
 240
 gtgccgaata tcattaatat cggaaTccaa gccgcgggtg tggcgattat ggccttcggt
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<210> 638

<211> 99

<212> PRT

<213> Homo sapiens

<400> 638

Met	Ile	Trp	Lys	Gly	Lys	Ile	Ile	Val	Thr	Thr	Thr	Ser	Pro	Ala	Thr
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Thr	Gln	Arg	Pro	Ser	Val	Gly	Arg	Lys	Val	Gly	Ser	Trp	Ser	Leu	Asn
			20					25					30		
Pro	Trp	Cys	Phe	Cys	Arg	Pro	Leu	Leu	Phe	Phe	Gly	Met	Val	Arg	Phe
		35					40					45			
Ile	Ala	Ile	Pro	Val	Phe	Leu	Thr	Val	Pro	Asn	Ile	Ile	Asn	Ile	Gly
	50					55					60				
Ile	Gln	Ala	Ala	Val	Val	Ala	Ile	Met	Ala	Phe	Gly	Met	Thr	Phe	Val
65					70				75					80	
Ile	Val	Thr	Ser	Gly	Ile	Asp	Leu	Ser	Val	Gly	Ser	Val	Ala	Ala	Leu
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Ser	Ala	Met													

<210> 639

<211> 330

<212> DNA

<213> Homo sapiens

<400> 639

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 120
 gaggccgggg acgcgcaggt ctacgacttc tgtgacaacc aggtgcccg aaccaccgag
 180
 aaggatcggg actactggcg ggacgtggga actatcgatg cctaccacga cgcgcacatg
 240
 gacctcgtgt cggtggaacc ggagttcaac ctctacaacc ccgactggcc gatctggagc
 300
 atccaggaac aggcaccggg agcgaaattt
 330

<210> 640

<211> 110

<212> PRT

<213> Homo sapiens

<400> 640

```

Xaa Ala Ser Met Gly Asn Tyr Ile Phe Ser Arg Asp Ala Leu Val Glu
 1           5           10          15
Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly
          20          25          30
Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr
          35          40          45
Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp
          50          55          60
Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met
          65          70          75          80
Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn Pro Asp Trp
          85          90          95
Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe
          100          105          110

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<210> 641

<211> 491

<212> DNA

<213> Homo sapiens

<400> 641

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120
ggcgacatcc accgcaacaa gcgcaagggtc ttctccaaga tcttcagcca cgaggccctg
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gagagttacc tgcccaagat ccagctggtg atccaggaca cactgcgcgc ctggagcagc
240
caccgcgagg ccatcaacgt gtaccaggag gcgcagaagc tgaccttcg catggccatc
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cgggtgctgc tgggcttcag catccctgag gaggaccttg ggcacctctt tgaggctctac
360
cagcagtttg tggacaatgt cttctccctg cctgtcgacc tgcccttcag tggctaccgg
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491

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<210> 642

<211> 163

<212> PRT

<213> Homo sapiens

<400> 642

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Arg Val Thr Gly Ala Glu Asn Val Arg Lys Ile Leu Met Gly Glu His
 1           5           10          15
His Leu Val Ser Thr Glu Trp Pro Arg Ser Thr Arg Met Leu Leu Gly
          20          25          30
Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg
          35          40          45
Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

```

```

      50              55              60
Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65              70              75              80
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
      85              90              95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
      100             105             110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
      115             120             125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
      130             135             140
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
145             150             155             160
Leu Gln Cys

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<210> 643
 <211> 628
 <212> DNA
 <213> Homo sapiens

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<400> 643
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gccatcacgc tgcgggaagg ccagtatgtg gaggtcctgg atgcagccca cccactgcgc
120
tggttgtcc gcaccaagcc caccaagtcc agccctcac ggcagggctg ggtgtcacca
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gcctacctgg acaggaggct caagctgtca cctgagtggg gggccgctga ggccctgag
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600
atccaggagt tctacaagaa atacgcgt
628

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<210> 644
 <211> 209
 <212> PRT
 <213> Homo sapiens

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<400> 644
Xaa Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu Pro Leu Gly
1           5           10          15
Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val

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<210> 645
<211> 417
<212> DNA
<213> Homo sapiens
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<210> 646
<211> 95
<212> PRT
<213> Homo sapiens
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763

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      1           5           10           15
Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp
      20           25           30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu
      35           40           45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile
      50           55           60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu
      65           70           75           80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser
      85           90           95

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<210> 647

<211> 421

<212> DNA

<213> Homo sapiens

<400> 647

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120
cggtagccat gcgtggcgaa ctcccttggc atgggaaaat cgggtgaggc caacggggcac
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240
ggatttccgt tgaatgaagg caagaagtcg ggcacgcac cacctgctac cgctcggtgg
300
tacgatagcc gcggcgccac caggttggt acattccaaa cgcaacgcag gaacccgcac
360
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420
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421

```

<210> 648

<211> 90

<212> PRT

<213> Homo sapiens

<400> 648

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Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
  1           5           10           15
Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
      20           25           30
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
      35           40           45
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
      50           55           60
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
      65           70           75           80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
      85           90

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<210> 649
 <211> 563
 <212> DNA
 <213> Homo sapiens

<400> 649
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 120
 cagtctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag
 180
 gaggggaagg caccaatgga aggtgggggc agggaaggag gtagcgttga caagttccaa
 240
 tgtctggctt tccctcctgg aaaccccgag ctggggctgg ccccccttc ccttcctgtc
 300
 tctctcgctc aagcacgtcc cttctaagag ccctctctg cagacgcccc cagtggaacc
 360
 aagcctagat tcgctgcaa gaaggccgac attttttaga cttgccacgt taaaggggcc
 420
 tgcacaggca cgcaactcaa tccccccctc catgtcctcc gcctgtgcac attcaggcaa
 480
 cccgaaacac acaaagacac ggttggacac agcggccacc tgtgcacaca ggaggtagca
 540
 catggagcgc atctgacccc ggg
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<210> 650
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 650
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro
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 20 25 30
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu
 35 40 45
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met
 50 55 60
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu
 65 70 75 80
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu
 85 90 95
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe
 100 105

<210> 651
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 651

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 cataatggag tccatgggggt caaagttatc tcctggagct cagcagttga tggatatggt
 120
 taggtgtcag cagcgggaatt gtattcccat tggagagcag cttcagtcgg tggtgggcaa
 180
 ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacia
 240
 gtcgtcctcc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa
 300
 cttacaagcg tacattgata aaagtacaca actgcctggt ggagagaatt c
 351

<210> 652

<211> 95

<212> PRT

<213> Homo sapiens

<400> 652

Met	Glu	Ser	Met	Gly	Ser	Lys	Leu	Ser	Pro	Gly	Ala	Gln	Gln	Leu	Met
1				5					10					15	
Asp	Met	Val	Arg	Cys	Gln	Gln	Arg	Asn	Cys	Ile	Pro	Ile	Gly	Glu	Gln
		20						25					30		
Leu	Gln	Ser	Val	Leu	Gly	Asn	Ser	Gly	Tyr	Lys	His	Met	Ile	Gly	Leu
		35				40						45			
Gln	Ser	Ser	Ser	Thr	Leu	Gly	Thr	Leu	Asn	Lys	Ser	Ser	Ser	Thr	Pro
		50				55					60				
Phe	Pro	Phe	Arg	Thr	Gly	Leu	Thr	Ser	Gly	Asn	Val	Thr	Glu	Asn	Leu
65					70					75				80	
Gln	Ala	Tyr	Ile	Asp	Lys	Ser	Thr	Gln	Leu	Pro	Gly	Gly	Glu	Asn	
				85					90					95	

<210> 653

<211> 399

<212> DNA

<213> Homo sapiens

<400> 653

nncccggtg gggctgggggt ggggccagca tcagaggagg acatgaccaa gctgtgcaac
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 caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgtctca
 120
 cactcttctc ctggagaggg agcgagcccc caaatgttcc aactgtgtc cccagggccc
 180
 ccctctgccc gccctccctg tcgagttcct cctacaactc cacttaatgg gggctcctggc
 240
 tcccttcccc cagaaccacc ctgagtttcc caggccttcc ccactctagc aggccttggg
 300
 gggcttttcc cccaaggct tgctgaccca gtcccttctg ggggcagtag cagccccgt
 360
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 399

<210> 654

<211> 133
 <212> PRT
 <213> Homo sapiens

<400> 654
 Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr
 1 5 10 15
 Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr
 20 25 30
 Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala
 35 40 45
 Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg
 50 55 60
 Pro Pro Cys Arg Val Pro Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly
 65 70 75 80
 Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu
 85 90 95
 Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro
 100 105 110
 Ser Gly Gly Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro
 115 120 125
 Ser Pro Ala Pro Pro
 130

<210> 655
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 655
 tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga
 60
 gatgaggtgg gaagtgcact gggatctggg ggaagaagcc cgggggttcaa gactcagcta
 120
 ctgactgcat ggtgtcaaag gattcgggca tcctctctga ggctgagtct tcagatgaca
 180
 gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg
 240
 cttgacaaat gcaaggtgcc atacaaacag gaactgcaca atctcaccgc ccggcctact
 300
 cagcattgtt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg
 360
 ttgttttc
 368

<210> 656
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 656
 Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp
 1 5 10 15
 Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

```

                20                25                30
Thr  Gln  Leu  Leu  Thr  Ala  Trp  Cys  Gln  Arg  Ile  Arg  Ala  Ser  Ser  Leu
          35                40                45
Arg  Leu  Ser  Leu  Gln  Met  Thr  Val  Arg  Thr  Gly  Thr  Pro  Ala  Leu  Pro
          50                55                60
Phe  Ser  Arg  Gly  Val  Trp  Ala  Pro  Met  Ser  Met  Leu  Asp  Lys  Cys  Lys
65                70                75                80
Val  Pro  Tyr  Lys  Gln  Glu  Leu  His  Asn  Leu  Thr  Ala  Arg  Pro  Thr  Gln
          85                90                95
His  Cys  Tyr  Phe  Tyr  Leu  Tyr  Ile  Tyr  Met  Lys  Met
          100                105

```

<210> 657
 <211> 330
 <212> DNA
 <213> Homo sapiens

```

<400> 657
gtcgaccacg gcatgaaaaa gccggggatg atcctcatca acaaccocctg gggcgagtcc
60
aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cggtgtcgag
120
cgtattcagg acagcgacct ggacgtggtg ccgcaattga ccccgctga aaaacgccgg
180
tgccgacacc ttgctgatgg tcggcaacgt cggcccttcg gcacaggtgg tcaagtcctt
240
ggaccgcatg ggttgggacg tgctgtggt gtctcactgg gggccggccg gnggtcgctt
300
tggcgagctg gcggggccta acgcttctcg
330

```

<210> 658
 <211> 102
 <212> PRT
 <213> Homo sapiens

```

<400> 658
Met  Lys  Lys  Pro  Gly  Met  Ile  Leu  Ile  Asn  Asn  Pro  Trp  Gly  Glu  Ser
1                5                10                15
Asn  Glu  Ala  Gly  Phe  Lys  Arg  Ala  Leu  Glu  Glu  Arg  Gly  Met  Ala  Asn
          20                25                30
Ala  Gly  Val  Glu  Arg  Ile  Gln  Asp  Ser  Asp  Leu  Asp  Val  Val  Pro  Gln
          35                40                45
Leu  Thr  Pro  Pro  Glu  Lys  Arg  Arg  Cys  Arg  His  Leu  Ala  Asp  Gly  Arg
          50                55                60
Gln  Arg  Arg  Pro  Phe  Gly  Thr  Gly  Gly  Gln  Val  Pro  Gly  Pro  His  Gly
65                70                75                80
Leu  Gly  Arg  Ala  Cys  Gly  Val  Ser  Leu  Gly  Ala  Gly  Arg  Xaa  Ser  Leu
          85                90                95
Trp  Arg  Ala  Gly  Gly  Ala
          100

```

<210> 659
 <211> 1505

<212> DNA

<213> Homo sapiens

<400> 659

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tctcctgtc catcctgggg
60
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac
120
aaccctgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgctg gaggcagagt
180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccagc catgctgcag
240
gcagtgcgag ccctgatgat cgtaggcatc gtctctgggtg ccattggcct cctggatatcc
300
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgccaa agccaacatg
360
acactgacct ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct
420
gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat gtacaccggc
480
atgggtggga tggcgcagac tgctcagacc aggtacacat ttggcgcggc tctgttcgtg
540
ggctgggtcg ctggaggcct cacactaatt ggggtgtga tgatgtgcat cgctgccgg
600
ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggcacagc
660
gttgcctaca agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac
720
aagaagatat acgatggagg tgcccgacac gaggacgagg tacaatctta tcttccaag
780
cacgactatg tgtaatgctc taagacctct cagcacgggc ggaagaaact cccggagagc
840
tcacccaaaa aacaaggaga tcccatctag atttcttctt gcttttgact cacagctgga
900
agttagaata gcctcgattt catctttgga gaggccaagt ggtcttagcc tcagtctctg
960
tctctaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac
1020
atcttcaatc ctctatttct ttttttaaat ataactttct actctgatga gagaatgtgg
1080
ttttaatctc tctctcacat ttgatgatt tagacagact cccctcttc ctctagtca
1140
ataaacccat tgatgatcta ttcccgact tatccccaag aaaacttttg aaaggaaaga
1200
gtagacccaa agatgttatt ttctgctgtt tgaattttgt ctccccaccc ccaacttggc
1260
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag
1320
cccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa agtcattttc
1380
agtttgaggc aacaaacct ttctactgct gttgacatct tcttattaca gcaacaccat
1440
tctaggagt tctgagctc tccactggag tctccctt ctgtcgtct ctgcagcgg
1500

tacc

1505

<210> 660

<211> 261

<212> PRT

<213> Homo sapiens

<400> 660

```

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
 1           5           10           15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20           25           30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35           40           45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50           55           60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
 65           70           75           80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
 85           90           95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100           105           110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115           120           125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130           135           140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145           150           155           160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165           170           175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180           185           190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195           200           205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210           215           220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225           230           235           240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245           250           255
Lys His Asp Tyr Val
260

```

<210> 661

<211> 451

<212> DNA

<213> Homo sapiens

<400> 661

```

nnacgcgtgt agtttgtgta tcggcgcgga actcgccgag tctgatctcg aggagcttcc
60
cccattggacg agattttaac cttgcttgcc ggaggcgggtg acgacgagcc agagtggcat
120

```


gacaaggcat tatgtgcca gactgatccg gaggcattct tccctgaaaa gggatggatcc
 180
 acccgtgagg ccaagcgcac ctgtgagtc tgtgaggtcc gccaggagt cttggagtag
 240
 gcccttgcca atgacgagag gttcggaaac tggggcggat tgtccgagat ggagaggcgt
 300
 cggtctgcga agcgggctgt acctgacgtc ggagcgcggg tattgacacg gcccggtaaa
 360
 atgccctgtc tgcccgggat ggctgtctgc acgatgcggc atatgcgatg atcgacagcg
 420
 tgggtgtgcat cccgtgctcc atgacgtcga c
 451

<210> 662

<211> 85

<212> PRT

<213> Homo sapiens

<400> 662

Met	Asp	Glu	Ile	Leu	Thr	Leu	Leu	Ala	Gly	Gly	Gly	Asp	Asp	Glu	Pro
1				5					10					15	
Glu	Trp	His	Asp	Lys	Ala	Leu	Cys	Ala	Gln	Thr	Asp	Pro	Glu	Ala	Phe
			20					25					30		
Phe	Pro	Glu	Lys	Gly	Gly	Ser	Thr	Arg	Glu	Ala	Lys	Arg	Ile	Cys	Glu
			35				40					45			
Ser	Cys	Glu	Val	Arg	Gln	Glu	Cys	Leu	Glu	Tyr	Ala	Leu	Ala	Asn	Asp
		50				55				60					
Glu	Arg	Phe	Gly	Ile	Trp	Gly	Gly	Leu	Ser	Glu	Met	Glu	Arg	Arg	Arg
65					70				75					80	
Leu	Arg	Lys	Arg	Ala											
					85										

<210> 663

<211> 552

<212> DNA

<213> Homo sapiens

<400> 663

ctcgagcgtc tcgacgcca cgccgccag ggagccaagg aagacctctc gcagcgcgac
 60
 ccctacgacg tgctcgtcgt aggggagggt cccgccgggt ccgaggccgc cgtgtacgag
 120
 gctcgtaagg gcattcgac cgccatgggt gggctctcga tcggcggcca ggtactcgat
 180
 accgaggcca tcgacaacct catctcgggt ccgcacacca ccggtccgag tctggccgac
 240
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc
 300
 gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgcggggc
 360
 cgctcagtca tcgtggccac cgggtgcccgc tggcgcaacc ttggcgtagg tggcgaggag
 420
 gaataccgca ccaaggggtgt gacctactgc ccgcactgag atggcccgtt attcacaggc
 480

aaaaagggtgg ccgtcgtcgg aggtggaaac tccggtattg aggccgctat cgacctcgcc
 540
 ggcgtcgtcg ac
 552

<210> 664
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 664
 Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu
 1 5 10 15
 Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala
 20 25 30
 Gly Ala Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala
 35 40 45
 Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile
 50 55 60
 Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp
 65 70 75 80
 Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg
 85 90 95
 Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His
 100 105 110
 Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly
 115 120 125
 Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr
 130 135 140
 Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly
 145 150 155 160
 Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala
 165 170 175
 Ile Asp Leu Ala Gly Val Val Asp
 180

<210> 665
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 665
 acgcgtacag ttcgccgtcg aggttgaaca ccacgatcgg tgtaccggtc acttcgtcga
 60
 acacgctctt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct
 120
 cgctcacgcg gtggccccgg ccagcggcctt ttccaggatc tcgaaacgca ggctcgtcgcg
 180
 cttgggggatg ccgaatcggt cgtcgccata cgggaacggc ttcttgatgc cggtgcgagc
 240
 gtagccgcgg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcattctgca
 300
 ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa
 352

<210> 666
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 666
 Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp
 1 5 10 15
 Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg
 20 25 30
 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr
 35 40 45
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg
 50 55 60
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Arg Thr Ala Ala Gly
 65 70 75 80
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly
 85 90 95
 Val Gln Pro Arg Arg Arg Thr Val Arg
 100 105

<210> 667
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 667
 nacgcgtacg aatcggtggt gcgtcgcaac ccaggggagg ccgagttcca ccaggctgtg
 60
 cgggagatct ttgaatctct cggcccgggtg ctgcacaaga atccgcagta cgtggaggca
 120
 gccgtgttgt cgcgcatctg cgaaccggaa cgccagatca ttttcgggt gccgtgggtt
 180
 gacgacgagg gcaagatccg tatcaaccgt ggcttcgcg ttgaatatcc gtcggtactg
 240
 gggccgtata aggggtggatt gcgattccac ccctcgggtg acttaggaac gattaagtcc
 300
 cttggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcggaag
 360
 ggtgggtcgg actttgatcc ccatgacgcg t
 391

<210> 668
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 668
 Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe
 1 5 10 15
 His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp
 20 25 30
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

```

      35          40          45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
      50          55          60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
65      70      75      80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
      85      90      95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
      100      105      110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
      115      120      125
Asp Ala
      130

```

<210> 669
 <211> 707
 <212> DNA
 <213> Homo sapiens

```

<400> 669
nngagtcctt tccccgtcta agctcatcgt ggtggtgctg gcatggccgt caacaagga
60
attgagaaca cccttgctgc cttcgccac gcggtcgagg tgggatgcac ctacctgaa
120
actgacgttc acgcgaccag cgacggggtg ctagtgcct tccacgatcc gatactcat
180
cgcgctcactg aatcaggcgg agtcatcgcc gccatgccgt ggcacaaggc caaacaagcc
240
aagggttggtg gcgaaccgat cccacacctta gatgagattt tcgacgcctt tcccgcgcg
300
ttcatcaata tcgacatcaa gcatgatggc gccaccatgc cgctcatcga cgttctttcc
360
cgtcaccggg cttggagtcg ggtttgcgtc gggtcgttca gcagtaaagc catccagacc
420
ttcgtcgcc tgggttcaggg acgcactgcg actgcagtgg ggtcggtggg agtcnnggt
480
gggctgtcat cagccctcat agcatgcaga tggcacagtc ccatgggaat gcgtaccagg
540
tgccgcaccg cttgaccggg tnatggggtg ccccttgatga caccgacctt cattaaagct
600
gcccatcgtc aggggagcgc tggtcatgtc tggacgggta atgagatctc tgaggctcga
660
gaactgatgg atatgggggt cgacggcatc gtcacagatc gtccgga
707

```

<210> 670
 <211> 170
 <212> PRT
 <213> Homo sapiens

```

<400> 670
Met Ala Val Asn Lys Gly Ile Glu Asn Thr Leu Ala Ala Phe Gly His
1      5      10      15
Ala Val Glu Val Gly Cys Thr Tyr Leu Glu Thr Asp Val His Ala Thr

```

```

      20      25      30
Ser Asp Gly Val Leu Val Ala Phe His Asp Pro Ile Leu Asp Arg Val
      35      40      45
Thr Glu Ser Gly Gly Val Ile Ala Ala Met Pro Trp His Lys Val Lys
      50      55      60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
      65      70      75      80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
      85      90      95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
      100      105      110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
      115      120      125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
      130      135      140
Xaa Ala Gly Leu Ser Ser Ala Leu Ile Ala Cys Arg Trp His Ser Pro
      145      150      155      160
Met Gly Met Arg Thr Arg Cys Arg Thr Ala
      165      170

```

<210> 671

<211> 444

<212> DNA

<213> Homo sapiens

<400> 671

```

acgcgtgggc cttcgggttg atgggatcag aaggggacgg gacctgtaga aaggggcctg
60
cagctcagag catggggcgg ccttggtcca ctacgcctgc agctgtgaat tcgttctccg
120
gtgctggaga gggatctggt tatctccatt ctcttgtctc cacgtggaaa ggaaggacgt
180
gcgctctcat cctacgtgtt ttgagaaatc gcattgtccc cagctctgcg ggaggatctg
240
gggacgcagt ggggaaccag acaggcagtt ggaggtctag tgcgcgccag aagccagttc
300
ccaccaggg tgccatttgc tgggcgcctt agggagctgc gtgggcatcc agaggagtga
360
gtcggccctt gctctgctca gtgccactt ccccgggcag ggcaggcggtt attaacgtag
420
agggagaaca cccatgcaca caac
444

```

<210> 672

<211> 103

<212> PRT

<213> Homo sapiens

<400> 672

```

Met Gly Ser Glu Gly Asp Gly Thr Cys Arg Lys Gly Pro Ala Ala Gln
1      5      10      15
Ser Met Gly Arg Pro Trp Leu Thr Thr Pro Ala Ala Val Asn Ser Phe
      20      25      30
Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr

```

```

      35          40          45
Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
      50          55          60
Ile Val Pro Ser Ser Ala Gly Gly Ser Gly Asp Ala Val Gly Asn Gln
65          70          75          80
Thr Gly Ser Trp Arg Ser Ser Ala Arg Gln Lys Pro Val Pro Thr Gln
      85          90          95
Gly Ala Ile Cys Trp Ala Pro
      100

```

<210> 673

<211> 452

<212> DNA

<213> Homo sapiens

<400> 673

```

acgcgtccct gcagaaatcc tctcggccta ggatcatccgc aagatgtggc agggcatgca
60
ccgtgaaagc cttcaagtct gccgcagcaa gaccgcacgc ctgctgaaat tcgcagttgt
120
gccgcggtcc ctgatgcgga caaactcggc caccacgatc agcctgacgc ttgcggacca
180
acgttcaaact actgtgcact tgaaacgtcc gggccgcac acctgggtga ctttgtgcga
240
ccgacattac ttatgttcac gctctttcag ttcttgtcaa taccgtattt ttcgtcgacg
300
tctccatcag aaaaatgtcg gtgttaccgc accgcagacg atgcgtaccc ttgcgctgac
360
gatggaggcc ttgaaaagtg cattagccac tactggggcga atctacggca aaaagctgtt
420
actaggcggg gattggggag gcccgtagtg gc
452

```

<210> 674

<211> 134

<212> PRT

<213> Homo sapiens

<400> 674

```

Met Trp Gln Gly Met His Arg Glu Ser Leu Gln Val Cys Arg Ser Lys
1          5          10          15
Thr Ala Arg Leu Leu Lys Phe Ala Val Val Pro Arg Ser Leu Met Arg
      20          25          30
Thr Asn Ser Ala Thr Thr Ile Ser Leu Thr Leu Ala Asp Gln Arg Ser
      35          40          45
Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
      50          55          60
Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
65          70          75          80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
      85          90          95
Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
      100          105          110
Ala Leu Ala Thr Thr Gly Arg Ile Tyr Gly Lys Lys Leu Leu Leu Gly

```

115
Gly Asp Trp Gly Gly Pro
130

120

125

<210> 675

<211> 8564

<212> DNA

<213> Homo sapiens

<400> 675

atgtcgggct ccacacagct tgtggcacag acgtggaggg ccaactgagcc ccgtacccg
60
ccccacagcc tttcctaccc agtgcagatc gcccggacgc acacggacgt cgggctcctg
120
gagtaccagc accactcccg cgactatgcc tcccacctgt cgccgggctc catcatccag
180
ccccagcggc ggaggccctc cctgctgtct gagttccagc ccgggaatga acggtcccag
240
gagctccacc tgcggccaga gtcccaactca tacctgcccg agctggggaa gtcagagatg
300
gagttcattg aaagcaagcg ccctcggcta gagctgctgc ctgaccccct gctgcgaccg
360
tcacccctgc tggccacggg ccagcctgcg ggatctgaag acctcaccaa ggaccgtagc
420
ctgacgggca agctggaacc ggtgtctccc ccagccccc cgcacactga ccctgagctg
480
gagctggtgc cgccacggct gtccaaggag gagctgatcc agaacatgga ccgcgtggac
540
cgagagatca ccatggtaga gcagcagatc tctaagctga agaagaagca gcaacagctg
600
gaggaggagg ctgccaagcc gcccgagcct gagaagcccg tgtcacccgc gcccatcgag
660
tcgaagcacc gcagcctggt gcagatcatc tacgacgaga accggaagaa ggctgaagct
720
gcacatcgga ttctggaagg cctggggccc caggtggagc tgccgctgta caaccagccc
780
tccgacccc ggagctatca tgagaacatc aaaataaacc aggcgatgag gaagaagcta
840
atcttgact tcaagaggag gaatcacgct cggaacaat gggagcagaa gttctgccag
900
cgctatgacc agctcatgga ggcctgggaa aaaaagggtg agcgcatcga gaacaacccc
960
cggcggcggg ccaaggagag caaggtgcgc gactactacg aaaagcagtt ccctgagatc
1020
cgcaagcagc gcgagctgca ggagcgcagc cagggcaggg tgggccagcg gggcagtggt
1080
ctgtccatgt cggccgcccc cagcgagcac gaggtgtcag agatcatcga tggcctctca
1140
gagcaggaga acctggagaa gcagatgcgc cagctggccg tgatcccgcc catgctgtac
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<211> 2518

<212> PRT

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<400> 676

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Pro	Arg	Tyr	Pro	Pro	His	Ser	Leu	Ser	Tyr	Pro	Val	Gln	Ile	Ala	Arg
			20					25					30		
Thr	His	Thr	Asp	Val	Gly	Leu	Leu	Glu	Tyr	Gln	His	His	Ser	Arg	Asp
		35				40						45			
Tyr	Ala	Ser	His	Leu	Ser	Pro	Gly	Ser	Ile	Ile	Gln	Pro	Gln	Arg	Arg
	50				55					60					
Arg	Pro	Ser	Leu	Leu	Ser	Glu	Phe	Gln	Pro	Gly	Asn	Glu	Arg	Ser	Gln
65				70					75					80	
Glu	Leu	His	Leu	Arg	Pro	Glu	Ser	His	Ser	Tyr	Leu	Pro	Glu	Leu	Gly
			85					90					95		
Lys	Ser	Glu	Met	Glu	Phe	Ile	Glu	Ser	Lys	Arg	Pro	Arg	Leu	Glu	Leu
			100				105						110		
Leu	Pro	Asp	Pro	Leu	Leu	Arg	Pro	Ser	Pro	Leu	Leu	Ala	Thr	Gly	Gln
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Pro	Ala	Gly	Ser	Glu	Asp	Leu	Thr	Lys	Asp	Arg	Ser	Leu	Thr	Gly	Lys
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Leu	Glu	Pro	Val	Ser	Pro	Pro	Ser	Pro	Pro	His	Thr	Asp	Pro	Glu	Leu
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Glu	Leu	Val	Pro	Pro	Arg	Leu	Ser	Lys	Glu	Glu	Leu	Ile	Gln	Asn	Met

783

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 Lys Pro Pro Ala Thr Leu Gly Ala Asp Gly Pro Pro Pro Gly Pro Pro
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 Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr

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Glu Pro Asn Lys Thr	Ser Val Leu Gly Gly Gly	Glu Asp Gly Ile Glu	
	2210	2215	2220
Pro Val Ser Pro Pro	Glu Gly Met Thr Glu Pro	Gly His Ser Arg Ser	
2225	2230	2235	2240
Ala Val Tyr Pro Leu	Leu Tyr Arg Asp Gly Glu	Gln Thr Glu Pro Ser	
	2245	2250	2255
Arg Met Gly Ser Lys	Ser Pro Gly Asn Thr Ser	Gln Pro Pro Ala Phe	
	2260	2265	2270
Phe Ser Lys Leu Thr	Glu Ser Asn Ser Ala Met	Val Lys Ser Lys Lys	
	2275	2280	2285
Gln Glu Ile Asn Lys	Lys Leu Asn Thr His Asn	Arg Asn Glu Pro Glu	
	2290	2295	2300
Tyr Asn Ile Ser Gln	Pro Gly Thr Glu Ile Phe	Asn Met Pro Ala Ile	
2305	2310	2315	2320
Thr Gly Thr Gly Leu	Met Thr Tyr Arg Ser Gln	Ala Val Gln Glu His	

2325 2330 2335
 Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu Met
 2340 2345 2350
 Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala
 2355 2360 2365
 Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile
 2370 2375 2380
 Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly Gly
 2385 2390 2395 2400
 Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys
 2405 2410 2415
 Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val Ser
 2420 2425 2430
 Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn
 2435 2440 2445
 Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro
 2450 2455 2460
 Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser Pro
 2465 2470 2475 2480
 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro His
 2485 2490 2495
 His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu
 2500 2505 2510
 Thr Leu Ser Asp Ser Glu
 2515

<210> 677
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 677
 gtaatgcaag gtgaacgccc aatggctgcg cagaacaaga gcattggtca gttcaccctt
 60
 gagggatatag ctccggcacg ccgtgggtgtt ccacagattg aagttacttt cgatatcgat
 120
 gccaacggta tcttgaatgt gagcgcaaag gataaggcta ccggttaagga acagaagatt
 180
 cgcacgaag cttcaagtgg tttgagtcag gaagaaatcg acagaatgaa agctgaggca
 240
 gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct
 300
 gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn
 345

<210> 678
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 678
 Val Met Gln Gly Glu Arg Pro Met Ala Ala Gln Asn Lys Ser Ile Gly
 1 5 10 15
 Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

```

      20      25      30
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
      35      40      45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
      50      55      60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
      65      70      75      80
Glu Gln Asn Ala Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
      85      90      95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
      100      105      110

```

<210> 679

<211> 362

<212> DNA

<213> Homo sapiens

<400> 679

```

acgcgtgacg tcaccgctcc atggggaaga tgacgactat ccctgtgaaa gtaaagcata
60
atgggaaaaa tgtacgttaa atgtgctaac gcgcagtatg atgtatctat gaatcttgag
120
ggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcattgtgcc acccgaacgc
180
caaaaagtac tcatcaaggg aggattgcta aaagacgata ccccatagg taaagtgggt
240
gcgcgtgcag gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
300
gaaaaaacctg tgctgttctt ggaggatttg ccggaagacg agctcaacaa ggctaaggat
360
cc
362

```

<210> 680

<211> 100

<212> PRT

<213> Homo sapiens

<400> 680

```

Met Gly Lys Met Tyr Val Lys Cys Ala Asn Ala Gln Tyr Asp Val Ser
1      5      10      15
Met Asn Leu Glu Gly Thr Gly Leu Asp Phe Lys Arg Ala Ile Ala Asp
      20      25      30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
      35      40      45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
      50      55      60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
      65      70      75      80
Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
      85      90      95
Lys Ala Lys Asp
      100

```

<210> 681
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 681
 acgcgtccaa atggacaaac gcttgatgat ttctaccatg aaattagagc aaaatatcca
 60
 gaacaattac tgatggcaga ctgttcaaca gtagaagaaa tgattcacgc tgatgaactc
 120
 ggttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa
 180
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta
 240
 attgcagaag gcaatatcga tacacctgaa aagggtgaaac gtgtgcttga gttaggcgcg
 300
 tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcatcacgaa aaaattt
 357

<210> 682
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 682
 Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg
 1 5 10 15
 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu
 20 25 30
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr
 35 40 45
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn
 50 55 60
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu
 65 70 75 80
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu
 85 90 95
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro
 100 105 110
 Gln Leu Ile Thr Lys Lys Phe
 115

<210> 683
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 683
 ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg
 60
 aatattgttt tgcccgcagc gtggttgcatt gattgcgtca gttaccctaa aaaccatgta
 120
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt
 180

aattaccccca aacaatactt attagcaatt catcatgcaa tttcagcgca cagtgtcagt
 240
 ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat
 300
 gcgctagggg caattggcgt ggctcgttgc attcaagtaa gtagccagtt acagcgccca
 360
 ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g
 411

<210> 684

<211> 137

<212> PRT

<213> Homo sapiens

<400> 684

Xaa	Ser	Asp	Arg	Val	Val	Lys	Leu	Ala	Thr	Leu	Ile	Ala	Glu	Asp	Glu
1				5					10					15	
Gln	Ala	Glu	Met	Asn	Ile	Val	Leu	Pro	Ala	Ala	Trp	Leu	His	Asp	Cys
			20					25					30		
Val	Ser	Tyr	Pro	Lys	Asn	His	Val	Leu	Arg	Ala	Gln	Ser	Ala	Leu	His
			35				40					45			
Ala	Ala	Asp	Lys	Ala	Ile	Val	Phe	Leu	Arg	Ser	Ile	Asn	Tyr	Pro	Lys
	50					55					60				
Gln	Tyr	Leu	Leu	Ala	Ile	His	His	Ala	Ile	Ser	Ala	His	Ser	Val	Ser
65					70				75					80	
Gly	Lys	Ile	Gln	Ala	Met	Ser	Leu	Glu	Ala	Gln	Ile	Val	Gln	Asp	Ala
			85					90					95		
Asp	Arg	Leu	Asp	Ala	Leu	Gly	Ala	Ile	Gly	Val	Ala	Arg	Cys	Ile	Gln
			100				105						110		
Val	Ser	Ser	Gln	Leu	Gln	Arg	Pro	Leu	Tyr	Ser	Glu	Val	Asp	Pro	Phe
			115				120					125			
Ser	Glu	Thr	Arg	Ser	Leu	Val	Cys	Met							
	130					135									

<210> 685

<211> 417

<212> DNA

<213> Homo sapiens

<400> 685

acgcgttgcg ttgcggagtg aacccggaac gatggatgga ttgacactat tcggcctggt
 60
 cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact gggtcgtgct
 120
 gctgttcgcg gccgcttggc gctcggttcg gcctacggct tcctccaagg cgcttgccg
 180
 ttcggttcg tcgaggcgat atgggcgctc gttgcctgcg gcgtggtgga cgatcaggcc
 240
 gcgatgaccg catcgctccg ctttaagccc gaaacgaaac cgaccagtgc gctgggttga
 300
 tgggcggcgc gtcgctggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc
 360
 gtgcatgccg acgctgtcgc tcatcgcgct acgctcgacc acggcgcgcg gcaatag
 417

<210> 686
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 686
 Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro
 1 5 10 15
 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val
 20 25 30
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly
 35 40 45
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu
 50 55 60
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln
 65 70 75 80
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg
 85 90 95
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile
 100 105 110

<210> 687
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 687
 nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgac
 60
 gacggcatcg atattccgctc tggggcgatt attgaaagct gccgcacctt atcagccggt
 120
 ctcgatgaaa cccacggtgg tcgcacgata gagcttcggg taccacctgc gtgcgcggtt
 180
 caattggcgg ccattgagtc gggccccaac caccaccggg gcactccgcc caatgtggcc
 240
 gagaccgacc ctgtcacctt cctgcagttg gcaactggct tctcacactg gccagaaatg
 300
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc
 360
 ccagtcggtg atatggccgg ggttttcgc gacatttttg ccgacgacta ga
 412

<210> 688
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 688
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala
 1 5 10 15
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu
 20 25 30
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg

```

      35          40          45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
      50          55          60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
      65          70          75          80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85          90          95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100          105          110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115          120          125
Phe Arg Asp Ile Phe Ala Asp Asp
      130          135

```

<210> 689

<211> 499

<212> DNA

<213> Homo sapiens

<400> 689

```

cgcgctcgcg tactcgacgt cgattttcat cacggtaacg gcacccagaa cattttttac
60
ccgcgcaatg acgtgatgtt catatcgctg cacggcgagc cggccgtgtc ctatccctac
120
tattcgggggt tcagcgatga agtcggcgca ggtgttggtc aaggggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg cctgtctgca tgcttgcagg
240
aaactccagc aattctcgcc gcaggtattg gtgatctcac tgggggtcga caccttcaag
300
gacgacccga tcagtcactt cctgtctggaa ggcgaggatt tcatcgggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcgc ttgagcatcc
480
gcccgaagac ggcgtgata
499

```

<210> 690

<211> 157

<212> PRT

<213> Homo sapiens

<400> 690

```

Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
  1          5          10          15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20          25          30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35          40          45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50          55          60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```

```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
          85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
          100          105          110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
          115          120          125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
          130          135          140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

<210> 691

<211> 336

<212> DNA

<213> Homo sapiens

<400> 691

```

ntgctgcgtg aaaacgtgca gcgcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggccctg ggagttggcc tgcgacatcg cgctgccgtg cgccaccag
120
aacgaactgg acgccgacgc cggccgcacg ctgctgcgca acggctgcct ttgctggct
180
ggaggcgcca atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcgggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggcggcgctgg ccgtgagtgg cctggaaatg
300
tcgcagaacg ccatgcgcct gctgtggacc gccggc
336

```

<210> 692

<211> 112

<212> PRT

<213> Homo sapiens

<400> 692

```

Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
 1          5          10          15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
          20          25          30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
          35          40          45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
          50          55          60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65          70          75          80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
          85          90          95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
          100          105          110

```

<210> 693

<211> 580

<212> DNA

<213> Homo sapiens

<400> 693

```

ngggcaaccc ggaaggtccg gcgtcccagc cgcctacctc gctgggaccc tggctcttgc
60
gtcccccgct ggcctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
120
gccacctgcg cactcaacca gtgggccctg gacttcgagg gcaatttgca aagaatttta
180
aagagtattg aaattgccaa aaacagagga gcaagataca ggcttgacc agagctggaa
240
atatgcggct gcggatgttg ggatcattat tacgagtcgg acaccctctt gcaactgttt
300
caagtccctag cggcccttgc ggagtctccc gtcactcagg acatcatctg cgacgtgggg
360
atactgttaa tgcaccgaaa cgtccgctac aactgcagag tgatattcct caacaggaag
420
atcctgctca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
480
tggttcacc cgtggctcgag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
540
gttaagcacc tccgctgtgt gtagccttgg gtcctgatca
580

```

<210> 694

<211> 136

<212> PRT

<213> Homo sapiens

<400> 694

```

Met Gly Arg Lys Val Thr Val Ala Thr Cys Ala Leu Asn Gln Trp Ala
1      5      10      15
Leu Asp Phe Glu Gly Asn Leu Gln Arg Ile Leu Lys Ser Ile Glu Ile
20     25     30
Ala Lys Asn Arg Gly Ala Arg Tyr Arg Leu Gly Pro Glu Leu Glu Ile
35     40     45
Cys Gly Cys Gly Cys Trp Asp His Tyr Tyr Glu Ser Asp Thr Leu Leu
50     55     60
His Ser Phe Gln Val Leu Ala Ala Leu Val Glu Ser Pro Val Thr Gln
65     70     75     80
Asp Ile Ile Cys Asp Val Gly Ile Pro Val Met His Arg Asn Val Arg
85     90     95
Tyr Asn Cys Arg Val Ile Phe Leu Asn Arg Lys Ile Leu Leu Ile Arg
100    105    110
Pro Lys Met Ala Leu Ala Asn Glu Gly Asn Tyr Arg Glu Leu Arg Trp
115    120    125
Phe Thr Pro Trp Ser Arg Ser Arg
130    135

```

<210> 695

<211> 439

<212> DNA

<213> Homo sapiens

<400> 695

ntgggtgactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtcctcgacc
 60
 atcatggctc tgcgagggc tgattacctg ctcgatatcg agacttcggt gcccggatc
 120
 ggcgacaagt tcgtcccga cgtctggggc aaactcaaac tcggcaagga caacgagcac
 180
 accgctctgc cctggtaactt cggcccgttc gtcgtgacgt acaacaagga cattttcaag
 240
 gatgttgcc tcgatccga aatcccgccg aagacgatga ccgagtacct cgacttcgcc
 300
 aagaaaatca ccgctgccgg caagcaggcg gtctatggca acacgtcgtg gtacatgctc
 360
 gcggaatggc gtgccctcg cgtcaaggtc atgaatgacg acttcaccaa gttcactttt
 420
 gcctcggaat ccaacgcgt
 439

<210> 696

<211> 146

<212> PRT

<213> Homo sapiens

<400> 696

Xaa	Val	Thr	Gln	Ala	Ser	Asn	Gly	Thr	Met	Ala	Asp	Val	Val	Asn	Met
1				5					10					15	
Pro	Ser	Ser	Thr	Ile	Met	Ala	Leu	Ser	Arg	Ala	Asp	Tyr	Leu	Leu	Asp
			20						25				30		
Ile	Glu	Thr	Ser	Val	Pro	Gly	Ile	Gly	Asp	Lys	Phe	Val	Pro	Asp	Val
		35					40					45			
Trp	Gly	Lys	Leu	Lys	Leu	Gly	Lys	Asp	Asn	Glu	His	Thr	Ala	Leu	Pro
	50					55				60					
Trp	Tyr	Phe	Gly	Pro	Phe	Val	Val	Thr	Tyr	Asn	Lys	Asp	Ile	Phe	Lys
65					70					75				80	
Asp	Val	Gly	Leu	Asp	Pro	Glu	Ile	Pro	Pro	Lys	Thr	Met	Thr	Glu	Tyr
				85					90					95	
Leu	Asp	Phe	Ala	Lys	Lys	Ile	Thr	Ala	Ala	Gly	Lys	Gln	Ala	Val	Tyr
			100					105					110		
Gly	Asn	Thr	Ser	Trp	Tyr	Met	Leu	Ala	Glu	Trp	Arg	Ala	Leu	Gly	Val
		115				120					125				
Lys	Val	Met	Asn	Asp	Asp	Phe	Thr	Lys	Phe	Thr	Phe	Ala	Ser	Glu	Ser
	130					135					140				
Asn	Ala														
145															

<210> 697

<211> 368

<212> DNA

<213> Homo sapiens

<400> 697

nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggg
 60

tgtcgggtgat ggggtcggag atgtcgccct cccacaactt gaacttgatc ggaccaaccc
 120
 tttccaccct ggagagactc gcctgccttg aaagtcttct tgccttctt gggcaactga
 180
 tcgcccctccc gaacgagata atccaagctc aagcgaccgc ccaccttgtc gcgcgcctcc
 240
 acaccgacgg aatgcgatgc cgggatcgca tcgatgctag cggcgggtgcg tgcaatgaca
 300
 atcttgtctt cacgcagcga tacgggcccc ccgttggaat cgaacacaaa caccttgaag
 360
 gcgttgtn
 368

<210> 698
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 698
 Met Pro Met Lys Arg Leu Ser Val Met Gly Ser Glu Met Ser Pro Ser
 1 5 10 15
 His Asn Leu Asn Leu Ile Gly Pro Thr Leu Ser Thr Leu Glu Arg Leu
 20 25 30
 Ala Cys Leu Glu Ser Leu Leu Ala Leu Leu Gly Gln Leu Ile Ala Leu
 35 40 45
 Pro Asn Glu Ile Ile Gln Ala Gln Ala Thr Ala His Leu Val Ala Arg
 50 55 60
 Leu His Thr Asp Gly Met Arg Cys Arg Asp Arg Ile Asp Ala Ser Gly
 65 70 75 80
 Gly Ala Cys Asn Asp Asn Leu Val Phe Thr Gln Arg Tyr Gly Pro Ala
 85 90 95
 Val Gly Ile Glu His Lys His Leu Glu Gly Val Val
 100 105

<210> 699
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 699
 nacgcgtaca caaatagtat cggaatcatt tcctatcatg ctgctatgac gagattttctc
 60
 cacacctcag attggcaact ggggatgact cggcactacc tgtcgaagcg cggcgacgac
 120
 gaccacagg caccgtttac tgccgatcga atcgagacgg tgccgaggct gggcgacgtt
 180
 gcccggaagg agggctgcga gtttgtcgtc gtgcgcggag atgtcttcga aaccacaaat
 240
 gtctccactc agatcattgc ccgcgcgtgt gaggcgatag cctccattga tctccccgtg
 300
 tacctgctgc ccggaaatca cgacagctta gagccggggg gtctctggga tgggccagaa
 360
 ttc
 363

<210> 700
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 700
 Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met
 1 5 10 15
 Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His
 20 25 30
 Tyr Leu Ser Lys Arg Gly Asp Asp Asp Pro Gln Ala Arg Phe Thr Ala
 35 40 45
 Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu
 50 55 60
 Gly Cys Glu Phe Val Val Ala Gly Asp Val Phe Glu Thr His Asn
 65 70 75 80
 Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile
 85 90 95
 Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro
 100 105 110
 Gly Cys Leu Trp Asp Gly Pro Glu Phe
 115 120

<210> 701
 <211> 585
 <212> DNA
 <213> Homo sapiens

<400> 701
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 60
 ttccggctacg tccattgcgc ggatgtctgc ccgctgacac tgggcaacat ggtctcggcc
 120
 ctcgatcgcc tgggctcccg ggcggacggc atcggtccga tcttcatctc cgtcgatccg
 180
 gcccgcgaca caccgcgct ggtcggacag tatgtcgcgc atttctcgcc gcggatcgtc
 240
 gggctgaccg gcaccgcagc gcagctggcg ccggtactgg cggagttcca catcaccgcg
 300
 cgcgccgaac ctgcggcaca cgacatggcc gccgacatgt atgccgtcga ccacagcgcc
 360
 ctctctctatc tgatggacgg caacaaccgc ctgttgcggg tgatggcggt cagcgccgac
 420
 gctgcctcgc tgacgcacca gctggcgggc ggcctggccg gggcaagaat gagaccatga
 480
 aagcgatcgg accgacggac gccccgaac aggcagcgcc gggctggtcg ttcggcatca
 540
 tctgtctgct cggcatcgcc ggcattgctg atttcgtcga ccggt
 585

<210> 702
 <211> 159
 <212> PRT

<213> Homo sapiens

<400> 702

```

Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
 1           5           10           15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
 20           25           30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
 35           40           45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
 50           55           60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
 65           70           75           80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
 85           90           95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
100          105          110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
115          120          125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
130          135          140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
145          150          155

```

<210> 703

<211> 390

<212> DNA

<213> Homo sapiens

<400> 703

```

ttctctgctc catcacacc tcagcagaat ggcatcgccg agcgcaagaa cataactctt
60
attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagtt ctggcctgaa
120
gccattgata ctgcttgatc caccatcaac cgcgtttatc ttcacaagggt tttggagaaa
180
acctcttatg agttcctaac tggttaagaaa cccaatgtaa gctatttcag agtatttggt
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaat ttgcaccgaa agcacatgaa
300
ggttttatgc ttggttacgg aaaggattcg cactcctaca gactcttcaa cctctttcac
360
tataaagtgg ttcaaactgt ggatgtgcgn
390

```

<210> 704

<211> 130

<212> PRT

<213> Homo sapiens

<400> 704

```

Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
 1           5           10           15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```

```

      20      25      30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
      35      40      45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
      50      55      60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
65      70      75      80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
      85      90      95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
      100      105      110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
      115      120      125
Val Arg
      130

```

<210> 705
 <211> 513
 <212> DNA
 <213> Homo sapiens

```

<400> 705
acgcgtattt cgtccaaatg attcaaatca aaacgccgcc gttaaaaacg atgcaggcga
60
agacaatgcg aataaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgacaaag ttgagaaaga ctatgcaaat tatggggatg aagctacttt cggtgccgga
240
aaatcaattc gtgatggtat ggctcaaaat cctaattgta caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcggattta aaaatgggta tatttttaag attggtaaag ctggaaaccc agatataatg
420
gataacggtg acatcatcat tgggtgcaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

```

<210> 706
 <211> 140
 <212> PRT
 <213> Homo sapiens

```

<400> 706
Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
1      5      10      15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
      20      25      30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
      35      40      45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg

```

```

      50              55              60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile
65              70              75              80
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr
      85              90              95
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val
      100             105             110
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys
      115             120             125
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His
      130             135             140

```

<210> 707

<211> 409

<212> DNA

<213> Homo sapiens

<400> 707

```

acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaaagccg
60
gcacactaca cagtgcacag gtgaagccct caggggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat ttcatggca gtgtctatgg acggctcccc ttggcatggt
180
gctgggtggc aatcctggct gtagctgcca cccctgccc tttttgcttc cctccgaggg
240
cattgtgatc atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagtagggg ttcccagcct gtctggccat cccccccag cccagcccct cctgctgggt
360
gacgtgtcga gttcgcccc tgctgtactg ggaggggggt aggagcata
409

```

<210> 708

<211> 136

<212> PRT

<213> Homo sapiens

<400> 708

```

Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val
1              5              10              15
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly
      20              25              30
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn
      35              40              45
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly
      50              55              60
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg
65              70              75              80
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro
      85              90              95
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His
      100             105             110
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu

```

115 120 125
 Trp Trp Ser Glu Asp Ala Thr Arg
 130 135

<210> 709
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 709
 acgcgtctga cggagagcct cctgagtctc cccacgcaga ggactcagaa agggaatcgg
 60
 tgaccacacc tgggccagcg acgtgtggtg cgccagcctc cccagcggat cacctcctcc
 120
 tccccctcca ggaggagagt ttctccgaag tccccatgag tgaagcaagc tcagcgaaag
 180
 acactccact ctttaggatg gagggagagg atgcccttgt gactcagtat cagagcaaag
 240
 ccagtgacca cgaaggttta ttgtctgacc ccttgagtga ccttcagttg gtctcagatt
 300
 ttaaattctcc aatcatggcc gatctgaact taagccttcc ttccattcct gaagtcgcat
 360
 cggatgatga aagaatagat cagggttgaag atgacggaga tcagggttga gatgatggag
 420
 agacagcaaa gtcgtcaact ctggacatag gagctttgtc cttgggcttg gtagtcccc
 480
 gtcctgagag gggaaagggg cccagtggcg aggcagatag gttggtactg ggggagggcc
 540
 tgtgtgattt caggctgcaa gcacccagc catctgtgac agtccttca gagcagacca
 600
 cagagttcgg aattcacaaa ccacatcttg gcaagagctc aagcttggat aaacagctgc
 660
 caggccccag tgggtgtgag gaagaaaaac cgatgggaaa tgggagtcca agcccgctc
 720
 ctggcacatc cctggacaat cctgtaccca gcccctcccc ttctgagatc t
 771

<210> 710
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 710
 Met Ser Glu Ala Ser Ser Ala Lys Asp Thr Pro Leu Phe Arg Met Glu
 1 5 10 15
 Gly Glu Asp Ala Leu Val Thr Gln Tyr Gln Ser Lys Ala Ser Asp His
 20 25 30
 Glu Gly Leu Leu Ser Asp Pro Leu Ser Asp Leu Gln Leu Val Ser Asp
 35 40 45
 Phe Lys Ser Pro Ile Met Ala Asp Leu Asn Leu Ser Leu Pro Ser Ile
 50 55 60
 Pro Glu Val Ala Ser Asp Asp Glu Arg Ile Asp Gln Val Glu Asp Asp
 65 70 75 80
 Gly Asp Gln Val Glu Asp Asp Gly Glu Thr Ala Lys Ser Ser Thr Leu


```

      85              90              95
Asp Ile Gly Ala Leu Ser Leu Gly Leu Val Val Pro Cys Pro Glu Arg
      100              105              110
Gly Lys Gly Pro Ser Gly Glu Ala Asp Arg Leu Val Leu Gly Glu Gly
      115              120              125
Leu Cys Asp Phe Arg Leu Gln Ala Pro Gln Ala Ser Val Thr Ala Pro
      130              135              140
Ser Glu Gln Thr Thr Glu Phe Gly Ile His Lys Pro His Leu Gly Lys
      145              150              155              160
Ser Ser Ser Leu Asp Lys Gln Leu Pro Gly Pro Ser Gly Gly Glu Glu
      165              170              175
Glu Lys Pro Met Gly Asn Gly Ser Pro Ser Pro Pro Pro Gly Thr Ser
      180              185              190
Leu Asp Asn Pro Val Pro Ser Pro Ser Pro Ser Glu Ile
      195              200              205

```

<210> 711
 <211> 432
 <212> DNA
 <213> Homo sapiens

```

<400> 711
nnggatccga cggcgcaaag ccttaatgaa gggtaggcag ttacctcttt ttctgtagga
60
attctcctgt tttatatcta ctcccccta ggttcacccat actccctcat cttctgagct
120
aatgtgcccg ctttatttgc acttgcatgg aatatgatta tgaacacagt tttatcatt
180
gatgaccacc ccgttatcag gttggcgatt cgtatgttgt tggaacacga ggggtataag
240
gtcgttggtg aaacggacaa cggttgtgac gcgatccaaa tgggtcgcga atgcctgccg
300
gacctgatca tcctggatat cagcatcccg aaactcgacg gcctcgaagt gctctgccga
360
ttcaacgccca tgaacacatc catgaaaacc ctgattctta cgcgccagag tccgacgttg
420
ttcgccacgc gt
432

```

<210> 712
 <211> 93
 <212> PRT
 <213> Homo sapiens

```

<400> 712
Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg
1      5      10      15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly
20      25      30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu
35      40      45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu
50      55      60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu

```

```

65              70              75              80
Ile Leu Thr Ala Gln Ser Pro Thr Leu Phe Ala Thr Arg
              85              90

<210> 713
<211> 465
<212> DNA
<213> Homo sapiens

<400> 713
atcctgatcg ccaacggtgg tatgcagaac ccggtgggcg cggtgttcaa ccccgacacc
60
atgcgcatgg aaatgaccga ctctgccgcg gtgatcttca acccggtggc gcaggccaag
120
ttcgtgcata cggtcagcgc gggctacgtg gccggcgcca tgttcgtcat gtcgatcagc
180
gcctggtacc tgetcaaggg ccgccacacc gacctggcca agcgctcgat ggcggtcgcc
240
gccagcttcg gcctggcgtc ggcgctgtcg gtcgtcgtgc tgggtgacga aagcggttat
300
ctcaccaccg aacaccagaa gatgaagatc gcggccatgg aatccatgtg gcacaccgag
360
ccggcgcccg cgtccttcaa cctgatcgcg ctgccaacc aggccgaacg caagaacgac
420
ttgccatcg agattcccta cgtcatgngc ctcatcgga cgcgt
465

```

```
<210> 714
<211> 155
<212> PRT
<213> Homo sapiens
```

```

<400> 714
Ile Leu Ile Ala Asn Gly Gly Met Gln Asn Pro Val Gly Ala Val Phe
  1                    5                      10                15
Asn Pro Asp Thr Met Arg Met Glu Met Thr Asp Phe Ala Ala Val Ile
      20                      25                30
Phe Asn Pro Val Ala Gln Ala Lys Phe Val His Thr Val Ser Ala Gly
      35                      40                45
Tyr Val Ala Gly Ala Met Phe Val Met Ser Ile Ser Ala Trp Tyr Leu
      50                      55                60
Leu Lys Gly Arg His Thr Asp Leu Ala Lys Arg Ser Met Ala Val Ala
65                      70                      75                80
Ala Ser Phe Gly Leu Ala Ser Ala Leu Ser Val Val Val Leu Gly Asp
      85                      90                95
Glu Ser Gly Tyr Leu Thr Thr Glu His Gln Lys Met Lys Ile Ala Ala
      100                      105                110
Met Glu Ser Met Trp His Thr Glu Pro Ala Pro Ala Ser Phe Asn Leu
      115                      120                125
Ile Ala Leu Pro Asn Gln Ala Glu Arg Lys Asn Asp Phe Ala Ile Glu
      130                      135                140
Ile Pro Tyr Val Met Xaa Leu Ile Gly Thr Arg
145                      150                155

```

<210> 715
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 715
 nnaccggtgg atgccaacga atatcgtagc gagctgaaag tcggcgccat caccaccgcc
 60
 cagaccggcc tgctgcctca ggcactggtg cgtttgcgcc aggcagcgcc gacggtggag
 120
 tgcaagttgg taccgggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg
 180
 gactcggcga tcacattcg cccgcccttt gatttgccca aggagttgca cgtacaggta
 240
 ctgcgcaagg agccgtttgt gttgatcgtg ccccgaggcg tcgggggtga tgaccgttg
 300
 caactgctcg aagctcatcc ccacgtgcgc tacgaccgag ctctggttgg cggg
 354

<210> 716
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 716
 Xaa Pro Val Asp Ala Asn Glu Tyr Arg Gly Glu Leu Lys Val Gly Ala
 1 5 10 15
 Ile Thr Thr Ala Gln Thr Gly Leu Leu Pro Gln Ala Leu Val Arg Leu
 20 25 30
 Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser
 35 40 45
 Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile
 50 55 60
 Ile Ile Arg Pro Pro Phe Asp Leu Pro Lys Glu Leu His Val Gln Val
 65 70 75 80
 Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly
 85 90 95
 Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp
 100 105 110
 Arg Ala Ser Phe Gly Gly
 115

<210> 717
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 717
 acgcgtatct ttccggtaaa cctactaatt ttccattcaa cgctcgacgc ccaggtaaag
 60
 ccgttaagtc atctaaatag gccattctgt ggctctccat cagtaagaac caaatccata
 120
 ggagaagttg agcggatagt aatgcatcaa attgatgctg agaaaccgaa aaatgggaca
 180

atataatcaa gctgacaata ctgatcaaac cactcgcatg aaagctacta ccgcttgacc
 240
 accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag
 300
 accaggtggt agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgag
 360
 attcaacggc gtagcaccag cacagcaaca tagccactag t
 401

<210> 718
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 718
 Met Leu Leu Cys Trp Cys Tyr Ala Val Glu Ser His Trp Ile Ser Phe
 1 5 10 15
 His Phe Leu Glu Arg Pro Ile Phe Asn Leu Ala Thr Thr Trp Ser Ser
 20 25 30
 Phe Leu Leu Trp Thr Ile Leu Phe Leu Ser Ile Ser Leu Val Phe Ser
 35 40 45
 Ala Trp Trp Ser Ser Gly Ser Ser Phe His Ala Ser Gly Leu Ile Ser
 50 55 60
 Ile Val Ser Leu Ile Ile Leu Ser His Phe Ser Val Ser Gln His Gln
 65 70 75 80
 Phe Asp Ala Leu Leu Ser Ala Gln Leu Leu Leu Trp Ile Trp Phe Leu
 85 90 95
 Leu Met Glu Ser His Arg Met Ala Tyr Leu Asp Asp Leu Thr Ala Leu
 100 105 110
 Pro Gly Arg Arg Ala Leu Asn Glu Lys Leu Val Gly Leu Pro Lys Arg
 115 120 125
 Tyr Ala
 130

<210> 719
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 719
 tatatagggc tatctacctt attcacagca cattccatct acacaacctt gtagcggtca
 60
 ctcttgaagg cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc
 120
 aatctccctg cgttggtaac tgggcaaaaag aaagacctct gcagtccagc aacctcatcg
 180
 tgcaaatgcc gtggcggtgt caactctgac ggcttggaag ctgcagacct tgtcaaagga
 240
 cctcggccga aattcaccct tgatctcttt gtcttggtcca actcttggtcc ctgagaatga
 300
 aactgtcttc tgagagtcca tcaatgcgac gctgactcgt gagaagtgct gaatcacgtc
 360
 gccattttgg agacctgcc aacgagctct ggaacctgcc aggacgcctt ccacaacacc
 420

agaacgcagc gactttgcgt taaatccaag ctcaaacc tcttgctcca caggcctgag
 480
 cataaaaagg tattctgcga cgggaaatgt aaagtctgag cttaggtgca gaggaccgcc
 540
 atcgatcagt gtctgatact gcttgccgc gacttctttg ccgagcaatg ggtatagcgt
 600
 tttcaaccaa gtggaagcag tcgtttgctc accctggcga ttccggcgag ttagggacat
 660
 gaccacgtca tcgatgggat tttgc
 685

<210> 720

<211> 161

<212> PRT

<213> Homo sapiens

<400> 720

Met	Ser	Leu	Thr	Arg	Arg	Asn	Arg	Gln	Gly	Glu	Gln	Thr	Thr	Ala	Ser
1				5				10						15	
Thr	Trp	Leu	Lys	Thr	Leu	Tyr	Pro	Leu	Leu	Gly	Lys	Glu	Val	Ala	Asp
			20					25						30	
Lys	Gln	Tyr	Gln	Thr	Leu	Ile	Asp	Gly	Gly	Thr	Leu	His	Leu	Ser	Ser
			35				40					45			
Asp	Phe	Thr	Phe	Pro	Val	Ala	Glu	Tyr	Leu	Phe	Met	Leu	Arg	Pro	Val
	50					55					60				
Glu	Gln	Glu	Val	Phe	Glu	Leu	Gly	Phe	Asn	Ala	Lys	Ser	Leu	Arg	Ser
65					70				75						80
Gly	Val	Val	Glu	Gly	Val	Leu	Ala	Gly	Ser	Arg	Ala	Ala	Leu	Ala	Gly
			85					90						95	
Leu	Gln	Asn	Gly	Asp	Val	Ile	Gln	His	Phe	Ser	Arg	Val	Ser	Val	Ala
			100					105					110		
Leu	Met	Asp	Ser	Gln	Lys	Thr	Val	Ser	Phe	Ser	Gly	Thr	Arg	Val	Gly
		115					120					125			
Gln	Asp	Lys	Glu	Ile	Lys	Gly	Glu	Phe	Arg	Pro	Arg	Ser	Phe	Asp	Lys
	130					135					140				
Val	Cys	Ser	Phe	Gln	Ala	Val	Arg	Val	Asp	His	Ala	Thr	Ala	Phe	Ala
145					150					155					160
Arg															

<210> 721

<211> 579

<212> DNA

<213> Homo sapiens

<400> 721

aagcttgagg tcagggtgtg gcagtgtggc gggagtgtgg aggtcctgcc ctgctcacgg
 60
 attgccaca ttgagcgagc ccacaagccc tacacagagg acctcaccgc ccatgtccgc
 120
 aggaacgctc tcagggtggc tgaagtctgg atggatgaat ttaaaagcca cgtctactgg
 180
 catggaacat accaggagga ctcaggaatt gacattgggg acatcactgc aaggaaggct
 240

ctcaggaaac agctgcagtg caagaccttc cggtggtacc tggtcagcgt gtaccagag
 300
 atgaggatgt actccgacat cattgcctat ggagtgtctgc agaattctct gaagactgat
 360
 ttgtgtcttg accaggggcc agatacagag aatgtcccca tcatgtacat ctgccatggg
 420
 atgacgcctc agaacgtgta ctacacgagc agtcagcaga tccatgtggg cattctgagc
 480
 cccaccgtgg atgatgatga caaccgatgc ctggtggacg tcaacagccg gccccggctc
 540
 atcgaatgca gctacgcca agccaagagg atgaagctt
 579

<210> 722

<211> 193

<212> PRT

<213> Homo sapiens

<400> 722

Lys	Leu	Gly	Ile	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Val	Glu	Val	Leu
1			5						10				15		
Pro	Cys	Ser	Arg	Ile	Ala	His	Ile	Glu	Arg	Ala	His	Lys	Pro	Tyr	Thr
			20					25				30			
Glu	Asp	Leu	Thr	Ala	His	Val	Arg	Arg	Asn	Ala	Leu	Arg	Val	Ala	Glu
		35					40				45				
Val	Trp	Met	Asp	Glu	Phe	Lys	Ser	His	Val	Tyr	Trp	His	Gly	Thr	Tyr
	50					55				60					
Gln	Glu	Asp	Ser	Gly	Ile	Asp	Ile	Gly	Asp	Ile	Thr	Ala	Arg	Lys	Ala
65					70				75					80	
Leu	Arg	Lys	Gln	Leu	Gln	Cys	Lys	Thr	Phe	Arg	Trp	Tyr	Leu	Val	Ser
			85					90				95			
Val	Tyr	Pro	Glu	Met	Arg	Met	Tyr	Ser	Asp	Ile	Ile	Ala	Tyr	Gly	Val
		100					105					110			
Leu	Gln	Asn	Ser	Leu	Lys	Thr	Asp	Leu	Cys	Leu	Asp	Gln	Gly	Pro	Asp
		115				120					125				
Thr	Glu	Asn	Val	Pro	Ile	Met	Tyr	Ile	Cys	His	Gly	Met	Thr	Pro	Gln
	130					135					140				
Asn	Val	Tyr	Tyr	Thr	Ser	Ser	Gln	Gln	Ile	His	Val	Gly	Ile	Leu	Ser
145					150				155					160	
Pro	Thr	Val	Asp	Asp	Asp	Asp	Asn	Arg	Cys	Leu	Val	Asp	Val	Asn	Ser
			165				170					175			
Arg	Pro	Arg	Leu	Ile	Glu	Cys	Ser	Tyr	Ala	Lys	Ala	Lys	Arg	Met	Lys
		180					185					190			

Leu

<210> 723

<211> 384

<212> DNA

<213> Homo sapiens

<400> 723

acgcgtcctc ttacgctcag ttttgacaat gcgtgctggc agccaaccga agccgtaaaa
 60

ctcaacgaaa tgctctcgct taaaccgtgc gaaggaaccc caccgcaatg gcgcttattc
 120
 cgcgaaagggg attaccaaatt gcgcattgat acgcgctccg gaacgcctac gctgatgctt
 180
 accgtacaaa gtgtaaccga caaacctgtt acggacgtca ctcgacaatg tcctaaatgg
 240
 gacggcaagc ccctcaccct tgacgtaacg aatacattcc cggaaggctc cgtcgtacga
 300
 gacttctaca gcaagcaaac cgctatgggtg cagcaaggta aaatcacact tcagcctgcc
 360
 gctaacagca atggcctgct gctg
 384

<210> 724
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 724
 Thr Arg Pro Leu Thr Leu Ser Phe Asp Asn Ala Cys Trp Gln Pro Thr
 1 5 10 15
 Glu Ala Val Lys Leu Asn Glu Met Leu Ser Leu Lys Pro Cys Glu Gly
 20 25 30
 Thr Pro Pro Gln Trp Arg Leu Phe Arg Glu Gly Asp Tyr Gln Met Arg
 35 40 45
 Ile Asp Thr Arg Ser Gly Thr Pro Thr Leu Met Leu Thr Val Gln Ser
 50 55 60
 Val Thr Asp Lys Pro Val Thr Asp Val Thr Arg Gln Cys Pro Lys Trp
 65 70 75 80
 Asp Gly Lys Pro Leu Thr Leu Asp Val Thr Asn Thr Phe Pro Glu Gly
 85 90 95
 Ser Val Val Arg Asp Phe Tyr Ser Lys Gln Thr Ala Met Val Gln Gln
 100 105 110
 Gly Lys Ile Thr Leu Gln Pro Ala Ala Asn Ser Asn Gly Leu Leu Leu
 115 120 125

<210> 725
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 725
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<210> 726

<211> 124

<212> PRT

<213> Homo sapiens

<400> 726

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		20						25				30			
Glu	Met	Ser	His	Arg	Arg	Leu	Phe	Leu	Val	His	Ile	Cys	Pro	Ser	Arg
		35				40					45				
Ser	Thr	Pro	Ser	Pro	Ser	Ser	Cys	Ser	Leu	Pro	Glu	Arg	Leu	Cys	Trp
	50				55				60						
Glu	Trp	Cys	Ile	Gly	Gly	Leu	Gln	Ala	Leu	Leu	Gly	Ser	Arg	Cys	Ser
65				70					75					80	
Phe	Pro	Gly	Ser	Phe	Pro	Ala	Met	Ser	Leu	Phe	Leu	Pro	Pro	Ser	Phe
			85					90						95	
Pro	Ser	Gln	Gln	Pro	Pro	Ser	Ser	Phe	His	Gln	Thr	Trp	Glu	Pro	Ser
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<210> 727

<211> 629

<212> DNA

<213> Homo sapiens

<400> 727

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 360
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 480
 tcggtggacg acaccaacct gctgaagttc tgaggagggt accgtgactg tcttggaac
 540

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 629

<210> 728
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 728
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 Gly Ile Val Gly Phe Leu Thr Arg Arg Asn Ala Leu Val Ala Phe Met
 20 25 30
 Ser Val Glu Leu Met Leu Asn Ala Ala Asn Leu Ala Leu Val Thr Phe
 35 40 45
 Ala His Val His Gly Ser Leu Asp Gly Gln Val Gly Val Phe Phe Val
 50 55 60
 Met Ile Val Ala Ala Ala Glu Val Val Val Gly Leu Ala Ile Ile Val
 65 70 75 80
 Thr Ile Phe Arg Ser Arg Arg Thr Thr Ser Val Asp Asp Thr Asn Leu
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 Leu Lys Phe

<210> 729
 <211> 4716
 <212> DNA
 <213> Homo sapiens

<400> 729
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 4200
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<210> 730

<211> 797

<212> PRT

<213> Homo sapiens

<400> 730

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Thr	Asp	Thr	Val	Arg	Leu	Thr	Ser	Val	Val	Thr	Pro	Arg	Pro	Phe	Gly
			20					25					30		
Ser	Gln	Thr	Arg	Gly	Ile	Ser	Ser	Leu	Pro	Arg	Ser	Tyr	Thr	Met	Asp
		35					40					45			
Asp	Ala	Trp	Lys	Tyr	Asn	Gly	Asp	Val	Glu	Asp	Ile	Lys	Arg	Thr	Pro
	50					55				60					
Asn	Asn	Val	Val	Ser	Thr	Pro	Ala	Pro	Ser	Pro	Asp	Ala	Ser	Gln	Leu
65					70					75				80	
Ala	Ser	Ser	Leu	Ser	Ser	Gln	Lys	Glu	Val	Ala	Ala	Thr	Glu	Glu	Asp
			85						90				95		
Val	Thr	Arg	Leu	Pro	Ser	Pro	Thr	Ser	Pro	Phe	Ser	Ser	Leu	Ser	Gln
			100					105					110		
Asp	Gln	Ala	Ala	Thr	Ser	Lys	Ala	Thr	Leu	Ser	Ser	Thr	Ser	Gly	Leu
	115					120						125			
Asp	Leu	Met	Ser	Glu	Ser	Gly	Glu	Gly	Glu	Ile	Ser	Pro	Gln	Arg	Glu
	130					135					140				
Val	Ser	Arg	Ser	Gln	Asp	Gln	Phe	Ser	Asp	Met	Arg	Ile	Ser	Ile	Asn

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Gln	Thr	Pro	Gly	Lys	Ser	Leu	Asp	Phe	Gly	Phe	Thr	Ile	Lys	Trp
				165					170					175
Ile	Pro	Gly	Ile	Phe	Val	Ala	Ser	Val	Glu	Ala	Gly	Ser	Pro	Ala
			180					185					190	
Phe	Ser	Gln	Leu	Gln	Val	Asp	Asp	Glu	Ile	Ile	Ala	Ile	Asn	Asn
		195				200						205		Thr
Lys	Phe	Ser	Tyr	Asn	Asp	Ser	Lys	Glu	Trp	Glu	Glu	Ala	Met	Ala
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Ala	Gly	Ser	Pro	Glu	Thr	Lys	Trp	Ile	Asp	Ala	Thr	Ser	Gly	Ile
				245					250					255
Asn	Ser	Glu	Lys	Ser	Ser	Asn	Leu	Ser	Val	Thr	Thr	Asp	Phe	Ser
		260					265						270	Glu
Ser	Leu	Gln	Ser	Ser	Asn	Ile	Glu	Ser	Lys	Glu	Ile	Asn	Gly	Ile
	275					280					285			His
Asp	Glu	Ser	Asn	Ala	Phe	Glu	Ser	Lys	Ala	Ser	Glu	Ser	Ile	Ser
	290					295					300			Leu
Lys	Asn	Leu	Lys	Arg	Arg	Ser	Gln	Phe	Phe	Glu	Gln	Gly	Ser	Ser
305					310					315				320
Ser	Val	Val	Pro	Asp	Leu	Pro	Val	Pro	Thr	Ile	Ser	Ala	Pro	Ser
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Trp	Val	Trp	Asp	Gln	Glu	Glu	Glu	Arg	Lys	Arg	Gln	Glu	Arg	Trp
		340						345				350		Gln
Lys	Glu	Gln	Asp	Arg	Leu	Leu	Gln	Glu	Lys	Tyr	Gln	Arg	Glu	Gln
	355					360					365			Glu
Lys	Leu	Arg	Glu	Glu	Trp	Gln	Arg	Ala	Lys	Gln	Glu	Ala	Glu	Arg
	370				375					380				Glu
Asn	Ser	Lys	Tyr	Leu	Asp	Glu	Glu	Leu	Met	Val	Leu	Ser	Ser	Asn
385					390					395				400
Met	Ser	Leu	Thr	Thr	Arg	Glu	Pro	Ser	Leu	Ala	Thr	Trp	Glu	Ala
			405						410				415	Thr
Trp	Ser	Glu	Gly	Ser	Lys	Ser	Ser	Asp	Arg	Glu	Gly	Thr	Arg	Ala
		420						425				430		Gly
Glu	Glu	Glu	Arg	Arg	Gln	Pro	Gln	Glu	Glu	Val	Val	His	Glu	Asp
	435					440						445		Gln
Gly	Lys	Lys	Pro	Gln	Asp	Gln	Leu	Val	Ile	Glu	Arg	Glu	Arg	Lys
	450				455					460				Trp
Glu	Gln	Gln	Leu	Gln	Glu	Glu	Gln	Glu	Gln	Lys	Arg	Leu	Gln	Ala
465				470					475					480
Ala	Glu	Glu	Gln	Lys	Arg	Pro	Ala	Glu	Glu	Gln	Lys	Arg	Gln	Ala
			485					490					495	Glu
Ile	Glu	Arg	Glu	Thr	Ser	Val	Arg	Ile	Tyr	Gln	Tyr	Arg	Arg	Pro
		500					505					510		Val
Asp	Ser	Tyr	Asp	Ile	Pro	Lys	Thr	Glu	Glu	Ala	Ser	Ser	Gly	Phe
	515					520						525		Leu
Pro	Gly	Asp	Arg	Asn	Lys	Ser	Arg	Ser	Thr	Thr	Glu	Leu	Asp	Asp
	530					535					540			Tyr
Ser	Thr	Asn	Lys	Asn	Gly	Asn	Asn	Lys	Tyr	Leu	Asp	Gln	Ile	Gly
545				550					555					560
Thr	Thr	Ser	Ser	Gln	Arg	Arg	Ser	Lys	Lys	Glu	Gln	Val	Pro	Ser
			565					570				575		Gly
Ala	Glu	Leu	Glu	Arg	Gln	Gln	Ile	Leu	Gln	Glu	Met	Arg	Lys	Arg

	580		585		590										
Pro	Leu	His	Asn	Asp	Asn	Ser	Trp	Ile	Arg	Gln	Arg	Ser	Ala	Ser	Val
	595						600					605			
Asn	Lys	Glu	Pro	Val	Ser	Leu	Pro	Gly	Ile	Met	Arg	Arg	Gly	Glu	Ser
	610					615						620			
Leu	Asp	Asn	Leu	Asp	Ser	Pro	Arg	Ser	Asn	Ser	Trp	Arg	Gln	Pro	Pro
	625				630				635					640	
Trp	Leu	Asn	Gln	Pro	Thr	Gly	Phe	Tyr	Ala	Ser	Ser	Ser	Val	Gln	Asp
			645					650					655		
Phe	Ser	Arg	Pro	Pro	Pro	Gln	Leu	Val	Ser	Thr	Ser	Asn	Arg	Ala	Tyr
		660						665					670		
Met	Arg	Asn	Pro	Ser	Ser	Ser	Val	Pro	Pro	Pro	Ser	Ala	Gly	Ser	Val
	675					680						685			
Lys	Thr	Ser	Thr	Thr	Gly	Val	Ala	Thr	Thr	Gln	Ser	Pro	Thr	Pro	Arg
	690					695					700				
Ser	His	Ser	Pro	Ser	Ala	Ser	Gln	Ser	Gly	Ser	Gln	Leu	Arg	Asn	Arg
	705				710				715					720	
Ser	Val	Ser	Gly	Lys	Arg	Ile	Cys	Ser	Tyr	Cys	Asn	Asn	Ile	Leu	Gly
			725					730					735		
Lys	Gly	Ala	Ala	Met	Ile	Ile	Glu	Ser	Leu	Gly	Leu	Cys	Tyr	His	Leu
		740					745					750			
His	Cys	Phe	Lys	Cys	Val	Ala	Cys	Glu	Cys	Asp	Leu	Gly	Gly	Ser	Ser
	755					760					765				
Ser	Gly	Ala	Glu	Val	Arg	Ile	Arg	Asn	His	Gln	Leu	Tyr	Cys	Asn	Asp
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Cys	Tyr	Leu	Arg	Phe	Lys	Ser	Gly	Arg	Pro	Thr	Ala	Met			
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<210> 731

<211> 513

<212> DNA

<213> Homo sapiens

<400> 731

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120

tcttcaaatg actgactggg gaaacagatt gttggaaaaa cactttcggg ttgcctcgat
180

ggggtcaata ctttatcagg ccacaggaaa gacaaaggaa aatgcttcct gctggagcat
240

gtgcacatat gttgttcctt taactccaaa tacgtatgca ggggtggtgg taggatcaga
300

aaatgtgtga tcagaaagt accagttccc caccattttg tgtgggtttt attttctttc
360

tgctccgtgt tgactctttt cccacaaca cggaagctgc ttaatccaaa gacttggacc
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513

<210> 732

<211> 113
 <212> PRT
 <213> Homo sapiens

<400> 732
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 35 40 45
 Leu Ile Leu Pro Pro Pro Leu His Thr Tyr Leu Glu Leu Lys Glu Gln
 50 55 60
 His Met Cys Thr Cys Ser Ser Arg Lys His Phe Pro Leu Ser Phe Leu
 65 70 75 80
 Trp Pro Asp Lys Val Leu Thr Pro Ser Arg Gln Pro Glu Ser Val Phe
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 Pro Thr Ile Cys Phe Pro Ser Gln Ser Phe Glu Glu Ser Arg Glu Ala
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 Glu

<210> 733
 <211> 4366
 <212> DNA
 <213> Homo sapiens

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<210> 734

<211> 364

<212> PRT

<213> Homo sapiens

<400> 734

Met	Val	Val	Pro	Ser	Leu	Lys	Leu	Gln	Asp	Leu	Ile	Glu	Glu	Ile	Arg
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Gly	Ala	Lys	Thr	Gln	Ala	Gln	Glu	Arg	Glu	Val	Ile	Gln	Lys	Glu	Cys
			20					25					30		
Ala	His	Ile	Arg	Ala	Ser	Phe	Arg	Asp	Gly	Asp	Pro	Val	His	Arg	His
		35					40					45			
Arg	Gln	Leu	Ala	Lys	Leu	Leu	Tyr	Val	His	Met	Leu	Gly	Tyr	Pro	Ala
		50				55					60				
His	Phe	Gly	Gln	Met	Glu	Cys	Leu	Lys	Leu	Ile	Ala	Ser	Ser	Arg	Phe
65					70					75				80	
Thr	Asp	Lys	Arg	Val	Gly	Tyr	Leu	Gly	Ala	Met	Leu	Leu	Leu	Asp	Glu
			85						90					95	
Arg	His	Asp	Ala	His	Leu	Leu	Ile	Thr	Asn	Ser	Ile	Lys	Asn	Asp	Leu
			100					105					110		
Ser	Gln	Gly	Ile	Gln	Pro	Val	Gln	Gly	Leu	Ala	Leu	Cys	Thr	Leu	Ser
		115					120					125			
Thr	Met	Gly	Ser	Ala	Glu	Met	Cys	Arg	Asp	Leu	Ala	Pro	Glu	Val	Glu
	130					135					140				
Lys	Leu	Leu	Leu	Gln	Pro	Ser	Pro	Tyr	Val	Arg	Lys	Lys	Ala	Ile	Leu
145					150					155				160	
Thr	Ala	Val	His	Met	Ile	Arg	Lys	Val	Pro	Glu	Leu	Ser	Ser	Val	Phe
			165						170					175	
Leu	Pro	Pro	Cys	Ala	Gln	Leu	Leu	His	Glu	Arg	His	His	Gly	Ile	Leu
			180					185					190		
Leu	Gly	Thr	Ile	Thr	Leu	Ile	Thr	Glu	Leu	Cys	Glu	Arg	Ser	Pro	Ala
	195						200					205			
Ala	Leu	Arg	His	Phe	Arg	Lys	Val	Val	Pro	Gln	Leu	Val	His	Ile	Leu
	210					215					220				
Arg	Thr	Leu	Val	Thr	Met	Gly	Tyr	Ser	Thr	Glu	His	Ser	Ile	Ser	Gly
225					230					235				240	
Val	Ser	Asp	Pro	Phe	Leu	Gln	Val	Gln	Ile	Leu	Arg	Leu	Leu	Arg	Ile
			245						250					255	
Leu	Gly	Arg	Asn	His	Glu	Glu	Ser	Ser	Glu	Thr	Met	Asn	Asp	Leu	Leu
			260					265					270		
Ala	Gln	Val	Ala	Thr	Asn	Thr	Asp	Thr	Ser	Arg	Asn	Ala	Gly	Asn	Ala

```

      275              280              285
Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp Ile Arg Ser Ala Ala
      290              295              300
Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly Arg Phe Leu Leu Asn
305              310              315              320
Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Arg Leu
      325              330              335
Val Gln Ser Asp His Ser Ala Val Gln Arg His Arg Pro Thr Val Val
      340              345              350
Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser Arg
      355              360

```

<210> 735
 <211> 597
 <212> DNA
 <213> Homo sapiens

```

<400> 735
gtcgactagc caaaccgccc gggaaagtct tgtaccaccg atcctgggtt atgcggatct
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120
tgcttggtgt cctcgatccc gctctgaccg cccactggac cgctcaaccc aggacatcct
180
cagtgccatc cagcagctgg ctgcaccgct ggcactaccc atcttcgtgg tgggtgccac
240
agcgcgcgac attctgctga cacacgtggt cggtatcgag accggacgtg ccacgctcga
300
cgtggatttc gccgttgccg tagaacattg gccgcagttc gaaaacatca agcagcacct
360
gctagccaac gaccatttcg actctgccgc cagcatcacc catcgactgc tctatcgcac
420
gagcgacaac acgatcgccc ggccaatcga tctcatccca ttcggcggca tcgaacagcc
480
gccagccacc atcaaattggc cgcccagacat ggctgtcatg atgaatgttg ctggctacgc
540
agatgcctgg cgggcgcgag tcgaagtaga gtttgtgccc gggcgcagca tacgcgt
597

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<210> 736
 <211> 175
 <212> PRT
 <213> Homo sapiens

```

<400> 736
Met Asp Ser Arg Asn Leu Glu Thr Ala Asn Leu Ile Pro Glu Lys Ile
1              5              10              15
Ile Ala Trp Cys Pro Arg Ser Arg Ser Asp Arg Pro Leu Asp Arg Ser
20              25              30
Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala
35              40              45
Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr
50              55              60
His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe

```

```

65              70              75              80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
              85              90              95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
              100              105              110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
              115              120              125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
              130              135              140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145              150              155              160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
              165              170              175

```

<210> 737
 <211> 497
 <212> DNA
 <213> Homo sapiens

```

<400> 737
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cgcgccggca tcgttgggta cggatacgat cccaaccctc acgccgaccg tgccgacctt
120
caccctgccc tgcctgggat cagccacgtc accttcgtta aaactgtcag tgtgggggat
180
accatcggtt acggcagaac atggacagcc agcgaaacga caaaaatcgc caccgtccca
240
gtcggttacg ccgacggact gtcccgagga ctgtcaaata aaggacacgt tctcattaga
300
gggtccgttc atcccatcgt cggtcggatc tgcattggacc aattcatggt cgatcttggc
360
cccgattcga acgtcacggt gggagatgag gtggtgctca ttggaacca ggaggacgaa
420
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480
gccatttcca aacgcgt
497

```

<210> 738
 <211> 165
 <212> PRT
 <213> Homo sapiens

```

<400> 738
Xaa Arg Leu Ala Asn Ser Gly Ala Ile Leu Gly His Asp Leu Gly Lys
1              5              10              15
Thr Ser Met Val Arg Ala Gly Ile Val Gly Tyr Gly Tyr Asp Pro Asn
              20              25              30
Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
              35              40              45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
              50              55              60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro

```

```

65          70          75          80
Val Gly Tyr Ala Asp Gly Leu Ser Arg Gly Leu Ser Asn Lys Gly His
          85          90          95
Val Leu Ile Arg Gly Ser Val His Pro Ile Val Gly Arg Ile Cys Met
          100          105          110
Asp Gln Phe Met Val Asp Leu Gly Pro Asp Ser Asn Val Thr Val Gly
          115          120          125
Asp Glu Val Val Leu Ile Gly Thr Gln Glu Asp Glu Thr Leu Thr Ala
          130          135          140
Asp Asp Met Ala Glu Leu Leu Gly Thr Ile Ser Tyr Glu Ile Thr Cys
145          150          155          160
Ala Ile Ser Lys Arg
          165

```

<210> 739
 <211> 438
 <212> DNA
 <213> Homo sapiens

```

<400> 739
cggctgctggg aagagcgggc gcacgcgctc aagaccaagg aaaagctggc acagaccgcc
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acggcctcat cagcagctgt gggctcaggc cccctcccg aggcggagca ggcgtggccg
120
cagagcagcg gggaggagga gctgcagctc cagctggccc tggccatgag caaggaggag
180
gccgaccagc ccccgctctg cggccccgag gacgacgccc agctccagct ggcccttagt
240
ttgagccgag aagagcatga taaggaggag cggatccgtc gcggggatga cctgcggctg
300
cagatggcaa tcgaggagag caagagggag actgggggca aggaggagtc gtcctcatg
360
gaccttgctg acgtcttcac gccccagct cctgccccga ccaagacccc ctggggggggc
420
ccagcaccca tggctgct
438

```

<210> 740
 <211> 146
 <212> PRT
 <213> Homo sapiens

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<400> 740
Arg Leu Arg Glu Glu Arg Ala His Ala Leu Lys Thr Lys Glu Lys Leu
1          5          10          15
Ala Gln Thr Ala Thr Ala Ser Ser Ala Ala Val Gly Ser Gly Pro Pro
          20          25          30
Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu Leu
          35          40          45
Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp Gln Pro
          50          55          60
Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln Leu Gln Leu Ala Leu Ser
65          70          75          80
Leu Ser Arg Glu Glu His Asp Lys Glu Glu Arg Ile Arg Arg Gly Asp

```

```

      85              90              95
Asp Leu Arg Leu Gln Met Ala Ile Glu Glu Ser Lys Arg Glu Thr Gly
      100              105              110
Gly Lys Glu Ser Ser Leu Met Asp Leu Ala Asp Val Phe Thr Pro
      115              120              125
Pro Ala Pro Ala Pro Thr Thr Asp Pro Trp Gly Gly Pro Ala Pro Met
      130              135              140
Ala Ala
145

```

```

<210> 741
<211> 726
<212> DNA
<213> Homo sapiens

```

```

<400> 741
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aatttgccgg tcattctgctt cgtcggggccc actgctagcg gaaaatcagg gctagcggtg
120
cgagtgtgcc gccgcttgta tgtcgatgag caccgcgccg aaattattaa tactgactcg
180
atgggtggtgt atcgcgggat ggacattggc actgccaccc ctacactgcg cgagcagcgc
240
acggtagtgc atcaacctggt gtcgattctt gatgtgactg tgccctcctc gctagtactg
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atgcagacgc tggcccgtag tgccgtcgag gattgtctgt cgcgtggtgt catccctgtc
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480
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600
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720
gtcgac
726

```

```

<210> 742
<211> 242
<212> PRT
<213> Homo sapiens

```

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<400> 742
Ala Ser Leu Arg Pro Arg Cys Cys Lys Asp Val Ala Thr Val Arg Lys
1      5      10      15
Asn Glu Tyr Val Asn Leu Pro Val Ile Cys Leu Val Gly Pro Thr Ala
20     25     30
Ser Gly Lys Ser Gly Leu Ala Val Arg Val Cys Arg Arg Leu Tyr Val

```

```

      35              40              45
Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
  50              55              60
Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
  65              70              75              80
Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
      85              90              95
Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
      100              105              110
Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
      115              120              125
Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Pro Thr Asp Pro Glu
      130              135              140
Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
      145              150              155              160
Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
      165              170              175
Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
      180              185              190
Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
      195              200              205
Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
      210              215              220
Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
      225              230              235              240
Val Asp

```

<210> 743

<211> 430

<212> DNA

<213> Homo sapiens

<400> 743

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naaaaaagtg atggtttcgg atctgtggcc agtcgtcttg caagaaatca ttatgacgtg
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gatgagggga acagcancat tcatgttaat caagacattg cgcgcagaac agggacggga
120
aagctatttg tacgagtgtg cccggcgcac gtgtactcag aggagcccgga tggcactatt
180
tccgtggagt acgcagcgtg tctggagtgt ggcacttgct tggcgggtgc tgcgccaggg
240
tcgcttgaat ggcactatcc cgcagggtgca atgggtatatt cgttcagaga aggatgaagt
300
ccttgtgggc gactgtaaag cgacatggcc gtcgctcggg aggaggaatt gtggtgtccg
360
caccaaatag tgctcaggat gaagttcgtc atggaaatcc ggctccaacc gtttcgggag
420
ctggtcgcga
430

```

<210> 744

<211> 98

<212> PRT

<213> Homo sapiens

<400> 744

```

Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn
 1           5           10           15
His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp
      20           25           30
Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro
      35           40           45
Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr
      50           55           60
Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala Ala Pro Gly
65           70           75           80
Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg
      85           90           95
Glu Gly

```

<210> 745

<211> 362

<212> DNA

<213> Homo sapiens

<400> 745

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60
gcgtcgtggt ggcgcatggc gcggtatttc atcgccgagc ttgaacgcag cagcgagttg
120
tatgagcagg cggcggtttac ccgcatctg gaaagctcgc tgatcaaggg cctgacctc
180
gcccagccga acaactactc cgaagaactg cgcgacgtac tcggcggtgaa gctgccgcat
240
tacttgattc ggcgcgggca gtacatccac gacaacgcc gcgaagccgt gcatctggaa
300
gacctggaaa ccgctgccgg ggtatcgagg ttcaagttgt tcgatgcgtt tcgcaaatac
360
tt
362

```

<210> 746

<211> 108

<212> PRT

<213> Homo sapiens

<400> 746

```

Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg
 1           5           10           15
Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala
      20           25           30
Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu
      35           40           45
Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val
      50           55           60
Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

```


65 70 75 80
 Ala Arg Glu Ala Val His Leu Glu Asp Leu Glu Thr Ala Ala Gly Val
 85 90 95
 Ser Arg Phe Lys Leu Phe Asp Ala Phe Arg Lys Tyr
 100 105

<210> 747
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 747
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 ctgaatgccg atggcacgcc taaagccacc ggcacgctgc tcaagaaccc agcgctggcc
 120
 gccgtgttca aacgtatcgc caaggaagga ccggacgcgc tgtaccacgg gccgattgcc
 180
 gacgagatcg cgcgcaaggt tcagggcaac cgcaatgcgg gcagcctgtc gcaagcggac
 240
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 300
 gtgtgcggca tgccaccgcc gtcgtcaggc gggattgcgg tggcgcagat cctcggcacg
 360
 ctgcaggccg tggaagcccg cgaccacgc ctggccatcg ccccatgaa accggt
 416

<210> 748
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 748
 Xaa Ala Leu Ile Ala Ala Asp Arg Phe Ile Pro Gln Ser Pro Asp Met
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 Ala Ala Tyr Phe Leu Asn Ala Asp Gly Thr Pro Lys Ala Thr Gly Thr
 20 25 30
 Leu Leu Lys Asn Pro Ala Leu Ala Ala Val Phe Lys Arg Ile Ala Lys
 35 40 45
 Glu Gly Pro Asp Ala Leu Tyr His Gly Pro Ile Ala Asp Glu Ile Ala
 50 55 60
 Arg Lys Val Gln Gly Asn Arg Asn Ala Gly Ser Leu Ser Gln Ala Asp
 65 70 75 80
 Leu Lys Ala Tyr Thr Ala Lys Glu Arg Thr Pro Leu Cys Thr Asp Tyr
 85 90 95
 Lys Gln Tyr Gln Val Cys Gly Met Pro Pro Pro Ser Ser Gly Gly Ile
 100 105 110
 Ala Val Ala Gln Ile Leu Gly Thr Leu Gln Ala Val Glu Ala Arg Asp
 115 120 125
 Pro Arg Leu Ala Ile Ala Pro Met Lys Pro
 130 135

<210> 749
 <211> 1211

<212> DNA

<213> Homo sapiens

<400> 749

nagtcctaga cgccagaccc gctcagaccc tcttgccagg tgacagccgc caagatgggg
60
tcttggggccc tgctgtggcc tcccctgctg ttcaccgggc tgctcgccg acccccgggg
120
accatggccc aggcccagta ctgctctgtg aacaaggaca tctttgaagt agaggagaac
180
acaaatgtca ccgagccgct ggtggacatc cacgtcccgg agggccagga ggtgaccctc
240
ggagccttgt ccaccccctt tgcatttcgg atccaggga accagctgtt tctcaacgtg
300
actcctgatt acgaggagaa gtcactgctt gaggtcagc tgctgtgtca gagcggaggc
360
acattggtga ccagctaag ggtgttcgtg tcagtgtgtg acgtcaatga caatgcccc
420
gaattcccct ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccacc
480
gtcatccccg agacgcaact gcaggctgag gaccgcgaca aggacgacat tctgttctac
540
accctccagg aaatgacagc aggtgccagt gactacttct ccctgggtgag tgtaaaccgt
600
ccgcccctga ggctggaccg gcccctggac ttctacgagc ggccgaacat gaccttctgg
660
ctgctggtgc gggacactcc gggggagaat gtggaacca gccacactgc caccgccaca
720
ctagtgtga acgtggtgcc cgccgacctg cgccccccgt ggttcctgcc ctgcacctc
780
tcagatggct acgtctgcat tcaagctcag taccacgggg ctgtccccac ggggcacata
840
ctgccatctc cctcgtcct gcgtcccgga cccatctacg ctgaggacgg agaccgaggc
900
atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatggtac attcatcatc
960
caccagact cgggcaacct caccgtggcc aggagtgtcc ccagcccat gaccttctc
1020
ctgctggtga agggccaaca ggccgacctt gcccgtact cagtgaacca ggtcaccgtg
1080
gagggtgtg gctgcggccg ggagcccgcc ccgcttcccc cagagcctgt atcgtggcac
1140
cgtggcgctg ggcgctggag cggcgcttgt ggtcaaggat gcagctgccc cttttcagcc
1200
tctgaggatc c
1211

<210> 750

<211> 385

<212> PRT

<213> Homo sapiens

<400> 750

Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

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1           5           10           15
Leu Val Arg Pro Pro Gly Thr Met Ala Gln Ala Gln Tyr Cys Ser Val
20           25           30
Asn Lys Asp Ile Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro
35           40           45
Leu Val Asp Ile His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala
50           55           60
Leu Ser Thr Pro Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu
65           70           75           80
Asn Val Thr Pro Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu
85           90           95
Leu Cys Gln Ser Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val
100          105          110
Ser Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr
115          120          125
Lys Glu Ile Arg Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile
130          135          140
Pro Glu Thr Gln Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu
145          150          155          160
Phe Tyr Thr Leu Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser
165          170          175
Leu Val Ser Val Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp
180          185          190
Phe Tyr Glu Arg Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr
195          200          205
Pro Gly Glu Asn Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val
210          215          220
Leu Asn Val Val Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys
225          230          235          240
Thr Phe Ser Asp Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala
245          250          255
Val Pro Thr Gly His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly
260          265          270
Pro Ile Tyr Ala Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile
275          280          285
Tyr Ser Ile Phe Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro
290          295          300
Asp Ser Gly Asn Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr
305          310          315          320
Phe Leu Leu Leu Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser
325          330          335
Val Thr Gln Val Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala
340          345          350
Pro Leu Pro Pro Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp
355          360          365
Ser Gly Arg Cys Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu
370          375          380
Asp
385

```

<210> 751

<211> 345

<212> DNA

<213> Homo sapiens

<400> 751

cgcgctcgcg tcacgtctcaa cgacatgagc gaggtcaaca tcgacgcggc gctgggtggcg
 60
 gcaggcgggc ggctgtcgcg caccgaggag aagctcgctc agatgtcgaa cggctgcacg
 120
 tgctgcacgc tgcgcgacga cctgatgcag gaagtggcga gactggcggg cgaaggccgc
 180
 ttgatgcgc tggatcatga gagcaccggc gtgtccgagc cgatgccggg cgccgccacg
 240
 ttcgatttcc gtgaccagga cggcgtctcg ctgcccgacg tcgcgcggct ggataccatg
 300
 gtcaccgtcg tcgacgccgc gtccttctcg cgcgactacg gctcg
 345

<210> 752

<211> 115

<212> PRT

<213> Homo sapiens

<400> 752

Arg	Val	Ala	Val	Ile	Val	Asn	Asp	Met	Ser	Glu	Val	Asn	Ile	Asp	Ala
1				5					10					15	
Ala	Leu	Val	Ala	Ala	Gly	Gly	Gly	Leu	Ser	Arg	Thr	Glu	Glu	Lys	Leu
		20						25					30		
Val	Glu	Met	Ser	Asn	Gly	Cys	Ile	Cys	Cys	Thr	Leu	Arg	Asp	Asp	Leu
		35					40					45			
Met	Gln	Glu	Val	Ala	Arg	Leu	Ala	Gly	Glu	Gly	Arg	Phe	Asp	Ala	Leu
	50					55					60				
Val	Ile	Glu	Ser	Thr	Gly	Val	Ser	Glu	Pro	Met	Pro	Val	Ala	Ala	Thr
65				70					75					80	
Phe	Asp	Phe	Arg	Asp	Gln	Asp	Gly	Val	Ser	Leu	Ala	Asp	Val	Ala	Arg
			85						90					95	
Leu	Asp	Thr	Met	Val	Thr	Val	Val	Asp	Ala	Ala	Ser	Phe	Leu	Arg	Asp
			100					105						110	
Tyr	Gly	Ser													
		115													

<210> 753

<211> 352

<212> DNA

<213> Homo sapiens

<400> 753

gcgcgccagt acgccaagac cgtccgcaag gaccgcaagg gcgaacggcg gcgtcggggc
 60
 gcgtcggact agtccacgat gcatccgaac cgcgcccttc gctttgccga tgatgtctcg
 120
 atgctegatt tcgcggccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg
 180
 cctatggtag cgcattgccc gggtacgccc ttcgacggag ccttcgctt ccatgtcgcg
 240
 cgcggaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgctcag catcagcgcg
 300

accgacggct atattcagccc gagctgggtac gccgacccgc agggaccaca gt
352

<210> 754

<211> 91

<212> PRT

<213> Homo sapiens

<400> 754

Met	His	Pro	Asn	Arg	Ala	Phe	Arg	Phe	Ala	Asp	Asp	Val	Ser	Met	Leu
1				5					10					15	
Asp	Phe	Ala	Ala	Lys	Arg	Ala	Phe	Ala	His	Ile	Phe	Val	Ser	Thr	Pro
		20						25					30		
Glu	Gly	Pro	Met	Val	Ala	His	Ala	Pro	Val	Thr	Pro	Phe	Asp	Gly	Ala
		35					40					45			
Phe	Arg	Phe	His	Val	Ala	Arg	Gly	Asn	Arg	Ile	Ala	Arg	His	Leu	Asp
	50					55				60					
Gly	Ala	Thr	Leu	Leu	Leu	Ser	Ile	Ser	Ala	Thr	Asp	Gly	Tyr	Ile	Ser
65				70					75					80	
Pro	Ser	Trp	Tyr	Ala	Asp	Pro	Gln	Gly	Pro	Gln					
				85					90						

<210> 755

<211> 301

<212> DNA

<213> Homo sapiens

<400> 755

tgggatgcag ggtcttttctt ctccaaggat ttcattctctg gagggagaaa agggccccag
60
ctgtctgccca tcaaaccggg ttgccgggct ggagctcctc ccaggcccgt gtgaggaaga
120
gcaaaggccg gcaggggctc gatgggacca gtcgctcgct caggcccagg aaaaccacac
180
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca
240
ggcccactct gcagacctca atgtctcagg tgcactgcag ggcaaccccg cctaccccgg
300
g
301

<210> 756

<211> 99

<212> PRT

<213> Homo sapiens

<400> 756

Met	Gln	Gly	Leu	Ser	Ser	Pro	Arg	Ile	Ser	Phe	Leu	Glu	Gly	Glu	Lys
1				5					10					15	
Gly	Pro	Ser	Cys	Leu	Pro	Ser	Asn	Arg	Val	Ala	Gly	Leu	Glu	Leu	Leu
		20					25					30			
Pro	Gly	Pro	Cys	Glu	Glu	Glu	Gln	Arg	Pro	Ala	Gly	Ala	Arg	Trp	Asp
		35				40					45				
Gln	Ser	Leu	Ala	Gln	Ala	Gln	Glu	Asn	His	Thr	Ala	Gly	Gly	Cys	Gln

```

      50              55              60
Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala
65              70              75              80
His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala
      85              90              95
Tyr Pro Gly

```

<210> 757
 <211> 311
 <212> DNA
 <213> Homo sapiens

```

<400> 757
actgaggcga tcgccagagg ggtgggctg cgagggctgc tcaacatcca gttcgccctg
60
gtctccgatg ttctctacgt catcgaggcc aacccaggg catcgcgac agtccccctc
120
gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag
180
acgatcgcc ctgctcaggcg ctccggccac ctgcccaggg ccgacgccgc cgtcaccgat
240
cccgatgacc cgatcgccgt caaggaggcg gtcctaccct tcaaacgatt ccgcaccacc
300
gagggacgcg t
311

```

<210> 758
 <211> 103
 <212> PRT
 <213> Homo sapiens

```

<400> 758
Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile
1              5              10              15
Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro
      20              25              30
Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln
      35              40              45
Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser
      50              55              60
Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Ala Val Thr Asp
65              70              75              80
Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg
      85              90              95
Phe Arg Thr Thr Glu Gly Arg
      100

```

<210> 759
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 759

```
<210> 760
<211> 130
<212> PRT
<213> Homo sapiens
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```
<210> 761
<211> 324
<212> DNA
<213> Homo sapiens
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833

cagatttcag ggaggggggg gcctaaaggg aagtagggat cttggtaggc tgcaaaattt
 300
 tcctcccat ccccatcca caga
 324

<210> 762
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 762
 Met Gly Asp Gly Glu Glu Asn Phe Ala Ala Tyr Gln Asp Pro Tyr Phe
 1 5 10 15
 Pro Leu Gly Pro Leu Pro Glu Ile Cys Thr Cys Ser Gln Thr Asp
 20 25 30
 Pro Ser Pro Gln Leu Ser Pro Ala Val Asn Gly Ser Gln Cys Pro Ala
 35 40 45
 Leu Pro Ser Leu Gly Glu Glu Pro Trp Gly Pro Leu Gly Gln Glu Val
 50 55 60
 Pro Asp Cys Pro Leu Ser Phe Ala Glu Lys Glu Leu Trp Gly Arg Glu
 65 70 75 80
 Gly Leu Ala Ser Pro Arg Arg Tyr Phe Leu Leu His Gln Gly Ser Lys
 85 90 95
 Lys Val Arg Pro Leu Trp Ala Tyr Leu
 100 105

<210> 763
 <211> 301
 <212> DNA
 <213> Homo sapiens

<400> 763
 acgcgttatg ggcggcccg atgggcgatg cgctatccca cacctcgatg atggcggaca
 60
 tcctcggcgg tgtgctggaa gtggcgcca atatcgcgat tactgcgggc ggcaccgctg
 120
 ccgcggtggc cgccaccggc ttaccgagg ccaccggcgg cctcggctgc ttctgctgg
 180
 gcgctgcctt gggcaccatt gccggcctgg ccatgagcaa cattggcgcg gacacagggc
 240
 tgaccaagat atgcaatgcc tttacaacg ccttatttgc gcccaccgtg catgcgaaca
 300
 t
 301

<210> 764
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 764
 Met Phe Ala Cys Thr Val Gly Ala Asn Lys Ala Leu Leu Lys Ala Leu
 1 5 10 15
 His Ile Leu Val Ser Pro Val Ser Ala Pro Met Leu Leu Met Ala Arg


```

      20      25      30
Pro Ala Met Val Pro Lys Ala Ala Pro Ser Arg Lys Gln Pro Arg Pro
      35      40      45
Pro Val Ala Ser Val Lys Pro Val Ala Ala Thr Ala Ala Ala Val Ala
      50      55      60
Pro Ala Val Ile Ala Ile Leu Ala Ala Thr Ser Ser Thr Pro Pro Arg
      65      70      75      80
Met Ser Ala Ile Ile Glu Val Trp Asp Ser Ala Ser Pro Ile Arg Ala
      85      90      95
Ala His Asn Ala
      100

```

<210> 765

<211> 831

<212> DNA

<213> Homo sapiens

<400> 765

```

ngcacactcc agcctctgtt ctttctctcc ttgtgccttt gcccttacca cggttcctca
60
taacattggt gttcctgtat ttaaggccct ataaacaggg agatgcgcca cctcatcagt
120
agcctccaga atcacaatca ccagctgaaa ggggaggtcc tgagatataa gcggaaattg
180
agagaagccc agtctgacct gaacaagaca cgctgcgta gtggtagtgc cctcctgcag
240
tcccagtcta gtactgagga cccgaaggat gagcctgcgg agctaaaacc agattctggg
300
gacttatact cccagtcctc agcttcaaag gcatctcagg aggatgccaa tgaaatcaag
360
tctaaacggg atgaagaaga acgagaacga gaaaggaggg agaaggagag ggaacgagaa
420
agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa
480
aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag
540
gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaag
600
gagatgaaac tattgctgga tatgtaccgt tctgccccaa aggaacagag agacaaagtt
660
cagctgatgg cagctgagaa gaagtctaag gcagagttgg aagatctaag gcaaagactc
720
aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg
780
aggaagatcc gggcagtgga ggagcagata gaatacctac agaagaagct a
831

```

<210> 766

<211> 243

<212> PRT

<213> Homo sapiens

<400> 766

Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

1	5	10	15
Gly Glu Val Leu Arg Tyr Lys Arg Lys Leu Arg Glu Ala Gln Ser Asp			
20	25	30	
Leu Asn Lys Thr Arg Leu Arg Ser Gly Ser Ala Leu Leu Gln Ser Gln			
35	40	45	
Ser Ser Thr Glu Asp Pro Lys Asp Glu Pro Ala Glu Leu Lys Pro Asp			
50	55	60	
Ser Gly Asp Leu Ser Ser Gln Ser Ser Ala Ser Lys Ala Ser Gln Glu			
65	70	75	80
Asp Ala Asn Glu Ile Lys Ser Lys Arg Asp Glu Glu Glu Arg Glu Arg			
85	90	95	
Glu Arg Arg Glu Lys Glu Arg Glu Arg Glu Arg Glu Arg Glu Lys Glu			
100	105	110	
Lys Glu Arg Glu Arg Glu Lys Gln Lys Leu Lys Glu Ser Glu Lys Glu			
115	120	125	
Arg Asp Ser Ala Lys Asp Lys Glu Lys Gly Lys His Asp Asp Gly Arg			
130	135	140	
Lys Lys Glu Ala Glu Ile Ile Lys Gln Leu Lys Ile Glu Leu Lys Lys			
145	150	155	160
Ala Gln Glu Ser Gln Lys Glu Met Lys Leu Leu Leu Asp Met Tyr Arg			
165	170	175	
Ser Ala Pro Lys Glu Gln Arg Asp Lys Val Gln Leu Met Ala Ala Glu			
180	185	190	
Lys Lys Ser Lys Ala Glu Leu Glu Asp Leu Arg Gln Arg Leu Lys Asp			
195	200	205	
Leu Glu Asp Lys Glu Lys Lys Glu Asn Lys Lys Met Ala Asp Glu Asp			
210	215	220	
Ala Leu Arg Lys Ile Arg Ala Val Glu Glu Gln Ile Glu Tyr Leu Gln			
225	230	235	240
Lys Lys Leu			

<210> 767

<211> 431

<212> DNA

<213> Homo sapiens

<400> 767

gctagctcgc tcgcactcat tctcgggagg cttccccgcg ccggccgcgt cccgccccgt
60
ccccggcacc agaagttcct ctgcgcgtcc gacggcgaca tgggcgtccc cacggccccg
120
gaggccggca gctggcgctg gggatccctg ctcttcgctc tcttcctggc tgcgtcccta
180
ggtccggtgg cagccttcaa ggtcgccacg ccgtattccc tgtatgtctg tcccaggggg
240
cagaacgtca ccctcacctg caggctcttg ggccctgtgg acaaagggca cgatgtgacc
300
ttctacaaga cgtggtaccg cagctcgagg ggcgaggtgc agacctgctc agagcgccgg
360
cccatccgca acctcacgtt ccaggacctt cacctgcacc atggaggcca ccaggctgcc
420
aacaccagcc a
431

<210> 768
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 768
 Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser
 1 5 10 15
 Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala
 20 25 30
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
 35 40 45
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
 50 55 60
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
 65 70 75 80
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
 85 90 95
 Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser
 100 105 110

<210> 769
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 769
 tgtacacctc gtaatacatg atcgcgatac cgcccgcgat gaccctaagc aactcattct
 60
 cgacttcgaa ctccatcaag tgatttttgc ggtcgacgaa tctggtttcc gtagtaaaga
 120
 acggtatggt ttgtatgtcg cggccctgcc actcaaact caccgtgtca cccacctcaa
 180
 aaaaatccc ggtcggccca caaataaatc aattgcgccg ctctccgag ttcttccatg
 240
 tcaacgatct cccctggctg ctcaagccaa ggccctcgcg gccgtgggac tccaagggtg
 300
 acgttgaccc gactgatttc ggaccagttg gcgtcggtat tgggggcagg gtagttaccg
 360
 cccatgtcga tgatctacat cgccaccggc agcgtgtctt cgtagtcgtc atgcctgac
 420
 an
 422

<210> 770
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 770
 Met Phe Cys Met Ser Arg Pro Cys His Ser Asn Leu Thr Val Ser Pro
 1 5 10 15
 Thr Ser Lys Lys Ser Arg Val Gly Pro Gln Ile Asn Gln Leu Arg Arg

```

                20                25                30
Ser Ser Glu Phe Phe His Val Asn Asp Leu Pro Trp Leu Leu Lys Pro
          35                40                45
Arg Pro Ser Arg Pro Trp Asp Ser Lys Val Asp Val Asp Pro Thr Asp
          50                55                60
Phe Gly Pro Val Gly Val Gly Ile Gly Gly Arg Val Val Thr Ala His
65                70                75                80
Val Asp Asp Leu His Arg His Arg Gln Arg Val Phe Val Val Val Met
          85                90                95
Pro Asp Xaa

```

<210> 771
 <211> 369
 <212> DNA
 <213> Homo sapiens

```

<400> 771
gcctacgcgc aattcctcgc gggatatggcg ttttaacaatg cgtctctcgg gtatgtgcat
60
gcaatggcgc atcagctggg cggttttttac gatctgccgc acggcgtgtg caatgcgata
120
ctgttgccac acgtgcagac gtttaactgc aaagtggcgg cctcgcgcct gcgtgattgc
180
gcccaggcca tgggtgtcga tgtcagtcaa atgacagcag aacagggcgc acaggcgtgt
240
atcgcagaga ttcgctctct ggcacgtcag gtgaatatcc cgggtgggatt gcgtgacctc
300
aacgtgaagg aagcggactt cccgattctg gcgaccaacg cgctaaaaga ccctgtgggt
360
ttgattaat
369

```

<210> 772
 <211> 123
 <212> PRT
 <213> Homo sapiens

```

<400> 772
Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
1                5                10                15
Gly Tyr Val His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asp Leu
          20                25                30
Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
          35                40                45
Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
          50                55                60
Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
65                70                75                80
Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
          85                90                95
Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
          100                105                110
Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn

```

115

120

<210> 773
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 773
 ccgccgttgc cggcgggtgga ttttctggta ggcttgaatc agcgccctggc tgccgacatc
 60
 ggttacttga tccgcgtgga gccgggcgta caaactccgg aattcaccct ggaaaacgcc
 120
 tccggttccct gccgggattc ggcggtggtg ctggtgcaac tgctgcgcaa cctgggcctg
 180
 gcggcgcgat ttgtgtctgg ctatctgac caactgaccg ccgacgtcaa agccctcgac
 240
 ggcccgctccg gcaccgaggt ggatttcacc gacctgcatg cctggtgcga agtgattttg
 300
 cccggcgcc
 309

<210> 774
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 774
 Pro Pro Leu Pro Ala Val Asp Phe Leu Val Gly Leu Asn Gln Arg Leu
 1 5 10 15
 Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr
 20 25 30
 Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala
 35 40 45
 Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe
 50 55 60
 Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp
 65 70 75 80
 Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys
 85 90 95
 Glu Val Tyr Leu Pro Gly Ala
 100

<210> 775
 <211> 4125
 <212> DNA
 <213> Homo sapiens

<400> 775
 nncaggatgg gcgcgaacaa tggcaaacag tacggcagtg agggcaaagg cagctcgagc
 60
 atctcatctg acgtgagttc aagtacagat cacacgccca ctaaagccca gaagaatgtg
 120
 gctaccagcg aagactccga cctgagcatg cgcacactga gcacgcccag cccagccctg
 180

atatgtccac cgaatctccc aggatttcag aatggaaggg gctcgtccac ctccctgtcc
240
tccatcacccg gggagacggt ggccatgggtg cactccccgc ccccgacccg cctcacacac
300
ccgctcatcc ggctcgctc cagaccccag aaggatcagg ccagcataga ccggctcccg
360
gaccactcca tgggtgcagat cttctccttc ctgcccacca accagctgtg ccgctgcgcg
420
cgagtgtgcc gccgctggta caacctggcc tgggaccgcg ggctctggag gactatccgc
480
ctgacgggcg agaccatcaa cgtggaccgc gccctcaagg tgctgaccgc cagactctgc
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 4020
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<210> 776

<211> 483

<212> PRT

<213> Homo sapiens

<400> 776

Tyr	Gly	Ser	Glu	Gly	Lys	Gly	Ser	Ser	Ser	Ile	Ser	Ser	Asp	Val	Ser
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Ser	Ser	Thr	Asp	His	Thr	Pro	Thr	Lys	Ala	Gln	Lys	Asn	Val	Ala	Thr
			20					25					30		
Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro
	35						40					45			
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly
	50					55					60				
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val
65					70				75					80	
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala
				85					90					95	
Ser	Arg	Pro	Gln	Lys	Asp	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His
		100						105					110		
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg
	115						120					125			
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg
	130					135					140				
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg
145					150				155					160	
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val
			165					170						175	
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr


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<210> 777
<211> 705
<212> DNA
<213> Homo sapiens
```

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<400> 777
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caccaatctg ctctttaatg ccagactgat ggctctaaca atccttatta actccttttt
120
gtgggttcaa ggaaaaacaa aaacctcttc tctcattcac cacctctagg ccaggagaaa
180
ttatttttgg ttcaggcttt cacagtgggg gtctgaaagt gaccagtcta gaaaaggatg
240
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actcagcaaa aggagagctc tgaaggtccc tgaggcggca cgggccagca ttattaggtc
 300
 acatggatatg acctgaaaca aatacgttct tcccaaatgt ggcaggaccg ggagagcttc
 360
 tcaccaggag ggaaccgccg caatgaccgc cggacgtcca gcaacacttg ttggtagtcc
 420
 ttgctcatct gccgtagggt cttccctgat ataggagggtg ggtcattggc attgacattg
 480
 aggagcttgg gccacacttt tcgtctgate tcatcagtca ggagccctcc ttcactgata
 540
 gccatgcgtc taagggcagc cacatcagtg ggatcactgt tcagagcctg gtgtatctct
 600
 aacactttct ttttcctttt ggcgtaaag tctgccttct ccgcgccgcc gtcccagtgg
 660
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 705

<210> 778

<211> 134

<212> PRT

<213> Homo sapiens

<400> 778

Met	Ala	Ser	Gly	Val	Arg	Arg	Gly	Arg	Pro	Thr	Ser	Gly	His	Trp	Asp
1				5					10					15	
Gly	Gly	Ala	Glu	Lys	Ala	Asp	Phe	Asn	Ala	Lys	Arg	Lys	Lys	Lys	Val
			20					25					30		
Leu	Glu	Ile	His	Gln	Ala	Leu	Asn	Ser	Asp	Pro	Thr	Asp	Val	Ala	Ala
		35					40					45			
Leu	Arg	Arg	Met	Ala	Ile	Ser	Glu	Gly	Gly	Leu	Leu	Thr	Asp	Glu	Ile
	50					55					60				
Arg	Arg	Lys	Val	Trp	Pro	Lys	Leu	Leu	Asn	Val	Asn	Ala	Asn	Asp	Pro
65					70				75					80	
Pro	Pro	Ile	Ser	Gly	Lys	Asn	Leu	Arg	Gln	Met	Ser	Lys	Asp	Tyr	Gln
			85					90					95		
Gln	Val	Leu	Leu	Asp	Val	Arg	Arg	Ser	Leu	Arg	Arg	Phe	Pro	Pro	Gly
		100						105				110			
Glu	Lys	Leu	Ser	Arg	Ser	Cys	His	Ile	Trp	Glu	Glu	Arg	Ile	Cys	Phe
		115					120					125			
Arg	Ser	Tyr	His	Val	Thr										
															130

<210> 779

<211> 322

<212> DNA

<213> Homo sapiens

<400> 779

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 120
 cgccttgccct ttgaaggaac ccagtgggaa ggctagacca agtaaataatg aatcaccaaa
 180

cgccagcaac ttcacgtca ggcattgtggc aactggcaaa gagggcactg atgatgagta
 240
 tgctaactca aactactact actcgatgtc tgccaatcga ctaggagacg aggaaacgga
 300
 ggaaatgata ggtttggcta cc
 322

<210> 780
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 780
 Met Cys Lys Gln Phe Asn Asp Val Val Arg Arg His Gly Val His His
 1 5 10 15
 Ser Val Thr Val Ser Asp Ser Glu Asp Thr Val Ala Pro Ser Gln Leu
 20 25 30
 Val Arg Ser Pro Arg Asn Ala Leu Pro Leu Lys Glu Pro Ser Gly Lys
 35 40 45
 Ala Arg Pro Ser Lys Tyr Glu Ser Pro Asn Ala Ser Asn Phe Ile Val
 50 55 60
 Arg His Val Ala Thr Gly Lys Glu Gly Thr Asp Asp Glu Tyr Ala Asn
 65 70 75 80
 Ser Asn Tyr Tyr Tyr Ser Met Ser Ala Asn Arg Leu Gly Asp Glu Glu
 85 90 95
 Thr Glu Glu Met Ile Gly Leu Ala Thr
 100 105

<210> 781
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 781
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 gtgtgtatgn gaatatgtgt gtgtatngta atgtgtgtgt gtgtttggaa tgtgtgtatg
 120
 gaatgtgtgt ctgtgtatgg aatatgtgtg agtatngaa tgtgtgtgtg tgtttggaat
 180
 gtatcgaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg
 240
 tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tgngaattgt tgtgtgt
 297

<210> 782
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 782
 Xaa Arg Val Pro Gly Met Cys Val Cys Val Cys Val Cys Met Tyr Val
 1 5 10 15
 Cys Met Glu Cys Val Cys Met Xaa Ile Cys Val Cys Met Xaa Met Cys

```

                20                25                30
Val Cys Val Trp Asn Val Cys Met Glu Cys Val Ser Val Tyr Gly Ile
                35                40                45
Cys Val Ser Met Xaa Met Cys Val Cys Val Trp Asn Val Ser Asn Val
                50                55                60
Cys Leu Cys Val Arg Asn Val Cys Val Trp Asn Val Phe Thr Cys Met
65                70                75                80
Cys Leu Glu Cys Val Cys Met Glu Cys Val Cys Met Cys Met Xaa Met
                85                90                95
Cys Val Cys

```

<210> 783
 <211> 612
 <212> DNA
 <213> Homo sapiens

```

<400> 783
accggtgacg taactgctcc cgctggcagc ttcgagggcg atgtcgattt gcgtgcccgg
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caccgggtcg agtgagctgc ccagcagcaa gcccaccaca tcggtgacca gaccgatcac
120
tttgttgagc acgtcgatga cgggcaactt caaggaaatc caggtgcgga cttgcgcggt
180
ccgcacaaaa atcggctggg tgtcgatcaa ctgcgggttg ccaatcgagc aatttgcgcg
240
gttcgatgac acgtgtcttc accgtgatat tcagcagccc cagtacgtcc accggcaact
300
cgacggccac cgcgctgggt ttgttgga gctgcacaaa gccctgaatc aggttgaaca
360
gttgacgggt gacgtccagg gcgctcttgt ccgtgccgtt ttgtatattg atcaggtcgc
420
ccaggtgcag gatctgcgtg cctggggcaa tcagcttgat tgcttcgagg ttattgatca
480
ccacctggac cgcattaccg cccagcttga gcacatcgat ggcggcctgg atcaactggc
540
cgacgggtcgc gtcggtcttg agcaactggt cgtagtgtgcc ggcgctgacg ttgaggcgga
600
tggccgacgc gt
612

```

<210> 784
 <211> 190
 <212> PRT
 <213> Homo sapiens

```

<400> 784
Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
1                5                10                15
Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
                20                25                30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
                35                40                45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu

```

```

      50              55              60
Phe Ala Arg Phe Asp Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65              70              75              80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
      85              90              95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
      100              105              110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
      115              120              125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
      130              135              140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145              150              155              160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
      165              170              175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
      180              185              190

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<210> 785
 <211> 408
 <212> DNA
 <213> Homo sapiens

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<400> 785
accttggact acttcactat cgaccctcgg ctaggcgacg acgatgactt cgatcacctg
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cttcaggccg cccacgctcg tggctctgtca gtactgctcg acggggtggt caaccacgtc
120
tcgcgtcgca accgcatcgt gcaggatgcg cagagtgtcg ggccagattc agacgccggc
180
cgtatggttc gctggtgtga ggggcgcctc gacgttttcg agggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgcatgtcgg gaacatgtca cccggatcat gaactattgg
300
tgcggtcgcg gtgttgacgg ctggcggtcg gacgccgcta ttccgtcaat cctgagttct
360
gggctgcggt gctgcctccg gtgcgagaga agcgcctga cgtgagga
408

```

<210> 786
 <211> 134
 <212> PRT
 <213> Homo sapiens

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<400> 786
Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp Asp
1      5      10      15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
      20      25      30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
      35      40      45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
      50      55      60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val

```

```

65              70              75              80
Ala Leu Asn His Asp Asn Pro Ala Val Arg Glu His Val Thr Arg Ile
              85              90              95
Met Asn Tyr Trp Cys Gly Arg Gly Val Asp Gly Trp Arg Leu Asp Ala
              100              105              110
Ala Ile Pro Ser Ile Leu Ser Ser Gly Leu Arg Cys Cys Leu Arg Cys
              115              120              125
Glu Arg Ser Ala Leu Thr
              130

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<210> 787
 <211> 310
 <212> DNA
 <213> Homo sapiens

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<400> 787
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gttggaacca cagacgatgc cacgcttgtg tcagcagtgc gacactggcc cacgtggcgt
120
ccttggtctc tcctcattgc tgccgtcact gtgtgctggg catgccctgc agttacccca
180
aagctttatg tcacaacatt gaggctggcg gagaaagacc ggccccctca cccacacctta
240
gacttctctg aagggccgcc cgggtccaca acctggcccc ttaactccct gggcagctgc
300
tgggggagaa
310

```

<210> 788
 <211> 90
 <212> PRT
 <213> Homo sapiens

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<400> 788
Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1              5              10              15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
              20              25              30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
              35              40              45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
              50              55              60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65              70              75              80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
              85              90

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<210> 789
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 789

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 tctgccagac agcagcgctg ggacctctcc cctccccagc aggatgggcc ggctctggaa
 120
 gcacgaggtg ttccaaagtg caaacaagct gctgttaaata aattattccc aaacgcaaaa
 180
 gcccttgcgtg gtttgcttgc ttgctttttt ctttttttgc ctgcacaga tatcgctagg
 240
 gcagagtatt gacatttcgt tttctttttg ttatgggtga taaagcacgg tgtttcttgt
 300
 gagtgtatgc ctgtatttcc ctgcagagct gattgccagt ccattttctt ctatcccatc
 360
 cccattttc
 369

<210> 790
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 790
 Met Asp Trp Gln Ser Ala Leu Gln Gly Asn Thr Gly Ile His Ser Gln
 1 5 10 15
 Glu Thr Pro Cys Phe Ile Thr His Asn Lys Lys Lys Thr Lys Cys Gln
 20 25 30
 Tyr Ser Ala Leu Ala Ile Ser Val Arg Gly Lys Lys Arg Lys Lys Gln
 35 40 45
 Ala Ser Lys Pro Ala Arg Ala Leu Ala Phe Gly Asn Asn Tyr Leu Thr
 50 55 60
 Ala Ala Cys Leu His Phe Gly Thr Pro Arg Ala Ser Arg Ala Gly Pro
 65 70 75 80
 Ser Cys Trp Gly Gly Glu Arg Ser Gln Arg Cys Cys Leu Ala Asp Leu
 85 90 95
 Gly Phe Gly Gly His Gln Lys Arg Gly Arg Leu Leu Ala Ala Ala Thr
 100 105 110
 Ser Arg

<210> 791
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 791
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 ggtcttccag ttcttggtgt gaaatgggtat cgaaataaat ctttactaga gccagatgaa
 120
 agaatacaaaa tggaaagagt gggtaatgtg tggttactgg aaatttctaa cattcaaaaa
 180
 ggagaagggg gagagtacat gtgtcatgct gtaaacatca taggggaagc aaagagcttt
 240
 gcaaatgtag acataatgcc ccaggaagaa agagtgggtg cactaccacc tccagtaaca
 300

catcagcatg tcatggagtt tgatttggaa cacaccacat catcaagaac accttctcct
 360
 caagaaattg tcctggaagt tgaattaagt gaaaaagacg ttaaagaatt tgagaagcag
 420

<210> 792
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 792
 Thr Lys Arg Lys Val Tyr Glu Asn Thr Thr Leu Gly Phe Ile Val Glu
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 Val Glu Gly Leu Pro Val Pro Gly Val Lys Trp Tyr Arg Asn Lys Ser
 20 25 30
 Leu Leu Glu Pro Asp Glu Arg Ile Lys Met Glu Arg Val Gly Asn Val
 35 40 45
 Cys Ser Leu Glu Ile Ser Asn Ile Gln Lys Gly Glu Gly Gly Glu Tyr
 50 55 60
 Met Cys His Ala Val Asn Ile Ile Gly Glu Ala Lys Ser Phe Ala Asn
 65 70 75 80
 Val Asp Ile Met Pro Gln Glu Glu Arg Val Val Ala Leu Pro Pro Pro
 85 90 95
 Val Thr His Gln His Val Met Glu Phe Asp Leu Glu His Thr Thr Ser
 100 105 110
 Ser Arg Thr Pro Ser Pro Gln Glu Ile Val Leu Glu Val Glu Leu Ser
 115 120 125
 Glu Lys Asp Val Lys Glu Phe Glu Lys Gln
 130 135

<210> 793
 <211> 479
 <212> DNA
 <213> Homo sapiens

<400> 793
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 ccgcgaacag tactgcggga acccaaacga tcatttttaa cccagacgt ccctgaacca
 120
 aagccaaagt ctacaggtca ctggggcaga ggccgcccga aaccagcttc cctcccggc
 180
 ctaggcgcgc caggtccccg ccagccggg gcgacccctt ggtcggacag tgaggttggg
 240
 agcccaccgc acccaagtcc gccgcatcca cccggcgag gcgacccccg acgggcagcc
 300
 gctcaccttc tcctggcccc gggttcagga aaactgcctg gaggtggccg gggttcccta
 360
 gcggaggctg ggcggcgggc ttgcgcctg cctcagtcct cccatccgtg gcccggggga
 420
 tggagcccgc tgcgcgagga ggctgcggca ggtcccagcc aggtgccctg gaacgtgga
 479

<210> 794

<211> 159
 <212> PRT
 <213> Homo sapiens

<400> 794
 Xaa Ala Cys Arg Phe Ser Glu Ile His Tyr Gly Asn Val Arg Val Val
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 Glu Met Leu Arg Pro Arg Thr Val Leu Arg Glu Pro Lys Arg Ser Phe
 20 25 30
 Leu Thr Pro Asp Val Pro Glu Pro Lys Pro Lys Ser Thr Gly His Trp
 35 40 45
 Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro
 50 55 60
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 Arg Arg Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu
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<210> 795
 <211> 1418
 <212> DNA
 <213> Homo sapiens

<400> 795
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<210> 796

<211> 176

<212> PRT

<213> Homo sapiens

<400> 796

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		20						25					30		
Ala	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr	Gln	Leu	Thr	Met	Asn	Val
		35					40					45			
Pro	Phe	Gln	Ala	Ile	His	Phe	Met	Thr	Tyr	Glu	Phe	Leu	Gln	Glu	His
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65				70					75					80	
Ala	Cys	Ala	Gly	Ala	Val	Ala	Ala	Ala	Ala	Thr	Thr	Pro	Leu	Asp	Val
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Cys	Lys	Thr	Leu	Leu	Asn	Thr	Gln	Glu	Ser	Leu	Ala	Leu	Asn	Ser	His
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Ile	Thr	Gly	His	Ile	Thr	Gly	Met	Ala	Ser	Ala	Phe	Arg	Thr	Val	Tyr
		115				120						125			
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Ile	Tyr	Gln	Ile	Pro	Ser	Thr	Ala	Ile	Ala	Trp	Ser	Val	Tyr	Glu	Phe
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165

170

175

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 <211> 585
 <212> DNA
 <213> Homo sapiens

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<210> 798
 <211> 195
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ser Ser Glu Ile Tyr Gly Arg Thr Lys Ser Gly Ile Ala Ile Gly Gly
 50 55 60
 Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Met Cys Val Glu
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 Ala Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Leu Leu Met
 85 90 95
 Asn Thr Gly Asp Lys Ala Val Lys Ser Lys His Gly Met Leu Thr Thr
 100 105 110
 Ile Ala Cys Gly Pro Arg Gly Glu Val Ala Tyr Ala Leu Glu Gly Ala
 115 120 125
 Val Phe Asn Gly Gly Ser Pro Val Gln Trp Leu Arg Asp Glu Leu Lys
 130 135 140
 Ile Ile Ala Asp Ala Thr Asp Thr Glu Tyr Phe Ala Gly Lys Val Lys

145		150		155		160									
Asp	Ser	Asn	Gly	Val	Tyr	Leu	Val	Pro	Ala	Phe	Thr	Gly	Leu	Gly	Ala
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Pro	Tyr	Trp	Asp	Pro	Tyr	Ala	Arg	Gly	Ala	Leu	Phe	Gly	Leu	Thr	Arg
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<210> 799

<211> 2152

<212> DNA

<213> Homo sapiens

<400> 799

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1200

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<211> 95

<212> PRT

<213> Homo sapiens

<400> 800

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			20					25						30	
Ala	Gln	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Glu	Ala	Glu	Ala	Gly
		35					40				45				
Gly	Ser	Arg	Asn	Pro	Ser	Thr	Leu	Arg	Gly	Arg	Gly	Gly	Gln	Ile	Met
	50				55					60					
Arg	Ser	Arg	Asp	Gln	Asp	His	Pro	Gly	Gln	Asn	Gly	Glu	Thr	Pro	Ser
65				70				75						80	
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<210> 801

<211> 424

<212> DNA

<213> Homo sapiens

<400> 801

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<213> Homo sapiens

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          20             25             30
Ile Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu Leu Ser His Leu Tyr
          35             40             45
Arg Leu His Ser Thr Lys Asn Lys Ile Thr Leu Asn Gly Lys Pro Leu
          50             55             60
Glu Ser Tyr Lys Gly Arg Glu Phe Ala Gln Leu Val Ala Val Leu Thr
          65             70             75             80
Gln Ser Arg Asp Ala Met Ile Asp Asp Phe Leu Val Lys Asp Ile Val
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<212> DNA

<213> Homo sapiens

<400> 803

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<210> 804
 <211> 1400
 <212> PRT
 <213> Homo sapiens

<400> 804
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 35 40 45
 Val Ser Cys Arg Val Cys Lys Val Ala Thr His Arg Lys Cys Glu Ala
 50 55 60
 Lys Val Thr Ser Ala Cys Gln Ala Leu Pro Pro Val Glu Leu Arg Arg
 65 70 75 80
 Asn Thr Ala Pro Val Arg Arg Ile Glu His Leu Gly Ser Thr Lys Ser
 85 90 95
 Leu Asn His Ser Lys Gln Arg Ser Thr Leu Pro Arg Ser Phe Ser Leu
 100 105 110
 Asp Pro Leu Met Glu Arg Arg Trp Asp Leu Asp Leu Thr Tyr Val Thr
 115 120 125
 Glu Arg Ile Leu Ala Ala Ala Phe Pro Ala Arg Pro Asp Glu Gln Arg
 130 135 140
 His Arg Gly His Leu Arg Glu Leu Ala His Val Leu Gln Ser Lys His
 145 150 155 160
 Arg Asp Lys Tyr Leu Leu Phe Asn Leu Ser Glu Lys Arg His Asp Leu
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 Thr Arg Leu Asn Pro Lys Val Gln Asp Phe Gly Trp Pro Glu Leu His
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 Ala Pro Pro Leu Asp Lys Leu Cys Ser Ile Cys Lys Ala Met Glu Thr
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 Trp Leu Ser Ala Asp Pro Gln His Val Val Val Leu Tyr Cys Lys Gly
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 Asn Lys Gly Lys Leu Gly Val Ile Val Ser Ala Tyr Met His Tyr Ser
 225 230 235 240
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 Lys Phe Cys Glu Asp Lys Val Ala Thr Glu Leu Gln Pro Ser Gln Arg
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Gly Pro Gln Gln Leu Cys Ile Ser Leu Glu Pro Ala Leu Leu Lys
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Gly Asp Val Met Val Thr Cys Tyr His Lys Gly Gly Arg Gly Thr Asp
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Arg Thr Leu Val Phe Arg Val Gln Phe His Thr Cys Thr Ile His Gly
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Pro Gln Leu Thr Phe Pro Lys Asp Gln Leu Asp Glu Ala Trp Thr Asp
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Glu Arg Phe Pro Phe Gln Ala Ser Val Glu Phe Val Phe Ser Ser Ser
      405              410              415
Pro Glu Lys Ile Lys Gly Ser Thr Pro Arg Asn Asp Pro Ser Val Ser
      420              425              430
Val Asp Tyr Asn Thr Thr Glu Pro Ala Val Arg Trp Asp Ser Tyr Glu
      435              440              445
Asn Phe Asn Gln His His Glu Asp Ser Val Asp Gly Ser Leu Thr His
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Thr Arg Gly Pro Leu Asp Gly Ser Pro Tyr Ala Gln Val Gln Arg Pro
465              470              475              480
Pro Arg Gln Thr Pro Pro Ala Pro Ser Pro Glu Pro Pro Pro Pro Pro
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Met Leu Ser Val Ser Ser Asp Ser Gly His Ser Ser Thr Leu Thr Thr
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Pro Gly Leu Ser Arg His Cys Ser Cys Arg Gln Gly Tyr Arg Glu Pro
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Cys Gly Val Pro Asn Gly Gly Tyr Arg Pro Glu Gly Thr Leu Glu
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      675              680              685
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      690              695              700
Gly Glu Gly Trp Ala Ser Glu Ala Gly Lys Pro Leu Leu His Pro Val
705              710              715              720
Arg Pro Gly His Pro Leu Pro Leu Leu Leu Pro Ala Cys Gly His His

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Tyr	Gly	His	Pro	Gly	Tyr	Pro	Ala	Leu	Val	Thr	Tyr	Ser	Tyr	Gly	Gly
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Leu	Pro	Arg	Ser	Pro	Arg	Asp	Ala	Pro	Cys	Ser	Ala	Ser	Ser	Glu	Leu
				885					890					895	
Ser	Gly	Pro	Ser	Thr	Pro	Leu	His	Thr	Ser	Ser	Pro	Val	Gln	Gly	Lys
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Glu	Ser	Thr	Arg	Arg	Gln	Asp	Thr	Arg	Ser	Pro	Thr	Ser	Ala	Pro	Thr
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Gln	Arg	Leu	Ser	Pro	Gly	Glu	Ala	Leu	Pro	Pro	Val	Ser	Gln	Ala	Gly
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Thr	Gly	Lys	Ala	Pro	Glu	Leu	Pro	Ser	Gly	Ser	Gly	Pro	Glu	Pro	Leu
945					950					955					960
Ala	Pro	Ser	Pro	Val	Ser	Pro	Thr	Phe	Pro	Pro	Ser	Ser	Pro	Ser	Asp
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Arg	Ser	Pro	Val	Pro	Thr	Thr	Leu	Pro	Gly	Leu	Arg	His	Ala	Pro	Trp
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 Cys Leu Arg Ile Pro Ser Lys Asp Pro Leu Glu Glu Thr Pro Glu Ala
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 Pro Val Pro Thr Asn Met Ser Thr Ala Ala Asp Leu Leu Arg Gln Gly
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 Arg Trp Thr Asn Pro Asp Gly Thr Thr Ser Lys Ile Phe Gly Phe Val
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 Ala Lys Lys Pro Gly Ser Pro Trp Glu Asn Val Cys His Leu Phe Ala
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<211> 550

<212> DNA

<213> Homo sapiens

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 420
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cacaagagaa aaagaagctg tacactgggg aggcctccgg ggtacctgtg cctgccatgt
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<210> 806
 <211> 118
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Met Leu Gly Arg Ala Thr Pro Met Asp Leu Ala Arg Thr Leu Ser His
 50 55 60
 Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg
 65 70 75 80
 Glu His Leu Gly Glu Gly Ser Val Glu Thr Arg Thr Gln Lys Asp Thr
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 Arg Glu Lys Glu Ala Val His Trp Gly Gly Phe Arg Gly Thr Cys Ala
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 Cys His Val Ser Glu Gly
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<210> 807
 <211> 287
 <212> DNA
 <213> Homo sapiens

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 180
 gcgccctgat tcgccaggac caggagcgaa gcgacggcct caggcagctt caaacgttga
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<210> 808
 <211> 93
 <212> PRT
 <213> Homo sapiens

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<211> 405
<212> DNA
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<211> 135
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<213> Homo sapiens
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866

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<210> 811
 <211> 642
 <212> DNA
 <213> Homo sapiens

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<210> 812
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 812
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 Ala His Pro Glu Val Leu Glu Ser Phe Leu Gln Glu Leu Arg Pro Lys
 35 40 45
 Ala Ser Arg Lys Glu Arg Xaa Thr Thr Asn Leu Ile Phe Thr Pro Phe
 50 55 60
 Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala
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 Val Thr Gly Ser Ser Ala Leu Tyr His Ser
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<210> 813
 <211> 558

<212> DNA

<213> Homo sapiens

<400> 813

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240
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<210> 814

<211> 151

<212> PRT

<213> Homo sapiens

<400> 814

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Ala Phe Gly Pro Leu Ala Phe Gly Gln Arg Ala Ala Gln Phe Gly Val
 35           40           45
Glu Asp Asp Pro Arg Pro Phe Asp Leu Asp His Asp Leu Gln Leu Pro
 50           55           60
Ala Ile Val Phe Ala Ala Asp Ile Gln Arg Ala Ala Ala His Gln Arg
 65           70           75           80
Leu Ala Gly Asp Gln Gly Glu Val Gln His His Leu Gln Arg Gly Leu
 85           90           95
Gly Gln Arg Leu Arg Phe His Pro Pro Val Glu Leu Arg Ala Leu Ile
100           105           110
Val Gly Asn Gln Pro Leu Val Arg Gly Phe Arg Phe Ala Arg Val Asp
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Leu Phe Ala Glu Pro Ala Gly Gly Ala Glu Gly Glu Ala Glu Glu Phe
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Glu Leu Val Gly Gly Tyr Ala
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<210> 815

<211> 315

<212> DNA

<213> Homo sapiens

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<210> 816

<211> 90

<212> PRT

<213> Homo sapiens

<400> 816

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Arg	Asp	Leu	Thr	Ser	Glu	Ala	Asp	Ser	Ala	Ser	Ala	Gln	Pro	Ser	Thr
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His	Ala	Glu	Val	Ser	Ser	Glu	Val	Thr	Ala	Thr	Ser	Ser	Ile	Asp	Glu
	50					55				60					
Gln	Val	Asp	Leu	Ile	Ala	Ala	Pro	Leu	Ser	Glu	Glu	Ser	Asn	Val	Ser
65					70					75				80	
Lys	Leu	Gly	Pro	Ser	Pro	Glu	Ala	Asp	Thr						
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<210> 817

<211> 321

<212> DNA

<213> Homo sapiens

<400> 817

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 aatacacttt tctcaaagct tcaaattaat caatccatta tattctgcaa ctctgttaat
 180
 agtgttgagc tgctggctaa aaaaataact gaactcgggtt attcatgctt ctacattcat
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 300
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 321

<210> 818
 <211> 107
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu
 50 55 60
 Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His
 65 70 75 80
 Ala Lys Met Leu Gln Asp His Arg Asn Arg Val Phe His Asp Cys Arg
 85 90 95
 Asn Gly Ala Cys Arg Asn Leu Val Cys Thr Asp
 100 105

<210> 819
 <211> 3422
 <212> DNA
 <213> Homo sapiens

<400> 819
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1740
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2280
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2340
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2400

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 2520
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 2580
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 3180
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 3240
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 ca
 3422

<210> 820

<211> 494

<212> PRT

<213> Homo sapiens

<400> 820

Met	Asn	Ser	Lys	Lys	Leu	Ser	Ser	Thr	Asp	Cys	Phe	Lys	Thr	Glu	Ala
1				5					10					15	
Phe	Thr	Ser	Pro	Glu	Ala	Leu	Gln	Pro	Gly	Gly	Thr	Ala	Leu	Ala	Pro
			20					25					30		
Lys	Lys	Arg	Ser	Arg	Lys	Gly	Arg	Ala	Gly	Ala	His	Gly	Leu	Ser	Lys
		35				40					45				
Gly	Pro	Leu	Glu	Lys	Arg	Pro	Tyr	Leu	Gly	Pro	Ala	Leu	Pro	Leu	Thr
	50					55					60				
Pro	Arg	Asp	Arg	Ala	Ser	Gly	Thr	Gln	Gly	Ala	Ser	Glu	Asp	Asn	Ser
65					70					75				80	
Gly	Gly	Gly	Gly	Lys	Lys	Pro	Lys	Met	Glu	Glu	Leu	Gly	Leu	Ala	Ser

<210> 821
<211> 420

<212> DNA

<213> Homo sapiens

<400> 821

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acgcgtccccg tcacctgcgg tatggaccaa gtgagttgtg tgctcgacaa tgggttcgcc
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gccatcatgg atgtgccggg tttcaactat cgcgcccatc gttacaccga agcctatcgg
120
cgtttgccgc aaaatgtggt gctaggttcg gaaacgacct cgacggtgag cagccgtggt
180
gtctacaagt ttcctgttgt gctgaagtcc gatgccatct atcccgacca tcagtcgtca
240
ggctacgaca cagagtattg ttcgtggtcg aacacccccg atgtcgattt cgcctcggc
300
gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcggtgaa
360
ccttcgcctt acgacaccga tgcctggccc tctcagcct ccctcttcgg cattgtcgac
420

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<210> 822

<211> 133

<212> PRT

<213> Homo sapiens

<400> 822

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Met Asp Gln Val Ser Cys Val Leu Asp Asn Gly Phe Ala Ala Ile Met
1          5          10          15
Asp Val Pro Gly Phe Asn Tyr Arg Ala His Arg Tyr Thr Glu Ala Tyr
20          25          30
Arg Arg Leu Pro Gln Asn Val Val Leu Gly Ser Glu Thr Thr Ser Thr
35          40          45
Val Ser Ser Arg Gly Val Tyr Lys Phe Pro Val Val Leu Lys Ser Asp
50          55          60
Ala Ile Tyr Pro Asp His Gln Ser Ser Gly Tyr Asp Thr Glu Tyr Cys
65          70          75          80
Ser Trp Ser Asn Thr Pro Asp Val Asp Phe Ala Leu Ala Glu Asp Tyr
85          90          95
Pro Trp Thr Met Gly Gln Phe Val Trp Thr Gly Phe Asp Tyr Leu Gly
100         105         110
Glu Pro Ser Pro Tyr Asp Thr Asp Ala Trp Pro Ser His Ala Ser Leu
115         120         125
Phe Gly Ile Val Asp
130

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<210> 823

<211> 550

<212> DNA

<213> Homo sapiens

<400> 823

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tctagattct tgggcagccg agccctctt gaattcctca gcctaccatc atgatcaaca
60
cctcccatgt tccgtccatg aatgaccgca ctgacagcac tggagagatt taatgggtca
120

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ccaattgagg cagtgaaggc actcatggca ctcagagctg gaatggggct gatctgagtt
 180
 gtactgttga ctgcagtggg gatgacaacc tgcattcctt tgctggctgc atcgacaact
 240
 gctttgtaaa tggcatctac ggaagcatca cctggggccac ccacaacgag gccatccttc
 300
 acctgttgac caagagatgg gtcaatcctc ggttgcaact cacaagggtg atcttgaaaa
 360
 ggtggaagtg tagtgtttgg attctcagga agtgctgtga gcccaggctg agtgcttatt
 420
 cttttgttta ggagagctgc atcttctcgc attctcacct gaaagttctg aaacagacaa
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 540
 ttctggtacc
 550

<210> 824
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 824
 Met Ala Cys Leu Phe Gln Asn Phe Gln Val Arg Met Gln Glu Asp Ala
 1 5 10 15
 Ala Leu Leu Asn Lys Arg Ile Ser Thr Gln Pro Gly Leu Thr Ala Leu
 20 25 30
 Pro Glu Asn Pro Asn Thr Thr Leu Pro Pro Phe Gln Asp Thr Pro Cys
 35 40 45
 Glu Leu Gln Pro Arg Ile Asp Pro Ser Leu Gly Gln Gln Val Lys Asp
 50 55 60
 Gly Leu Val Val Gly Gly Pro Gly Asp Ala Ser Val Asp Ala Ile Tyr
 65 70 75 80
 Lys Ala Val Val Asp Ala Ala Ser Lys Gly Met Gln Val Val Ile Thr
 85 90 95
 Thr Ala Val Asn Ser Thr Thr Gln Ile Ser Pro Ile Pro Ala Leu Ser
 100 105 110
 Ala Met Ser Ala Phe Thr Ala Ser Ile Gly Asp Pro Leu Asn Leu Ser
 115 120 125
 Ser Ala Val Ser Ala Val Ile His Gly Arg Asn Met Gly Gly Val Asp
 130 135 140
 His Asp Gly Arg Leu Arg Asn Ser Arg Gly Ala Arg Leu Pro Lys Asn
 145 150 155 160
 Leu

<210> 825
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 825
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 60

cagttgctgg atgagcgga gatgcgggc gtgctcgcc acgagctgat gcacgtgtac
 120
 aaccgcgata tcctcacctc ttcggtggcg gggggtatcg cctccatcat cggtagcatt
 180
 gcgcagattc tttcgtttgg cgcgatgttc ggtggatcca accgcgatgg tgaacgttcc
 240
 aacccccctcg ccatgttcgt ggttgctatg ctggctccca ttgctactca ggtcatccag
 300
 atggctatta gccgcaccgg tgaattc
 327

<210> 826

<211> 109

<212> PRT

<213> Homo sapiens

<400> 826

Ala	Phe	Ala	Thr	Gly	Arg	Asn	Pro	Gln	Asn	Ala	Ala	Val	Cys	Cys	Thr
1				5				10					15		
Glu	Gly	Ile	Leu	Gln	Leu	Leu	Asp	Glu	Arg	Glu	Met	Arg	Gly	Val	Leu
			20					25					30		
Gly	His	Glu	Leu	Met	His	Val	Tyr	Asn	Arg	Asp	Ile	Leu	Thr	Ser	Ser
			35				40					45			
Val	Ala	Ala	Gly	Ile	Ala	Ser	Ile	Ile	Gly	Thr	Ile	Ala	Gln	Ile	Leu
			50			55					60				
Ser	Phe	Gly	Ala	Met	Phe	Gly	Gly	Ser	Asn	Arg	Asp	Gly	Glu	Arg	Ser
65					70					75				80	
Asn	Pro	Leu	Ala	Met	Phe	Val	Val	Ala	Met	Leu	Ala	Pro	Ile	Ala	Thr
					85					90				95	
Gln	Val	Ile	Gln	Met	Ala	Ile	Ser	Arg	Thr	Arg	Glu	Phe			
			100					105							

<210> 827

<211> 534

<212> DNA

<213> Homo sapiens

<400> 827

nacgcgtacg tcaatatgca tcgtccagtc gttatcgcaa cgccgaaatc gatgctgcgc
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 aacaagatgg cgacctcgga tcccgaagag ttcaccaccg gtaggtggcg tcctgttcta
 120
 cccgacccat cgatcaccga cccgacggcc gttacgagga ttatcttggt ctctggcaag
 180
 gcgcgggtggg agctgggtcaa gcaacgtaag gccgccagtc ttgacggaca gctcgccatc
 240
 atcccgatgg agcgtctcta cccgctacca gtcgacgagt tggctgaggt ttttgccct
 300
 tacaccaacg tcacggatgt ccgctgggtc caagaagagc cagagaacca gggcgcttg
 360
 tactacatgc tgaccacact gcccaggcc atgtcggaga agctgccagg attctttgat
 420
 gggttagtcg gcatcaccgg cccaccgtcc tcagctccgt cgggtgggaca gcacagcgtc
 480

cacatccgtg aagagcagga gttactcgag aaggctatag cctgagcgac ctga
534

<210> 828

<211> 174

<212> PRT

<213> Homo sapiens

<400> 828

Xaa	Ala	Tyr	Val	Asn	Met	His	Arg	Pro	Val	Val	Ile	Ala	Thr	Pro	Lys
1				5					10					15	
Ser	Met	Leu	Arg	Asn	Lys	Met	Ala	Thr	Ser	Asp	Pro	Glu	Glu	Phe	Thr
		20						25					30		
Thr	Gly	Arg	Trp	Arg	Pro	Val	Leu	Pro	Asp	Pro	Ser	Ile	Thr	Asp	Pro
		35				40						45			
Thr	Ala	Val	Thr	Arg	Ile	Ile	Leu	Cys	Ser	Gly	Lys	Ala	Arg	Trp	Glu
	50					55					60				
Leu	Val	Lys	Gln	Arg	Lys	Ala	Ala	Ser	Leu	Asp	Gly	Gln	Leu	Ala	Ile
65					70					75				80	
Ile	Pro	Met	Glu	Arg	Leu	Tyr	Pro	Leu	Pro	Val	Asp	Glu	Leu	Ala	Glu
				85					90					95	
Val	Phe	Ala	Pro	Tyr	Thr	Asn	Val	Thr	Asp	Val	Arg	Trp	Val	Gln	Glu
		100						105					110		
Glu	Pro	Glu	Asn	Gln	Gly	Ala	Trp	Tyr	Tyr	Met	Leu	Thr	His	Leu	Pro
		115					120					125			
Gln	Ala	Met	Ser	Glu	Lys	Leu	Pro	Gly	Phe	Phe	Asp	Gly	Leu	Val	Gly
	130					135					140				
Ile	Thr	Arg	Pro	Pro	Ser	Ser	Ala	Pro	Ser	Val	Gly	Gln	His	Ser	Val
145					150					155				160	
His	Ile	Arg	Glu	Glu	Gln	Glu	Leu	Leu	Glu	Lys	Ala	Ile	Ala		
				165						170					

<210> 829

<211> 492

<212> DNA

<213> Homo sapiens

<400> 829

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atctggctgg acctgaagga ggccggtgac tttcacttcc agccagctgt gaagaagttt
120
gtcctgaaga attatggaga gaaccagaa gcctacaatg aagaactgaa gaagctggag
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240
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300
gccgctgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggag
360
atcaagtacg agcaggcctg tattttctcc aacnttgag cgctgcactc catgctgggg
420
gccatggaca agcgggtgtc tgaggagggc atgaaggtct cctgtaccca tttccagtgc
480

gcagccggcg cc
492

<210> 830
<211> 164
<212> PRT
<213> Homo sapiens

<400> 830
Xaa Trp Pro Gly Gly Arg Arg Val Pro Ala Ala Met Glu Ala Val Pro
1 5 10 15
Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His
20 25 30
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn
35 40 45
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln
50 55 60
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg
65 70 75 80
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly
85 90 95
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser
100 105 110
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile
115 120 125
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys
130 135 140
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys
145 150 155 160
Ala Ala Gly Ala

<210> 831
<211> 303
<212> DNA
<213> Homo sapiens

<400> 831
gcgttgctgc ggcgtggcga gacatgacg gcggagaatc agcgtgcca tgtgcgcatc
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gccgcaaacc acatcaagga ggttgcggtc gatcacgagg tcgttgtagc ccatggtaat
120
ggccccagg taggtctgtt ggctctgcaa tcgacagcct acgaggaagt cggtatctat
180
ccgctggatg tcttggggcg agagtcacag gccatgatcg gctacatgat cgagcaggaa
240
ctcggcaatg tgatgcctca ggatcagcag atcgtcacca tgatcacgat gacagtcgtc
300
gac
303

<210> 832
<211> 101
<212> PRT

<213> Homo sapiens

<400> 832

Ala Leu Leu Arg Arg Gly Glu Thr Met Thr Ala Glu Asn Gln Arg Ala
 1 5 10 15
 Asn Val Arg Ile Ala Ala Asn His Ile Lys Glu Val Ala Val Asp His
 20 25 30
 Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
 35 40 45
 Leu Gln Ser Thr Ala Tyr Glu Val Gly Ile Tyr Pro Leu Asp Val
 50 55 60
 Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
 65 70 75 80
 Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
 85 90 95
 Met Thr Val Val Asp
 100

<210> 833

<211> 466

<212> DNA

<213> Homo sapiens

<400> 833

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 catttgacga gggctgaaaa cgtcttctac cggctctgctg tgccgcctgg tgtcagcaaa
 120
 cgacgccatg atcgtccagt gggatcgcg ttgttctgcg gcgctggggg attcagttgc
 180
 ggattccacc aggccgggtg gcatgttgcg gcggcggttg agcacgacgt gtcggcgctc
 240
 ctgacctatg tcatgaatct cgctcggccc ggcgtcaaga ttcacatcga ccccgagcac
 300
 ccggagctgg gcccaagacc accgcgaacc aagaagaaga gcggcggcgc agtgccgttc
 360
 gatcgcatg tcggaactgg gtggatcgcc agcgagcccg ccgacgatcc cggctgcgaa
 420
 cacttctacg tgtacgacgt caagaacctc agcggcgagc ggatcc
 466

<210> 834

<211> 142

<212> PRT

<213> Homo sapiens

<400> 834

Gln Arg Lys Cys Ala Ala Gly His Leu Thr Arg Ala Glu Asn Val Phe
 1 5 10 15
 Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
 20 25 30
 Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
 35 40 45
 Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

```

      50              55              60
Ser Ala Ser Leu Thr Tyr Val Met Asn Leu Ala Arg Pro Gly Val Lys
65              70              75              80
Ile His Ile Asp Pro Glu His Pro Glu Leu Gly Pro Arg Pro Pro Arg
      85              90              95
Thr Lys Lys Lys Ser Gly Gly Ala Val Pro Phe Asp Ala His Val Gly
      100             105             110
Thr Gly Trp Ile Ala Ser Glu Pro Ala Asp Asp Pro Gly Cys Glu His
      115             120             125
Phe Tyr Val Tyr Asp Val Lys Asn Leu Ser Gly Glu Arg Ile
      130             135             140

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<210> 835
 <211> 482
 <212> DNA
 <213> Homo sapiens

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<400> 835
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aagctcagag caaagaacat cacaccacgt ccctcagtga ttgaagcagt gattgagtca
120
cagaataaat ctggaactca ggtcttctga tctttgctcc agatgtaga gacaaaacta
180
aaagtaaaat accaagttaa atcaaagcat cagcattgag ccagaacat gaaaaagaac
240
ttcctggccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct
300
ctggaataag attgatgttt ccatgctgtg aaagacgatg atgttccttc tcccagattc
360
ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa
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tgaagaacaa tcccatggcc atgcaggcac tcctccctc cactctctg cccttcacgc
480
gt
482

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<210> 836
 <211> 120
 <212> PRT
 <213> Homo sapiens

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<400> 836
Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln
1              5              10              15
Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys
      20              25              30
Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu
      35              40              45
Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser
      50              55              60
Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu
65              70              75              80
Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala

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85 90 95
 Lys Ile Arg Arg Pro Glu Phe Gln Ile Tyr Ser Val Thr Gln Ser Leu
 100 105 110
 Leu Gln Ser Leu Arg Asp Val Val
 115 120

<210> 837
 <211> 509
 <212> DNA
 <213> Homo sapiens

<400> 837
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 cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca
 120
 ctctgcacca gccaaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggg
 180
 gcctggcggg cgagcccctc ttatcctggg gaatgctggg gggcgcttct gagcagacct
 240
 gcctgctgcc cctgctggct ggcaactgcc ctccccggg gaaaggttgg gtgggtcccc
 300
 caggggaact caaagcaggg gagcccctgg agggcccaag tccctggaat atcttggcgc
 360
 tcagatggcc cccctcgaac accctcacac gggggggccg cgcggtggga ggtgaccag
 420
 cagccactct tacttggcga agacttttct cccaatgcga gcgcgggtgg tatcagcctg
 480
 agccttcagg ttggtgaggc tgggtacc
 509

<210> 838
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 838
 Met Ala Pro Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro
 1 5 10 15
 Ser Tyr Pro Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys
 20 25 30
 Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp
 35 40 45
 Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val
 50 55 60
 Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His
 65 70 75 80
 Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly
 85 90 95
 Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu
 100 105 110
 Gln Val Gly Glu Ala Gly Val
 115

<210> 839
 <211> 347
 <212> DNA
 <213> Homo sapiens

<400> 839
 acgcgtctcg tgttcgtgcg gcacggcagg acggcggttca atgtggaggg tcggctccag
 60
 ggccgtctcg acatgccggtt ggatgaggtg gggcgccgctc aggcactcac agtggctcaa
 120
 gtcacgccc agatggaacc tgacgcgatc atggcctctc cgctacaacg tgcgcgcgac
 180
 acagctcagg caatcggtgc ttgtgctgga ttgggcgtac agctggatga tcgactcatc
 240
 gagatcgatg tcggacgttg gtcgggacaa cgggctgcgg acctgcgtcg caacgatcct
 300
 gagtacgcag caagtgtggt cagccctatc gattaccggg tcggagn
 347

<210> 840
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 840
 Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu
 1 5 10 15
 Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg
 20 25 30
 Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp
 35 40 45
 Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala
 50 55 60
 Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile
 65 70 75 80
 Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg
 85 90 95
 Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr
 100 105 110
 Arg Val Gly
 115

<210> 841
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 841
 tccggaactc accccgacgc cgtcattatg gacgtcatga tgccgcgtct agatggcttg
 60
 gaagccaccc ggatgctgcg cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc
 120
 cgcgatgctg tcgacgatcg cggtgacggc ctcgacgctg gcgccgatga ctacatggtc
 180

aagcccttcg ccctcgacga actcctcgct cgccctacgcg ccctcactcg tcgttcccgt
 240
 cccgagccag agcaaaacga ggcccttgaa caactctcct tcgctgacct cacccttgat
 300
 ccaggcaccc gcgagatcac ccgcgggaac cgtcgcatca gtttgacgcg t
 351

<210> 842
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 842
 Ser Gly Thr His Pro Asp Ala Val Ile Met Asp Val Met Met Pro Arg
 1 5 10 15
 Leu Asp Gly Leu Glu Ala Thr Arg Met Leu Arg Ser Asn Gly Asn Asp
 20 25 30
 Val Pro Ile Leu Val Leu Thr Ala Arg Asp Ala Val Asp Asp Arg Val
 35 40 45
 Asp Gly Leu Asp Ala Gly Ala Asp Asp Tyr Met Val Lys Pro Phe Ala
 50 55 60
 Leu Asp Glu Leu Leu Ala Arg Leu Arg Ala Leu Thr Arg Arg Ser Arg
 65 70 75 80
 Pro Glu Pro Glu Gln Asn Glu Ala Pro Glu Gln Leu Ser Phe Ala Asp
 85 90 95
 Leu Thr Leu Asp Pro Gly Thr Arg Glu Ile Thr Arg Gly Asn Arg Arg
 100 105 110
 Ile Ser Leu Thr Arg
 115

<210> 843
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 843
 ctagcccagg ctctcgatcca cgaggggctg cgcgctgtgg cctctggggc aaaccgggtc
 60
 ggccctcaagc gcggtatcga gaaggctgtc gacgccgttg tggaggagct ccgctctatc
 120
 tcgcgcgcca tcgacaccac ctcgacatg gccagcgttg ccaccatctc cagccgtgac
 180
 gagaccatcg gcgccctcat cgctgaggcc ttcgacaagg ttggttaagga cgggggttate
 240
 accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc
 300
 gacaagggtt acctgtcgcc ctacatggtc accgaccagg ttcgcatgga ggctgtgate
 360
 gaggatcctt acatcctcat tcaactccgc aag
 393

<210> 844
 <211> 131
 <212> PRT

<213> Homo sapiens

<400> 844

```

Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
 1           5           10           15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
      20           25           30
Val Val Glu Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
      35           40           45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
      50           55           60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
65           70           75           80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
      85           90           95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
      100          105          110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
      115          120          125
Ser Arg Lys
      130

```

<210> 845

<211> 505

<212> DNA

<213> Homo sapiens

<400> 845

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gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
60
gaagcaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
120
ccctgcccc cgcggggct ccaggaccgg gagactcatc agccggaagc tcttgaggga
180
ggcggctgcc gtgaagacag gcacccttgc tcctgagagg ggcacccaga gaaccaagac
240
tcagcagagg gaacacaggg ctacgcccag gcccaggcc tgatatccag agtctaaatc
300
ccacctcagc ccagggggga gccttgagag gagctatgtc cctcatggac ccagtttcc
360
tctgcatacg ggctccgagc cctgcactgc ctccagggtg gtteccaagg tcttttccca
420
ttacctccta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
480
agccacagaa tcccaggcca cgcgt
505

```

<210> 846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 846

```

Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```

```

      1           5           10           15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu
      20           25           30
Lys Ala Pro Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly
      35           40           45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser
      50           55           60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg
      65           70           75           80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro
      85           90           95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro
      100          105          110
Ala Pro Ala Ala Val Ala Leu Leu Ser Cys Pro Cys Ser Leu Asp
      115          120          125
Val Pro
      130

```

<210> 847
 <211> 448
 <212> DNA
 <213> Homo sapiens

```

<400> 847
aagcttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct ccgcatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tcctgaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacaagaag
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatattgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaattc tgagaaatag tgccgttagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcca acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

```

<210> 848
 <211> 149
 <212> PRT
 <213> Homo sapiens

```

<400> 848
Lys Leu Leu Lys Lys Glu Gln Glu Asn Met Lys Glu Leu Val Val Asn Leu
      1           5           10           15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys
      20           25           30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met
      35           40           45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Lys Cys Glu

```

```

      50              55              60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65              70              75              80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
      85              90              95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
      100             105             110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
      115             120             125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
      130             135             140
Asp Val Arg Lys Ile
145

```

<210> 849
 <211> 463
 <212> DNA
 <213> Homo sapiens

```

<400> 849
nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggtga agtgataagt
60
cttttggaga tggggaatgc agccagacat acaggtacca ctcaaataaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggca
180
gctgaagatg gatcatggta ttccctcgg catattgtct caaagttcca ctttgtggat
240
ttggcaggat cagaaagagt aacaaaaacg gggaataactg gtgaacgggt caaagaatcc
300
attcaaataca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggaccca
360
cgcaggaaga gttcacatat tccatatagg gatgctaaaa ttaccgggct tctgaaagat
420
tctctgggag gcagtgctaa gactgtcatg atcacatgtg tca
463

```

<210> 850
 <211> 154
 <212> PRT
 <213> Homo sapiens

```

<400> 850
Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
1              5              10              15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
      20              25              30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
      35              40              45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
      50              55              60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65              70              75              80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg

```

<210> 853
<211> 423

<212> DNA

<213> Homo sapiens

<400> 853

acgcgttcag aaacttatgg tgaaatggcc gaactagaaa acctagtcga cgaatattac
 60
 caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa
 120
 gtccaagaaa cgcatttggt agaagagctt gcaggcatag aatcaggtga tgatggcgca
 180
 gtggtggaag agagcgtatt agaaggcctc gatacctatt tatgtgagat aaaagaagca
 240
 cagattcgtc atggattgca tcgtcttgga gaattaccag aagacgataa attggccgat
 300
 accttggtcg ccttattgcy tttaccccggt ggagtgaca ttaccagcaa ggggaatttg
 360
 catgccttaa tggcagattt agagttagaa caagacgatt ttgaccaat gcaaagcacg
 420
 cgt
 423

<210> 854

<211> 141

<212> PRT

<213> Homo sapiens

<400> 854

Thr	Arg	Ser	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Glu	Leu	Glu	Asn	Leu	Val
1				5					10					15	
Asp	Glu	Tyr	Tyr	Gln	Ala	Met	Gly	Met	Asp	Val	Arg	Arg	Glu	Thr	Trp
			20				25						30		
Leu	Arg	Glu	Gln	Ile	Leu	Lys	Lys	Val	Gln	Glu	Thr	His	Leu	Leu	Glu
			35				40					45			
Glu	Leu	Ala	Gly	Ile	Glu	Ser	Gly	Asp	Asp	Gly	Ala	Val	Val	Glu	Glu
			50				55				60				
Ser	Val	Leu	Glu	Gly	Leu	Asp	Thr	Tyr	Leu	Cys	Glu	Ile	Lys	Glu	Ala
65					70					75				80	
Gln	Ile	Arg	His	Gly	Leu	His	Arg	Leu	Gly	Glu	Leu	Pro	Glu	Asp	Asp
			85						90					95	
Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Leu	Leu	Arg	Leu	Pro	Arg	Gly	Ser
			100					105					110		
Asp	Ile	Thr	Ser	Lys	Gly	Ile	Leu	His	Ala	Leu	Met	Ala	Asp	Leu	Glu
			115				120					125			
Leu	Glu	Gln	Asp	Asp	Phe	Asp	Pro	Met	Gln	Ser	Thr	Arg			
			130				135					140			

<210> 855

<211> 338

<212> DNA

<213> Homo sapiens

<400> 855

acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga
 60

tgaatgtctg tgcggatggt gctcacagca agatagtgtc tggagcgatt ggcacttcga
 120
 acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag
 180
 cttggagcaa gaaggagctc caagcaagat ggagcttgca gcaggtgctt ctcagtgtaa
 240
 gatggagctc agagaagatg atgctcagag taagattgag ctcggtgatt ggcactccaa
 300
 acattgctct gagcccattg gagnctctga gcagaaag
 338

<210> 856

<211> 93

<212> PRT

<213> Homo sapiens

<400> 856

Met	Asn	Val	Cys	Ala	Asp	Val	Ala	His	Ser	Lys	Ile	Val	Leu	Gly	Ala
1				5					10					15	
Ile	Gly	Thr	Ser	Asn	Lys	Met	Glu	His	Gly	Ala	Asp	Gly	Ala	Leu	Ser
			20					25					30		
Lys	Met	Glu	Arg	Gly	Val	Asp	Arg	Ala	Trp	Ser	Lys	Lys	Glu	Leu	Gln
		35				40					45				
Ala	Arg	Trp	Ser	Leu	Gln	Gln	Val	Leu	Leu	Ser	Val	Arg	Trp	Ser	Ser
	50				55					60					
Glu	Lys	Met	Met	Leu	Arg	Val	Arg	Leu	Ser	Ser	Val	Ile	Gly	Thr	Pro
65				70					75					80	
Asn	Ile	Ala	Leu	Ser	Pro	Leu	Glu	Xaa	Leu	Ser	Arg	Lys			
			85						90						

<210> 857

<211> 435

<212> DNA

<213> Homo sapiens

<400> 857

ccggacagtg ggccaccagt gtttgccccc agcaatcatg tcagtgaagc ccaacctcgg
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 gagacacccc ggcccctcat gcctcctacc aagcctttcc tagcacctga gaccaccagc
 120
 cctggtgaca ggggtggagac ccctgtgggg gagagagccc caaccctgt ctcagcaagc
 180
 tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc
 240
 tctgagcagc ctccaacag cgtcctgcct gacaaactga aggtgagctg ggagaacccc
 300
 agccccagg aggccctgc tgcagagagt gcagaaccgt cccaggcacc ctgttctgag
 360
 acttctgagg ctgccccag ggagggtggg aagcccccta caccaccacc caagatctta
 420
 tcagagaaac tgaaa
 435

<210> 858

<211> 145
 <212> PRT
 <213> Homo sapiens

<400> 858
 Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser Glu
 1 5 10 15
 Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys Pro
 20 25 30
 Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr Pro
 35 40 45
 Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser
 50 55 60
 Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser Gly
 65 70 75 80
 Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val Ser
 85 90 95
 Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Ala Glu Ser Ala Glu
 100 105 110
 Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg Glu
 115 120 125
 Gly Gly Lys Pro Pro Thr Pro Pro Lys Ile Leu Ser Glu Lys Leu
 130 135 140
 Lys
 145

<210> 859
 <211> 561
 <212> DNA
 <213> Homo sapiens

<400> 859
 nacgcgtgggt gtggtaatcc ggtttctggt ggcgacggct gccaccctc gtggcaagac
 60
 atgccgttgc gtgccgatat gccatacgaa gcttggccta gtgcgaaaag ctcgctggaa
 120
 cctcgaaga ggcagggctg gcaggttacc gtggtcggtg tacgcatcgt ttcgacgatg
 180
 aacccattc tgggagcaga tatgacgacg taccagtacc tcattgtcgg tggcgggatg
 240
 gccgctgatt ctgccgcccg cggatatccg gacatcgaca agaaagggtc gatcgccatc
 300
 ctcagcgctg acgtcgacgc cccgtatcct cggccagcgc tgagcaagaa gctgtggact
 360
 gaccctgagt tcacctggga ccaggtcgac cttgctactg tcgctgacac cggcgcgga
 420
 ttgcggctcg gcaactgaggt gctcagcatt gaccgtgacg gcaagaccgt cctgaccgct
 480
 tccggccagg tattcggtta ccagaagttg ctgctcgta ccggccttac cccgtcgcgc
 540
 attgacgacg acggcgatgc c
 561

<210> 860

<211> 187
 <212> PRT
 <213> Homo sapiens

<400> 860
 Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro
 1 5 10 15
 Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp
 20 25 30
 Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln
 35 40 45
 Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu
 50 55 60
 Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met
 65 70 75 80
 Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly
 85 90 95
 Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro
 100 105 110
 Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln
 115 120 125
 Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly
 130 135 140
 Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala
 145 150 155 160
 Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu
 165 170 175
 Thr Pro Ser Arg Ile Asp Asp Asp Gly Asp Ala
 180 185

<210> 861
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 861
 ccatggggttt ctatgctctg aggtttcatc tgtggggaac agtattgact tacttacaaa
 60
 gagataatgg tcatacccta tggctactca ccatagtctg gcggtacatg gacttctcag
 120
 cccagtaag atctgtatcc acaggacact taaagtcacc ttacagaggg ctatcccagt
 180
 gcctgaggcc tattagaggc gtctcttttc agccatcagt gttagaggcc atctgcatgg
 240
 gatcccagag cctgcctcgg gaatggcaga agctggctgg tgcttggcgt gggctttgcc
 300
 tgtttcactg ctttcaggga ggctgccac aggggagaaa ctgggggggg ga
 352

<210> 862
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 862

```

Met Gly Phe Tyr Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
 1           5           10           15
Tyr Leu Gln Arg Asp Asn Gly His Thr Leu Trp Ser Leu Thr Ile Val
      20           25           30
Trp Arg Tyr Met Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
      35           40           45
His Leu Lys Ser Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
      50           55           60
Arg Gly Val Ser Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
      65           70           75           80
Ser Gln Ser Leu Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
      85           90           95
Gly Leu Cys Leu Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
      100          105          110
Asn Trp Gly Gly
      115

```

<210> 863

<211> 327

<212> DNA

<213> Homo sapiens

<400> 863

```

tccggatcga cccggacgaa ttccacggtc cagccattga ctccaaatg ctctttgaca
60
tacgccgtga catgttcaat gtccaactta cgcattgtcca cccgctcacc ggtctcattg
120
agtttgagct gcgagtagac gttgcggtag ttctcggtga ccgactgctc atacgagatg
180
tgcagaagca tcggtttgcg gccatcctcg gacggcattg gcttggttga catggccgct
240
tgccggaaca tggttcagggt aaagcccgac ttgaagttgt gcgacagggc agaaacacac
300
agcatttctg accggcgatg acccatn
327

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<210> 864

<211> 108

<212> PRT

<213> Homo sapiens

<400> 864

```

Met Gly His Arg Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
 1           5           10           15
Asn Phe Lys Ser Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
      20           25           30
Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
      35           40           45
His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
      50           55           60
Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
      65           70           75           80
Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

```

85 90 95
 Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro
 100 105

<210> 865
 <211> 729
 <212> DNA
 <213> Homo sapiens

<400> 865
 acgcgtcatc ctcattcaag aggcccagga ggagcaccac cctccgcata ttgcgcgtgc
 60
 agctctcggt ctggtctctg agcatgccca cggcgctctg cacacagctt ctcagcagcc
 120
 tgggtggtgtc caggatcgac acatcactgc ctccgagttc agaggtttcc tttcccacct
 180
 tctcagaact ttctgtttcc atggcctcct ctgccacctc tgccacctcc cctgatgtgc
 240
 tggcctccgt ctccatcgcc tctcatggc cgtcttcgc cgggtgttcc aagcccagct
 300
 caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat
 360
 cagaaacat gagggtgat ctccggaggt catcgatgtg gacagactgc cacagccctc
 420
 cgtggaagcc cacataggct gtctctcttc ccaccggga cagttttgtg atgaaataga
 480
 cgaagatacg gtcctcattt tctcgtattt tgttgatttc atttataaca gaatacttag
 540
 ctgaggcaat gagctgggcg ctacggattc catcttcaaa atctgtctga aaaatgagga
 600
 ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gactactcgg
 660
 tgtcaaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt
 720
 ctaaaattt
 729

<210> 866
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 866
 Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys
 1 5 10 15
 Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro
 20 25 30
 Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro
 35 40 45
 Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg
 50 55 60
 Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg
 65 70 75 80
 Thr Ala Gly

<210> 867
 <211> 640
 <212> DNA
 <213> Homo sapiens

<400> 867
 nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct
 60
 tcagggtggac tctcgttggg ggccggcgctc gctggccccc tcgcacccgg tcccgtgtca
 120
 catgctccag ggcgagctc ttgtccacct ttacctcacc gaaagccttg tttttgcctc
 180
 gggttaatccc ttcatgtagg gctttgatcc aggattcctt ctctctcccg gtgggtgcct
 240
 ggaatttgat gtcgctgacc ttgttccttg gggatcgag caggataaag cgggtgttttc
 300
 gcttgaggag ggacgaagg tcctggcact tctcatagct gccagctcc acagtctcca
 360
 cacacttctg atcatcctca ttctcataga ccagcagctg ggcttgagcag aggagcagat
 420
 atcgggtcttt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt
 480
 ccaccatctg tgctccccga ggcttctcac cggttctctt cacaccctcc tcctccatgg
 540
 cgagtcgcgc gaggtccgcg cgctccgcca ctgcttcca gcgcgcgcg ggctctgcca
 600
 ccgcgtctac gcccgccag gcggcgactc tccgcgttct
 640

<210> 868
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 868
 Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln
 1 5 10 15
 Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly
 20 25 30
 Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro
 35 40 45
 His Cys Ser Ser
 50

<210> 869
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 869
 ngggtgatgc tgctcgcggc attgagcatc tttgtgtca gcgcgctgtt tatcgacaac
 60

ttcctgtcgc cgctgaatat gcgcgggctg ggcctggcga tttcgacggt gggcatcgct
 120
 gcgtgcacca tgctgttctg cctggcgctg gggcatttcg acttgctcgtt gggctcgggtg
 180
 atgcctctgtg ccggtgtggt cgcggggatt gtgattcgtg acaccgatag cgtggcactc
 240
 ggcgtgtccg ctgcgttggc catgggcctg gtagtggggc tgatcaacgg catcgtgatc
 300
 gccaaagtgc gcatcaacgc g
 321

<210> 870

<211> 107

<212> PRT

<213> Homo sapiens

<400> 870

Xaa	Val	Met	Leu	Leu	Ala	Ala	Leu	Ser	Ile	Phe	Val	Leu	Ser	Ala	Leu
1				5					10					15	
Phe	Ile	Asp	Asn	Phe	Leu	Ser	Pro	Leu	Asn	Met	Arg	Gly	Leu	Gly	Leu
			20					25					30		
Ala	Ile	Ser	Thr	Val	Gly	Ile	Ala	Ala	Cys	Thr	Met	Leu	Phe	Cys	Leu
		35					40					45			
Ala	Ser	Gly	His	Phe	Asp	Leu	Ser	Val	Gly	Ser	Val	Ile	Ala	Cys	Ala
	50				55					60					
Gly	Val	Val	Ala	Gly	Ile	Val	Ile	Arg	Asp	Thr	Asp	Ser	Val	Ala	Leu
65					70				75					80	
Gly	Val	Ser	Ala	Ala	Leu	Ala	Met	Gly	Leu	Val	Val	Gly	Leu	Ile	Asn
			85					90						95	
Gly	Ile	Val	Ile	Ala	Lys	Leu	Arg	Ile	Asn	Ala					
			100					105							

<210> 871

<211> 320

<212> DNA

<213> Homo sapiens

<400> 871

agatcttcag agtcctcgtc ttttaaattg gggtaacagc agcaagtcct cagaggtgtc
 60
 ctgagcctca aaacacatcc tggtttgtaa cgtccgcagc ctcagcaggg gctaggcaca
 120
 gaacaagcat tcaggacctg gaaggtacca gcgacacctg gtcctccctt cccaggcaca
 180
 aggcagcccc tctccattca agctctgccc cagcccagca aagagagggg tcctcagcca
 240
 ctgcccccac cactaccaca atcatactca cctctcctgg tccatactg acaaaggacc
 300
 tgccacggcc agggagacaa
 320

<210> 872

<211> 98

<212> PRT

<213> Homo sapiens

<400> 872

```

Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
 1           5           10           15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
 20           25           30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
 35           40           45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
 50           55           60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
 65           70           75           80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
 85           90           95
Arg Gln

```

<210> 873

<211> 363

<212> DNA

<213> Homo sapiens

<400> 873

```

nttgttttagc atcggtttttt acgggtgtat cagcgcgttt agcagcgttt ttagcggatg
60
catcagcatg ttttgcgta cgtttttacaa ctgtgctacc gtgttttagca tcatttttga
120
cggaggtatc aatacggttta gcatcggtttt taacagatgt atcaacacgg ggttcacccg
180
cttttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atagagtcg
240
cagttgtttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaag
300
acaaagataa tttatttagt ttcattgttcg gagagaagtg tgcgaattcg gcgatacagt
360
cag
363

```

<210> 874

<211> 108

<212> PRT

<213> Homo sapiens

<400> 874

```

Met Lys Leu Asn Lys Leu Ser Leu Ser Leu Ala Ile Thr Leu Ala Leu
 1           5           10           15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
 20           25           30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
 35           40           45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
 50           55           60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

```

65 70 75 80
Lys Arg Asp Ala Lys His Ala Asp Ala Ser Ala Lys Asn Ala Ala Lys
 85 90 95
Arg Ala Asp Thr Pro Val Lys Asn Asp Ala Lys Gln
 100 105

```
<210> 875
<211> 355
<212> DNA
<213> Homo sapiens
```

```

<400> 875
acgcgtgaag gggaccctaa ctcgtctggg ctgtaggatg cgggcgaggc ttccacaaac
60
tcactgtctg ggggagaaga aaagcagaaa acaactcgaa tcgctaccat tcaggacgaa
120
cccgccaagc accagctcaa gcgcaggtcc ccgggaaaaa gcgcgggctt ctctctccca
180
gcgctcagaa tccctgagcc ggaggccccg cgggattcag accgccagat ccccagggag
240
tgacaaatcg ccgcagaaac ttggggggaca actcggccct ggcaccgcgc ggcttcagg
300
cgggggcagg cgcgcgccaa ctttccccgc gtgccacccc gcggctcccc cggcn
355

```

```
<210> 876
<211> 106
<212> PRT
<213> Homo sapiens
```

```

<400> 876
Met Arg Ala Arg Leu Pro Gln Thr His Cys Leu Gly Glu Lys Lys Ser
 1             5             10             15
Arg Lys Gln Leu Glu Ser Leu Pro Phe Arg Thr Asn Pro Pro Ser Thr
      20             25             30
Ser Ser Ser Ala Gly Pro Arg Glu Lys Ala Arg Ala Ser Leu Ser Gln
      35             40             45
Arg Ser Glu Ser Leu Ser Arg Arg Pro Arg Gly Ile Gln Thr Ala Arg
      50             55             60
Ser Pro Gly Ser Asp Lys Ser Pro Gln Lys Leu Gly Gly Gln Leu Gly
65             70             75             80
Pro Gly Thr Ala Arg Leu Pro Gly Ala Gly Arg Arg Ala Pro Thr Phe
      85             90             95
Pro Ala Cys His Pro Ala Ala Pro Pro Ala
      100             105

```

```
<210> 877
<211> 487
<212> DNA
<213> Homo sapiens
```

<400> 877
acgcgtactt tgggtaatga actgacgacc gctgagatcg actgccttta tctgtgttac
60

caatccacct atgctaaacg tggtcagcaa ggttatctca cacgagaatt ctttggtttg
 120
 ttggccaata ccatgggaga tcaaatcctt ttagtacagg cgtacagaga aggcgaagcg
 180
 atcgccgcgt cgtggtgttt ctttgatgat cattcactat atgggcgtta ttggggctgt
 240
 atggaagaag tggattgcct gcattttgaa gcttggtatt accaaggaat cgagttttgt
 300
 ctcgaaaaag ggttacagca tttcgatccg ggtacacaag gggaacacaa gattgcgcgc
 360
 ggctttgaac ctgttttttag ccacagcgtg cattacattg ctcacaaagg ttttcgtgaa
 420
 gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc
 480
 cacgcgt
 487

<210> 878

<211> 162

<212> PRT

<213> Homo sapiens

<400> 878

Thr	Arg	Thr	Leu	Gly	Asn	Glu	Leu	Thr	Thr	Ala	Glu	Ile	Asp	Cys	Leu
1				5					10					15	
Tyr	Leu	Cys	Tyr	Gln	Ser	Thr	Tyr	Ala	Lys	Arg	Gly	Gln	Gln	Gly	Tyr
			20					25				30			
Leu	Thr	Arg	Glu	Phe	Phe	Gly	Leu	Leu	Ala	Asn	Thr	Met	Gly	Asp	Gln
			35				40					45			
Ile	Leu	Leu	Val	Gln	Ala	Tyr	Arg	Glu	Gly	Glu	Ala	Ile	Ala	Ala	Ser
	50					55				60					
Trp	Cys	Phe	Phe	Asp	Asp	His	Ser	Leu	Tyr	Gly	Arg	Tyr	Trp	Gly	Cys
65				70					75					80	
Met	Glu	Glu	Val	Asp	Cys	Leu	His	Phe	Glu	Ala	Cys	Tyr	Tyr	Gln	Gly
				85					90					95	
Ile	Glu	Phe	Cys	Leu	Glu	Lys	Gly	Leu	Gln	His	Phe	Asp	Pro	Gly	Thr
			100				105					110			
Gln	Gly	Glu	His	Lys	Ile	Ala	Arg	Gly	Phe	Glu	Pro	Val	Phe	Ser	His
			115				120				125				
Ser	Val	His	Tyr	Ile	Ala	His	Gln	Gly	Phe	Arg	Glu	Ala	Ile	Gly	Asn
	130					135				140					
Phe	Cys	Glu	Glu	Glu	Ala	Gln	Ala	Val	Arg	Glu	Tyr	His	Gln	Asp	Thr
145				150					155					160	
His	Ala														

<210> 879

<211> 993

<212> DNA

<213> Homo sapiens

<400> 879

nncttagcat ttaagccaac gaggcagcta atgtcctctg aacagcaaag gaaattcagc
 60

agccagtcca gtagggctct gacccctcct tectacagta ctgctaaaaa ttcattggga
 120
 tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcatggggac
 180
 gagcacaggc agctcctctc tcacccaatg caaggccctg gactccgtgc agctacctca
 240
 tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggtg
 300
 accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tggctctcgac
 360
 ctggtgaagg ctgtcattaa agaggagggtt ttatggccag tgttgaggtc agacgcgttc
 420
 agtggactga cggccttacc tcggagcctc cttttatttg gacctcgggg gacaggcaaa
 480
 acattatttg gcagatgcat cgctagtcag ctggggggcca catttttcaa aattgccggt
 540
 tctggactag tcgccaaggg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt
 600
 gtggccagggt gtcgccagcc ctcggtgatt tttgttagtg acattgacat gcttctctcc
 660
 tctcaagtga atgaggaaca tagtccagtc agtcggatga gaaccgaatt tctgatgcaa
 720
 ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa
 780
 ccagaagaaa tagatgaatc ccttcggagg tacttcatga aacgactttt aatcccactt
 840
 cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt
 900
 ctcaatgaca aggagtgtgc actgctcgtc cagcgcacag aaggcttttc tggactagat
 960
 gtggctcatt tgtgtcagga agcagtgggtg ggc
 993

<210> 880

<211> 331

<212> PRT

<213> Homo sapiens

<400> 880

Xaa	Leu	Ala	Phe	Lys	Pro	Thr	Arg	Gln	Leu	Met	Ser	Ser	Glu	Gln	Gln
1				5				10					15		
Arg	Lys	Phe	Ser	Ser	Gln	Ser	Ser	Arg	Ala	Leu	Thr	Pro	Pro	Ser	Tyr
			20					25					30		
Ser	Thr	Ala	Lys	Asn	Ser	Leu	Gly	Ser	Arg	Ser	Ser	Glu	Ser	Phe	Gly
			35				40					45			
Lys	Tyr	Thr	Ser	Pro	Val	Met	Ser	Glu	His	Gly	Asp	Glu	His	Arg	Gln
	50					55					60				
Leu	Leu	Ser	His	Pro	Met	Gln	Gly	Pro	Gly	Leu	Arg	Ala	Ala	Thr	Ser
65					70					75				80	
Ser	Asn	His	Ser	Val	Asp	Glu	Gln	Leu	Lys	Asn	Thr	Asp	Thr	His	Leu
				85					90					95	
Ile	Asp	Leu	Val	Thr	Asn	Glu	Ile	Ile	Thr	Gln	Gly	Pro	Pro	Val	Asp
			100					105					110		
Trp	Asn	Asp	Ile	Ala	Gly	Leu	Asp	Leu	Val	Lys	Ala	Val	Ile	Lys	Glu

```

      115              120              125
Glu Val Leu Trp Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr
      130              135              140
Ala Leu Pro Arg Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys
      145              150              155              160
Thr Leu Leu Gly Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe
      165              170              175
Lys Ile Ala Gly Ser Gly Leu Val Ala Lys Gly Leu Gly Glu Ala Glu
      180              185              190
Lys Ile Ile His Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser
      195              200              205
Val Ile Phe Val Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn
      210              215              220
Glu Glu His Ser Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln
      225              230              235              240
Leu Asp Thr Val Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys
      245              250              255
Ala Thr Ser Lys Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe
      260              265              270
Met Lys Arg Leu Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln
      275              280              285
Ile Ile Val Gln Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys
      290              295              300
Glu Phe Ala Leu Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp
      305              310              315              320
Val Ala His Leu Cys Gln Glu Ala Val Val Gly
      325              330

```

<210> 881
 <211> 313
 <212> DNA
 <213> Homo sapiens

```

<400> 881
cgctgagcgc tcgacaatgc tccaggaacc ggtgtgtatg aggccgggga ttctaccggt
60
cgtggtttgc agggcatgcg tgagcgcgcc cgtatccatg gcggcaccgc gcgctggggc
120
gactcgcagt attatgaagg cggtttcaac gtcacggtgg agattccaac atgagcggcc
180
aaaggatgaa catggacacg acgcgcccc aacacggtcg gggcttgccg acgatcagcc
240
ggctgggtgc gcaccggttt tgccatggtg ctggattcgc aggacgacat cacggtggcc
300
tggaagccg acn
313

```

<210> 882
 <211> 57
 <212> PRT
 <213> Homo sapiens

```

<400> 882
Arg Val Ser Val Asp Asn Ala Pro Gly Thr Gly Val Tyr Glu Ala Gly

```

```

      1           5           10           15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile
      20           25           30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly
      35           40           45
Phe Asn Val Thr Val Glu Ile Pro Thr
      50           55

```

<210> 883

<211> 576

<212> DNA

<213> Homo sapiens

<400> 883

```

naattaagat ctgggggtccc agtgtcattg gtgaaggcct tgggattcga ggcagctgag
60
tcctcactga ccaaggcaag ccatgcttct gagtgcttga ggccaccgaa atgaacaaat
120
ggaaaacact cccatctttt tcaagcctac ctttttagcag aagaggcaga tacacaagcc
180
ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcaggctca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaaccca
300
gctctcctgt ctcccagtga agacttggat ggcagccatc agggaaggct ggggtcccagc
360
tgaggagtatg ggtgtgagct ctatagacca tcctctcttg caatcaataa acacttgcct
420
gtgaaagagg cccaagccac catccgcatg gacaccagtg caagtggccc caccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
540
tccttccttg tgaacgcctt agctaagcag gtcatg
576

```

<210> 884

<211> 105

<212> PRT

<213> Homo sapiens

<400> 884

```

Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu
1           5           10           15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro
      20           25           30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile
      35           40           45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp
      50           55           60
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
65           70           75           80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
      85           90           95
Val Asn Ala Leu Ala Lys Gln Val Met

```

100

105

<210> 885
 <211> 370
 <212> DNA
 <213> Homo sapiens

<400> 885
 actagtggcg ccctcatccg ggccgctgtc ccgctctcgg agtcggctgc gttggagtcc
 60
 ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc
 120
 aggcgggtgt cgcgcctcgg tgcgacgag ttgtcgtcga ccccggtccg cccagatccg
 180
 gtacgggctc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtagcgagc
 240
 ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt
 300
 gatccctggc ccgatgtcag cgatgaggct ctgctagcct gcgccgagga gtggcttgac
 360
 ctcgacgcgt
 370

<210> 886
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 886
 Thr Ser Gly Ala Leu Ile Arg Ala Ala Val Pro Leu Ser Glu Ser Ala
 1 5 10 15
 Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr
 20 25 30
 Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala
 35 40 45
 Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg
 50 55 60
 His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser
 65 70 75 80
 Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Arg Leu Ala Leu Ala His
 85 90 95
 Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu
 100 105 110
 Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala
 115 120

<210> 887
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 887
 cagggcggtg cgctcggctg cgtgctgccg atgggtcatgc tcggaggctt aaccgccatc
 60

attatctccg gctgcctgaa ccagcttggt aaacgctatc cgcattctgac cggcgaaggc
 120
 caactgatgc caaacctgac taatgctgat accacggctt cccaaccggc gttctccggt
 180
 aaagcggacg tgaccacat tgcctccggc gcgttgctgg ccgtgctgct ttacatggtg
 240
 ggtaggttgg ttcacaagtt gattggcctg cctgctccgg ttggcatgtt gtttgtggcg
 300
 gtgctggtca aactgtgcaa cggcgttctt ccccgctgc tcgaaggctc gcaggtggtt
 360
 tacaaattct tccagacctc cgtcacctat ccgattctgt tcgccgttgg cgtggcgatt
 420
 acgccgtggc aggaactggt caacgcg
 447

<210> 888
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 888
 Gln Gly Val Ala Leu Gly Arg Val Leu Pro Met Val Met Leu Gly Gly
 1 5 10 15
 Leu Thr Ala Ile Ile Ile Ser Gly Cys Leu Asn Gln Leu Gly Lys Arg
 20 25 30
 Tyr Pro His Leu Thr Gly Glu Gly Gln Leu Met Pro Asn Arg Ala Asn
 35 40 45
 Ala Asp Thr Thr Ala Ser Gln Pro Ala Phe Ser Gly Lys Ala Asp Val
 50 55 60
 Thr Thr Ile Ala Ser Gly Ala Leu Leu Ala Val Leu Leu Tyr Met Val
 65 70 75 80
 Gly Arg Leu Val His Lys Leu Ile Gly Leu Pro Ala Pro Val Gly Met
 85 90 95
 Leu Phe Val Ala Val Leu Val Lys Leu Cys Asn Gly Ala Ser Pro Arg
 100 105 110
 Leu Leu Glu Gly Ser Gln Val Val Tyr Lys Phe Phe Gln Thr Ser Val
 115 120 125
 Thr Tyr Pro Ile Leu Phe Ala Val Gly Val Ala Ile Thr Pro Trp Gln
 130 135 140
 Glu Leu Val Asn Ala
 145

<210> 889
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 889
 ggtaccaccc cacacctgac aagaggtggc cagggaggaa gggagggttc ttacctcccc
 60
 atctccccctc agtaaaattc aggatgccca gtgaagtttg aatgtcagat aaacaatttg
 120
 ttagtataag gatgtacctc gcattgaaat gatgccttgt aatttactaa atctgcaact
 180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg
 240
 gtgctgggga gatactgagg tcaggaaccc gtacacctct gcttctgcc tctcttcct
 300
 gtgccggcca caaggcaatg actcctgtgt ggggtgcagag gcagaaatgg gtctggaagg
 360
 ggattcccag tgtctggcaa gttctggtaa attctgcatt ggaggttctc tctgtagtaa
 420
 ggggagttgg cctggccgcc cttcacgcgt
 450

<210> 890
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 890
 Met Met Pro Cys Asn Leu Leu Asn Leu Gln Leu Cys Ser Leu Ile Ser
 1 5 10 15
 Trp Arg Ala Val Ala Val Ile Pro Gly Phe Arg Gly Gly Glu Gly Cys
 20 25 30
 Trp Gly Asp Pro Glu Val Arg Asn Pro Tyr Thr Ser Ala Ser Ala Leu
 35 40 45
 Ser Ser Leu Cys Arg Pro Gln Gly Asn Asp Ser Cys Val Gly Ala Glu
 50 55 60
 Ala Glu Met Gly Leu Glu Gly Asp Ser Gln Cys Leu Ala Ser Ser Gly
 65 70 75 80
 Lys Phe Cys Ile Gly Gly Ser Leu Cys Ser Lys Gly Ser Trp Pro Gly
 85 90 95
 Arg Pro Ser Arg
 100

<210> 891
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 891
 nncacgtcc ccgtactgga tccgcgcgag gatttcgccg actgcatgca cattgacgta
 60
 ctggatccct tccacactga caacaccagt gagcacagtg acctggccac agatggccag
 120
 actaacggcc cggctgatag cgggactggc acccactctg agcagggaaa ctccgacata
 180
 tctagccccg tcagctctag tgacgctgct aacaccaccg acagcactgc tggcaatacc
 240
 ggtgaaggta ctgccgcgaa tatgcctggt gacatggctc attcttcgac ggctacccac
 300
 ccctatgcaa gcaccggt
 318

<210> 892
 <211> 106
 <212> PRT

<213> Homo sapiens

<400> 892

```

Xaa Thr Val Pro Val Leu Asp Pro Arg Glu Asp Phe Ala Asp Cys Met
 1           5           10           15
His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
          20          25          30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
          35          40          45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
          50          55          60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
65          70          75          80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
          85          90          95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
          100          105

```

<210> 893

<211> 510

<212> DNA

<213> Homo sapiens

<400> 893

```

nnggatccta tccctgaatc taagggtggt gacacatgtg tttgggatag caaggtagag
60
aagtcacaga aaaagcctgt ggaaaacagg atgaaggagg acaaaagcag catcagggaa
120
gcaatcagca aagccaagag tacagcaaata ataaagacag aacaggaagg tgaggcatct
180
gagaagagct tgcattctgag cccacagcat atcacacacc agactatgcc tataggacag
240
agaggcagtg agcaaggcaa acgtgtggag aacattaatg gaacctccta ccctagtcta
300
cagcagaaaa ccaatgctgt taagaaatta cataaatgtg atgaatgtgg gaaatccttc
360
aaatataatt cccgccttgt tcaacataaa attatgcaca ctggggaaaa gcgctatgaa
420
tgtgatgact gtggagggac tttccggagc agctcgagcc ttcgggtcca caaacggatc
480
cacactgggt acggagagaa gacaacgcgt
510

```

<210> 894

<211> 170

<212> PRT

<213> Homo sapiens

<400> 894

```

Xaa Asp Pro Ile Pro Glu Ser Lys Val Gly Asp Thr Cys Val Trp Asp
 1           5           10           15
Ser Lys Val Glu Lys Ser Gln Lys Lys Pro Val Glu Asn Arg Met Lys
          20          25          30
Glu Asp Lys Ser Ser Ile Arg Glu Ala Ile Ser Lys Ala Lys Ser Thr

```

35	40	45
Ala Asn Ile Lys Thr Glu Gln Glu Gly Glu Ala Ser Glu Lys Ser Leu		
50	55	60
His Leu Ser Pro Gln His Ile Thr His Gln Thr Met Pro Ile Gly Gln		
65	70	75
Arg Gly Ser Glu Gln Gly Lys Arg Val Glu Asn Ile Asn Gly Thr Ser		
85	90	95
Tyr Pro Ser Leu Gln Gln Lys Thr Asn Ala Val Lys Lys Leu His Lys		
100	105	110
Cys Asp Glu Cys Gly Lys Ser Phe Lys Tyr Asn Ser Arg Leu Val Gln		
115	120	125
His Lys Ile Met His Thr Gly Glu Lys Arg Tyr Glu Cys Asp Asp Cys		
130	135	140
Gly Gly Thr Phe Arg Ser Ser Ser Ser Leu Arg Val His Lys Arg Ile		
145	150	155
His Thr Gly Tyr Gly Glu Lys Thr Thr Arg		160
165	170	

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<211> 1119

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<400> 895

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<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 900

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		115				120						125			
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Val	Leu	Glu	His	Lys	Thr	Leu	Asp	Ile	Phe	Ser	His	Ile	Thr	Thr	Leu
			165					170					175		
Lys	Ile	Asp	Gln	Lys	Pro	Leu	Pro	Thr	Thr	Asp	Ser	Thr	Val	Thr	Ser
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 Arg Asn Arg Arg Gln Arg Leu Gly Pro Thr Gln Gly Val Lys Ser Asn
 20 25 30
 Arg Lys Pro Phe Leu His Lys Ala Thr Met Gly Leu Pro Lys Ile Lys
 35 40 45
 Pro Cys His Pro Arg Asp Cys Ser Pro Ile Leu Tyr His His Glu Val
 50 55 60
 Gln Lys Ile Pro Ser Cys Glu Phe Ser Phe Lys Trp Pro Trp Ser Pro
 65 70 75 80
 Val Ser Leu Ala Met Trp Gln Lys Gln Thr Ile Leu Phe Gly Gly Tyr
 85 90 95
 Ile Phe Ile Leu Arg Leu
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<210> 905
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 905
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 ctcaacgaag acatcattat cgcggtgac cgggcagacg cggtgattag cgtatcccag
 120
 gggctctgcg acaggctggc tggacatggc gtgacctcaa cggtggttcc caacatcggt
 180
 gacgtcgagc tgtttgaccg tcctgatcga cgacatgagg ggacgatcgt cgtcagcgtc
 240

gccaccctca acccgggaaa gggcatgatt gagttagctc aggctgttga gcgtcttccc
 300
 gaggttcagt tgagaatcat cggagatgga cgcgagcggc accaactgga ggccattgcc
 360
 gctgataatc cacgcgt
 377

<210> 906
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 906
 Xaa Pro Glu Pro Val Val Trp Thr Glu His Asp Ser His Leu Ala His
 1 5 10 15
 Pro Asp Gln Arg Leu Asn Glu Asp Ile Ile Ile Ala Gly Asp Arg Ala
 20 25 30
 Asp Ala Val Ile Ser Val Ser Gln Gly Leu Cys Asp Arg Leu Ala Gly
 35 40 45
 His Gly Val Thr Ser Thr Val Val Pro Asn Ile Val Asp Val Glu Leu
 50 55 60
 Phe Asp Arg Pro Asp Arg Arg His Glu Gly Thr Ile Val Val Ser Val
 65 70 75 80
 Ala Thr Leu Asn Pro Gly Lys Gly Met Ile Glu Leu Ala Gln Ala Val
 85 90 95
 Glu Arg Leu Pro Glu Val Gln Leu Arg Ile Ile Gly Asp Gly Pro Gln
 100 105 110
 Arg His Gln Leu Glu Ala Ile Ala Ala Asp Asn Pro Arg
 115 120 125

<210> 907
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 907
 acgcgtagga tgatgaagtc cgtcactgga tcgttcttgg gtggcaaccg ggaagtcggt
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 gaccagttct tcaacggcga ggttcaactg aaccttgtgc cgcagggtac attcgccgag
 120
 cgcattcgtg ccggcgctgc tggattgca gcattcttca cgcctactgg ctatggtaca
 180
 gccgtgcaga aggggtgagct tgttcttaag tatgaaaaga aggacggtaa ggctgtgcc
 240
 gtcattgacgt ccaagccgcg tgaagtgcgc tcgtttgacg gccgtgacta tataatagaa
 300
 gaggttatta aggatgaata ggataggtg aa
 332

<210> 908
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 908

Thr Arg Arg Met Met Lys Ser Val Thr Gly Ser Phe Leu Gly Gly Asn
 1 5 10 15
 Arg Glu Val Gly Asp Gln Phe Phe Asn Gly Glu Val Gln Leu Asn Leu
 20 25 30
 Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
 35 40 45
 Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
 50 55 60
 Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
 65 70 75 80
 Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
 85 90 95
 Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
 100 105

<210> 909

<211> 318

<212> DNA

<213> Homo sapiens

<400> 909

acgcgtcggg catggcagct gtacagatct atcgcgtcag cagggcctac gcacacatga
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 tgccgcaggg gcaccgacgc tgcgccatc aaaagagccg cctcgcgccc gcagcgcctc
 120
 ccagggacgg cgactcacgt ggctcgacac gcgcgcgcga gtcgcgtggg tgtgtcacgc
 180
 cccttttttt cccaccccaa caccgaaccg gcgggccatg gctgaggatt cgcaccccat
 240
 tcgctccggc ttgcgcatgc tcaagcgctc ctggagctcg aatgagaatg taccgccgcc
 300
 acaaagctcg ccgccggc
 318

<210> 910

<211> 102

<212> PRT

<213> Homo sapiens

<400> 910

Met Ala Ala Val Gln Ile Tyr Arg Val Ser Arg Ala Tyr Ala His Met
 1 5 10 15
 Met Pro Gln Gly His Arg Arg Cys Arg His Gln Lys Ser Arg Leu Ala
 20 25 30
 Pro Ala Ala Pro Pro Arg Asp Gly Asp Ser Arg Gly Ser Thr Arg Ala
 35 40 45
 Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
 50 55 60
 Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
 65 70 75 80
 Cys Ala Cys Ser Ser Ala Pro Gly Ala Arg Met Arg Met Tyr Arg Arg
 85 90 95
 His Lys Ala Arg Arg Arg

100

<210> 911
 <211> 506
 <212> DNA
 <213> Homo sapiens

<400> 911
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 caaccttatg aggctggcct tgggggaacc ctgttttagg gatgagctga acttaccggg
 120
 aggctgcatg cgaggttggg gtgaaatgca tatctggctt tgtagctggg cggctcacct
 180
 ctgggggttg cacaggggag ggggttctgc catggctaga atgcgctaag ggggtgaaac
 240
 gaagcctgct gggcccgga accacagagc agcctggcct ttgaaggaga ccctgtggca
 300
 cccctgccc accccaagt ccagccattt cacttccctg gagatgggtg aaagcaagaa
 360
 aaaaaaaaa atccagtgtt ctcaggtcag cctccacca gccaggattc atcgtctgat
 420
 ctgtttgggg agagagcatg gagggtgga gatgggttg gcccagtggt tttctgatta
 480
 actcgagtt cacctgaaac attttg
 506

<210> 912
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 912
 Met Phe Gln Val Asn Cys Glu Leu Ile Arg Lys His Trp Gly Pro Thr
 1 5 10 15
 His Leu His His Ser Met Leu Ser Pro Gln Thr Asp Gln Thr Met Asn
 20 25 30
 Pro Gly Trp Trp Lys Ala Asp Leu Arg Thr Leu Asp Phe Phe Phe Phe
 35 40 45
 Leu Ala Leu His His Leu Gln Gly Ser Glu Met Ala Gly Leu Gly Gly
 50 55 60
 Gly Gln Gly Val Pro Gln Gly Leu Leu Gln Arg Pro Gly Cys Ser Val
 65 70 75 80
 Val Pro Gly Pro Ser Arg Leu Arg Phe His Pro Leu Ala His Ser Ser
 85 90 95
 His Gly Arg Thr Pro Ala Pro Val Pro Thr Pro Glu Val Ser Arg Pro
 100 105 110
 Ala Thr Lys Pro Asp Met His Phe Thr Pro Thr Ser His Ala Ala Ser
 115 120 125
 Arg

<210> 913
 <211> 339

<212> DNA

<213> Homo sapiens

<400> 913

cgcttcatgg cgtggttcag gcgtacgggt ccggctactg gtgactaccg tggcacgaaa
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 120
 ctgggcgcca cggacctgct tttcgccctc gactcgatcc cggcgctccta tggtttcacc
 180
 aacgaggggt accttatact taccgctaac gtctttgctc tcatgggctt gcgtcagttg
 240
 tatttcctta ttggaagcct gttggaacgt ctggtgtact tgcgctggg actggctgtg
 300
 attttgggct ttatcgccct caagctcatt ggccacgcg
 339

<210> 914

<211> 113

<212> PRT

<213> Homo sapiens

<400> 914

Arg	Phe	Met	Ala	Trp	Phe	Arg	Arg	Thr	Val	Pro	Ala	Thr	Gly	Asp	Tyr
1				5				10					15		
Arg	Gly	Thr	Lys	Phe	Phe	Val	Arg	Glu	Asn	Gly	Lys	Thr	Leu	Ala	Thr
			20				25					30			
Ser	Met	Phe	Met	Val	Cys	Val	Ala	Leu	Gly	Ala	Thr	Asp	Leu	Leu	Phe
		35				40					45				
Ala	Leu	Asp	Ser	Ile	Pro	Ala	Ser	Tyr	Gly	Phe	Thr	Asn	Glu	Gly	Tyr
	50				55					60					
Leu	Ile	Leu	Thr	Ala	Asn	Val	Phe	Ala	Leu	Met	Gly	Leu	Arg	Gln	Leu
65				70				75					80		
Tyr	Phe	Leu	Ile	Gly	Ser	Leu	Leu	Glu	Arg	Leu	Val	Tyr	Leu	Ser	Leu
			85				90					95			
Gly	Leu	Val	Val	Ile	Leu	Gly	Phe	Ile	Ala	Leu	Lys	Leu	Ile	Gly	His
		100				105						110			

Ala

<210> 915

<211> 663

<212> DNA

<213> Homo sapiens

<400> 915

nnggtacctg tcaatcagta tgtaaaccctc actttatgtc gtggttatcc acttcctgat
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 gacagtgaag atcctgttgt ggacattggt gctgtaccc ctgtcatcaa tggacagtca
 120
 ttaaccaagg gagagacttg catgaatcct caggatttta agccaggagc aatggttctg
 180
 gagcagaatg gaaaatcggg acacactttg actggtgatg gtctcaatgg accatcagat
 240

gcaagtgagc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgact
 300
 atccctttga ttaagggccc taaaggggtt gggtttgcaa ttgctgacag ccctactgga
 360
 cagaaggtga aaatgatact ggatagtcag tgggtgtcaag gccttcagaa aggagatata
 420
 attaaggaaa tataccatca aaatgtgcag aatttaacac atctccaagt ggtagagggtg
 480
 ctaaagcagt ttccagtagg tgctgatgta ccattgctta tcttaagagg aggtccccct
 540
 tcaccaacca aaagtgccaa aatgaaaaca gataaaaagg aaaatgcagg aagtttggag
 600
 gccataaatg agcctattcc tcagcctatg ccttttccac cgagcattat caggtcagga
 660
 tcc
 663

<210> 916

<211> 221

<212> PRT

<213> Homo sapiens

<400> 916

Xaa	Val	Pro	Val	Asn	Gln	Tyr	Val	Asn	Leu	Thr	Leu	Cys	Arg	Gly	Tyr
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Pro	Leu	Pro	Asp	Asp	Ser	Glu	Asp	Pro	Val	Val	Asp	Ile	Val	Ala	Ala
			20				25					30			
Thr	Pro	Val	Ile	Asn	Gly	Gln	Ser	Leu	Thr	Lys	Gly	Glu	Thr	Cys	Met
			35				40					45			
Asn	Pro	Gln	Asp	Phe	Lys	Pro	Gly	Ala	Met	Val	Leu	Glu	Gln	Asn	Gly
			50				55				60				
Lys	Ser	Gly	His	Thr	Leu	Thr	Gly	Asp	Gly	Leu	Asn	Gly	Pro	Ser	Asp
65					70					75				80	
Ala	Ser	Glu	Gln	Arg	Val	Ser	Met	Ala	Ser	Ser	Gly	Ser	Ser	Gln	Pro
			85					90						95	
Glu	Leu	Val	Thr	Ile	Pro	Leu	Ile	Lys	Gly	Pro	Lys	Gly	Phe	Gly	Phe
			100					105					110		
Ala	Ile	Ala	Asp	Ser	Pro	Thr	Gly	Gln	Lys	Val	Lys	Met	Ile	Leu	Asp
			115				120					125			
Ser	Gln	Trp	Cys	Gln	Gly	Leu	Gln	Lys	Gly	Asp	Ile	Ile	Lys	Glu	Ile
			130				135				140				
Tyr	His	Gln	Asn	Val	Gln	Asn	Leu	Thr	His	Leu	Gln	Val	Val	Glu	Val
145					150					155				160	
Leu	Lys	Gln	Phe	Pro	Val	Gly	Ala	Asp	Val	Pro	Leu	Leu	Ile	Leu	Arg
			165					170						175	
Gly	Gly	Pro	Pro	Ser	Pro	Thr	Lys	Ser	Ala	Lys	Met	Lys	Thr	Asp	Lys
			180					185					190		
Lys	Glu	Asn	Ala	Gly	Ser	Leu	Glu	Ala	Ile	Asn	Glu	Pro	Ile	Pro	Gln
			195				200					205			
Pro	Met	Pro	Phe	Pro	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Ser			
			210				215					220			

<210> 917

<211> 615

<212> DNA

<213> Homo sapiens

<400> 917

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 120
 caggagggcg acctggtgga ggtggtgctg tcggcctcgg ccaccttcga ggacttccag
 180
 atccgcccgc acgccctcac ggtgcactcc tategggcgc ctgccttctg tgatcactgc
 240
 ggggagatgc tcttcggcct agtgcgccag ggcctcaagt gcgatggctg cgggctgaac
 300
 taccacaagc gctgtgcctt cagcatcccc aacaactgta gtggggccccg caaacggcgc
 360
 ctgtcatcca cgtctctggc cagtggccac tcggtgcgcc tcggcacctc cgagtccctg
 420
 ccttcacagg ctgaagagga gccgtagcac caccgaactc ctgcctcgcc gtccccgtca
 480
 tcctcttctt cctcttctgc ctcacgtat acggggccgc ccattgagct ggacaagatg
 540
 ctgctctcca aggtcaaggt gccgcacacc ttcctcatcc acagctatac acggcccacc
 600
 gtttgccagg cttgc
 615

<210> 918

<211> 148

<212> PRT

<213> Homo sapiens

<400> 918

Ile Val Asp Gln Lys Phe Pro Glu Cys Gly Phe Tyr Gly Leu Tyr Asp
 1 5 10 15
 Lys Ile Leu Leu Phe Lys His Asp Pro Thr Ser Ala Asn Leu Leu Gln
 20 25 30
 Leu Val Arg Ser Ser Gly Asp Ile Gln Glu Gly Asp Leu Val Glu Val
 35 40 45
 Val Leu Ser Ala Ser Ala Thr Phe Glu Asp Phe Gln Ile Arg Pro His
 50 55 60
 Ala Leu Thr Val His Ser Tyr Arg Ala Pro Ala Phe Cys Asp His Cys
 65 70 75 80
 Gly Glu Met Leu Phe Gly Leu Val Arg Gln Gly Leu Lys Cys Asp Gly
 85 90 95
 Cys Gly Leu Asn Tyr His Lys Arg Cys Ala Phe Ser Ile Pro Asn Asn
 100 105 110
 Cys Ser Gly Ala Arg Lys Arg Arg Leu Ser Ser Thr Ser Leu Ala Ser
 115 120 125
 Gly His Ser Val Arg Leu Gly Thr Ser Glu Ser Leu Pro Cys Thr Ala
 130 135 140
 Glu Glu Glu Pro
 145

<210> 919
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 919
 accggtatgc gtcgctggc tgtgctcggc gacaacatca ccaccgacca tctatcgccg
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 acaaatgcga tcctgctcga tagcgcagcg ggtgagtacc tcgccaagat gggcccgccg
 120
 gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc
 180
 accttcgcca acccgacctt gctcaacgag atggccgtag tcgatggtga agtgaagaaa
 240
 ggctcgcttg cccgcgtgga accggaaggc catgtgatgc gcatgtggga agcc
 294

<210> 920
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 920
 Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp
 1 5 10 15
 His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu
 20 25 30
 Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala
 35 40 45
 Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn
 50 55 60
 Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys
 65 70 75 80
 Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp
 85 90 95
 Glu Ala

<210> 921
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 921
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 aaccaggacg tgctgttggt catcgacaac atcttccggt tctcccaggc tggttctgag
 120
 gtttcaaccc tgctaggtcg tatgccctcg gcggtgggct accagcccaa cttggccgac
 180
 gagatgggccc aattgcagga gcgaatcacc tcgaccctg gtcactccat cacctcgatg
 240
 caggccgtct acgtccccgc tgacgattac accgaccggg ctccggcgac gaccttcgcc
 300

cacctggatg ccaccaacgga gctttctcgt gagattgcct ctcgtggcct gtacccggcc
 360
 gtggatccgc tggcgctcg
 378

<210> 922
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 922
 Thr Arg Leu Arg Ile Ala Leu Thr Gly Leu Thr Met Ala Glu Tyr Phe
 1 5 10 15
 Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe
 20 25 30
 Arg Phe Ser Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met
 35 40 45
 Pro Ser Ala Val Gly Tyr Gln Pro Asn Leu Ala Asp Glu Met Gly Gln
 50 55 60
 Leu Gln Glu Arg Ile Thr Ser Thr Arg Gly His Ser Ile Thr Ser Met
 65 70 75 80
 Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala
 85 90 95
 Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Ser Arg Glu Ile
 100 105 110
 Ala Ser Arg Gly Leu Tyr Pro Ala Val Asp Pro Leu Ala Ser
 115 120 125

<210> 923
 <211> 571
 <212> DNA
 <213> Homo sapiens

<400> 923
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 120
 caacgcaaga atgtcgaaga agaagacatc ttcgccgccc accttgcgct attggaagac
 180
 cccacgctgc tggacgccgc cactggtgcc atcgaacacg gcagcgccgc caccacgcc
 240
 tggcgcgatg caatccaggc gcaatgcgcc gtgttgctgg ccctgggcaa accgctgttt
 300
 gccgagcgcg ccaacgacct gcgcgatctg caacagcgag tactgcgtgc gctgttgggg
 360
 gaagcctggc acttcgaatt gccggccggg ccgattttca ggnnggccat taacttacc
 420
 ccttcgcct tgttgcaact gagtgcccaa aacgccgtgg gtatttgcat ggccgaaggc
 480
 ggcgctacgt ctcacgtcgc gattttggcc cgaggcaaag gcttgccgtg cgtggctcgc
 540
 ctgggcgccg aagtgctcga cgtgccccaa g
 571

<210> 924
 <211> 190
 <212> PRT
 <213> Homo sapiens

<400> 924
 Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu
 1 5 10 15
 Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile
 20 25 30
 Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu
 35 40 45
 Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu
 50 55 60
 Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala
 65 70 75 80
 Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly
 85 90 95
 Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln
 100 105 110
 Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro
 115 120 125
 Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu
 130 135 140
 Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly
 145 150 155 160
 Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro
 165 170 175
 Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln
 180 185 190

<210> 925
 <211> 620
 <212> DNA
 <213> Homo sapiens

<400> 925
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 ncatggtgtg tgcacgtgtg cnactgtgta tgcattggtg tgtgcacgtg tgcactgtgt
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 gtggtgtgta tgcattggtg gtgcacgtgt gactgtgtgt tgtgtgtatg catgtgtgtg
 180
 cacgtgtgcc tgtgtgtatg catggtaatg tgcgtgtgca ctgtgtggtg tgtatgcatg
 240
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 300
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 420
 tgtgtgcatg tatgcatggt gtgtgcatac gtgtgcagca gcacctggtc ccattccag
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tgcccagcag catcacacgc actttggtgc ttataaatg catggtcagt gaggtgccca
 540
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 600
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 620

<210> 926
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 926
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
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 20 25 30
 Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val Cys
 35 40 45
 Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Val Cys Leu
 50 55 60
 Cys Val Cys Met Val Met Cys Val Cys Thr Val Trp Cys Val Cys Met
 65 70 75 80
 Cys Val His Val Cys Thr Val Tyr Ala
 85

<210> 927
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 927
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 aagaggcatt tggggctcctg ttcagatcat tccaacagca aaccggggcat ggagacccca
 120
 tctcaggtct gtgcttctct gggggccacc cagccatcct gcccaccagc tcagaggcag
 180
 ggacaaagcc ctcccaagag gcagcaggca gcaagggta gccagcgag tggggacagg
 240
 caggtacaac ctggaaaccc caaaggaccc cagatggcaa tgtgacacgg cccatccacc
 300
 aagcacctgt aatgccggct tcccacagag gcgagccaga tcctggcact attctttaag
 360

<210> 928
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 928
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 1 5 10 15
 Gly Val Leu Phe Arg Ser Phe Gln Gln Gln Thr Gly His Gly Asp Pro

	20		25		30										
Ile	Ser	Gly	Leu	Cys	Phe	Ser	Gly	Gly	His	Pro	Ala	Ile	Leu	Pro	Thr
	35		40		45										
Ser	Ser	Glu	Ala	Gly	Thr	Lys	Pro	Ser	Gln	Glu	Ala	Ala	Gly	Ser	Lys
	50		55		60										
Gly	Gln	Pro	Ala	Gln	Trp	Gly	Gln	Ala	Gly	Thr	Thr	Trp	Lys	Pro	Gln
65			70		75									80	
Arg	Thr	Pro	Asp	Gly	Asn	Val	Thr	Arg	Pro	Ile	His	Gln	Ala	Pro	Val
			85		90									95	
Met	Pro	Ala	Ser	His	Arg	Gly	Glu	Pro	Asp	Pro	Gly	Thr	Ile	Leu	
	100						105						110		

<210> 929

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 929

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aagcctcggg gctcatgtgc ggagcccact ttactgata cggaatggt ggctcacata
120
aacaacagcc ggctcaaggc caaggcgtg ggccagcacg acaacgcca gaactttggt
180
aaccagagct ttgaggagct gcgagcagcc tgtctaagaa agggggagct cttcaggagc
240
cccttattcc ctgctgaacc cagctcactg ggcttcaagg acctgggccc caactccaaa
300
aatgtgcaga acatctcctg gcagcggccc aaggatatca taaacaaccc tctattcatc
360
atggatggga tttctccaac agacatctgc caggggatcc tcggggactg ctggctgctg
420
gctgccatcg gctcccttac cacctgcccc aaactgctat accgcgtggt gccagagga
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540
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600
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660
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720
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780
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840
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960
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1080

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 1260
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 1320
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 1380
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 1440
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 1500
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 1740
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 1860
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 1920
 aagaaatgga tggacatctt cagagagtgt gaccaggacc attcaggcac cttgaactcc
 1980
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 2160
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 2340

<210> 930

<211> 702

<212> PRT

<213> Homo sapiens

<400> 930

Met	Val	Ala	His	Ile	Asn	Asn	Ser	Arg	Leu	Lys	Ala	Lys	Gly	Val	Gly
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Gln	His	Asp	Asn	Ala	Gln	Asn	Phe	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Leu
			20					25					30		
Arg	Ala	Ala	Cys	Leu	Arg	Lys	Gly	Glu	Leu	Phe	Glu	Asp	Pro	Leu	Phe

```

      35              40              45
Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser
  50              55              60
Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn
  65              70              75              80
Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln
      85              90              95
Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr
      100              105              110
Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe
      115              120              125
Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly
      130              135              140
Gln Trp Val Asn Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp
  145              150              155              160
Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala
      165              170              175
Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu
      180              185              190
Ser Gly Gly Ser Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val
      195              200              205
Ala Gln Ser Phe Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu
      210              215              220
Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu
  225              230              235              240
Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val
      245              250              255
Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg
      260              265              270
Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile
      275              280              285
Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val
      290              295              300
Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu
  305              310              315              320
Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu
      325              330              335
Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr
      340              345              350
Trp His Thr Thr Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala
      355              360              365
Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe
      370              375              380
Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly
  385              390              395              400
Asn Val Val Val Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp
      405              410              415
Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val
      420              425              430
Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu
      435              440              445
Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile
      450              455              460
Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly

```

465 470 475 480
 Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
 485 490 495
 Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
 500 505 510
 Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
 515 520 525
 Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
 530 535 540
 Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
 545 550 555 560
 Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
 565 570 575
 Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys
 580 585 590
 Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp
 595 600 605
 Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn
 610 615 620
 Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn
 625 630 635 640
 Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu
 645 650 655
 Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr
 660 665 670
 Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile
 675 680 685
 Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly
 690 695 700

<210> 931

<211> 297

<212> DNA

<213> Homo sapiens

<400> 931

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 acgaccgatc acaagacccg ctggtacgcc gagaagcagt acgccgagct cgtgggtgag
 120
 gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgccggtct ttcgtccatc
 180
 gagatcgagc gtcgctccga gcgcgtgacc attttccttt acgccgctcg cccgggcatc
 240
 gttatcgggc gcaatggccg ggaggccgag cgcgtgcgtn ntgagctcga aaagctt
 297

<210> 932

<211> 93

<212> PRT

<213> Homo sapiens

<400> 932

Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr

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1           5           10           15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
20           25           30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
35           40           45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
50           55           60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
65           70           75           80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
85           90

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<210> 933

<211> 305

<212> DNA

<213> Homo sapiens

<400> 933

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nnaacgcgtcg ccaagctggt gatggccgaa tacaaggggc tcaacgtcat cgtcaaaacc
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tccgccgatc cggcaagcca agccaatgcc gtgcaggatc tggcgggggc aggcacgac
120
gcgctggcca tcctgccgac cgacccggat cagctggttt cggcgatcca gcaggtcaag
180
gacgacggca agttcgtggc gctggtcgac cgtgcgccctt cagtcaacga caacacgac
240
cgcgatctct acgtggccgg caacaacccg gcgctcgccg aagtggcggg caaattcatg
300
ggcga
305

```

<210> 934

<211> 101

<212> PRT

<213> Homo sapiens

<400> 934

```

Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
1           5           10           15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
20           25           30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
35           40           45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
50           55           60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
65           70           75           80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
85           90           95
Gly Lys Phe Met Gly
100

```

<210> 935

<211> 333

<212> DNA

<213> Homo sapiens

<400> 935

acgcgtgaag ggctgatgag tgctatgaaa aagccagggg cccgaggaca ctgggggtgga
 60
 caggctcccc tggggaagtc ctcttagaac tgagggatca aactggagg agactgcaag
 120
 ggggtacggga taaatgttcc tgggtgaagga aacagcaggg gcaaaggccc tgcagcagaa
 180
 aggagcgagg ccctttggag taacagaaaag accatgggtga caggagctca gaaagaccac
 240
 tgggtgttaag actataagcc agtggaggcc agattgggga atgggatggg aggggtgctt
 300
 gaagaccatg gtgaggctct cttggtcttt act
 333

<210> 936

<211> 103

<212> PRT

<213> Homo sapiens

<400> 936

Met	Val	Phe	Lys	His	Pro	Ser	His	Pro	Ile	Pro	Gln	Ser	Gly	Leu	His
1				5					10					15	
Trp	Leu	Ile	Val	Leu	Thr	Pro	Val	Val	Phe	Leu	Ser	Ser	Cys	His	His
			20					25					30		
Gly	Leu	Ser	Val	Thr	Pro	Lys	Gly	Leu	Ala	Pro	Phe	Cys	Cys	Arg	Ala
			35				40					45			
Phe	Ala	Pro	Ala	Val	Ser	Phe	Thr	Arg	Asn	Ile	Tyr	Pro	Val	Pro	Leu
	50					55					60				
Ala	Val	Ser	Ser	Ser	Val	Asp	Pro	Ser	Val	Leu	Arg	Gly	Leu	Pro	Gln
65					70					75				80	
Gly	Ser	Leu	Ser	Thr	Pro	Val	Ser	Ser	Gly	Pro	Trp	Leu	Phe	His	Ser
				85					90					95	
Thr	His	Gln	Pro	Phe	Thr	Arg									
															100

<210> 937

<211> 464

<212> DNA

<213> Homo sapiens

<400> 937

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 120
 gaccgtgccc tggcagggtt gcgtgccagt cacgtcatcg acgaagctcg cgccgagggtg
 180
 cagcggcgtg ccgatctcgc ccgtggccat ctgccatcc ttcccgcagg cgatgcccgt
 240
 acggcggttg agaccctgtg cgacgagggtg ggttcccggg cggcctgaac cccgaccctg
 300

ccagnctgcg tcccatctcc tggccgggac cgctccagcg tctgctctct gacagctcat
 360
 cgttcttccg acaccaagga gtttctcgtg gcccgctatc tcgatctcat cggcattggg
 420
 cccggcaacc cggactggat caccctgggt gccgtcaagg ccan
 464

<210> 938
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 938
 Xaa Leu Ser Ala Glu Gly Val Ala Thr Leu Pro Thr Leu Met Leu Gln
 1 5 10 15
 Ala Ser Thr Asp Pro Ala Asp Asp Glu Leu Lys Asp Leu Leu Thr Ala
 20 25 30
 Asp Leu Met Asp Gln His Asn Leu Asp Arg Ala Leu Ala Gly Leu Arg
 35 40 45
 Ala Ser His Val Ile Asp Glu Ala Arg Ala Glu Val Gln Arg Arg Ala
 50 55 60
 Asp Leu Ala Arg Gly His Leu Ala Ile Leu Pro Ala Gly Asp Ala Arg
 65 70 75 80
 Thr Ala Leu Glu Thr Leu Cys Asp Glu Val Gly Ser Arg Ala Ala
 85 90 95

<210> 939
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 939
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 120
 acatggcggg ggatcgaggt tggcggctat gaaatccatc acgggcgtct gtcgttcgct
 180
 gaggacgctg aagccttcct cgacggcgta cacgtcggtc cggatatggg gacgatgtgg
 240
 cacggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac
 300
 gctggatcat cctggcgtcc gcaactccgac gagctgggtt atcaggctcg acgcgaggcg
 360
 atgatcgaac ccctcgccga cgcgt
 385

<210> 940
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 940
 Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val

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      1           5           10           15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
      20           25           30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
      35           40           45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
      50           55           60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
65           70           75           80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
      85           90           95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
      100          105          110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
      115          120          125

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<210> 941

<211> 348

<212> DNA

<213> Homo sapiens

<400> 941

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60
gaagccatgc aaaccatggt cgtgctggcc gggctgccgt tctcgggtggt gctgattttc
120
ttcatgttcg gtttcacaaa ggcgatgcgc caggacgtgg ccatggagca ggagcaggca
180
caattggctg aacgtggctg ccgtggtttc agcagcgcc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttcgctga tcaagggctg gaagtgcaga ccctgctt
348

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<210> 942

<211> 116

<212> PRT

<213> Homo sapiens

<400> 942

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Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
1           5           10           15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
20           25           30
Pro Phe Ser Val Val Leu Ile Phe Phe Met Phe Gly Leu His Lys Ala
35           40           45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Gln Ala Gln Leu Ala Glu
50           55           60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
65           70           75           80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
85           90           95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val

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100 105 110
 Gln Thr Leu Leu
 115

<210> 943
 <211> 439
 <212> DNA
 <213> Homo sapiens

<400> 943
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 60
 ctctcttaaat gcatcctggg ctctctgctaa ccctgtggga aacaccgtct cttctctcct
 120
 ttgccctctt ctgtgatcac atctcactt ctgagcctat ctgcccatcc agtcaatccc
 180
 ccttggttct gggatgctat ttccctggcc gctccctctt aggagtgtt agaaccctca
 240
 ctgtgggcag aagggaggga agatggctga ggtacctgga aagggacgtg tggatccccg
 300
 ggcattggaag gaaggaggca ggagagctag aaaaagggat gagatctaatt gttccctaag
 360
 gaacctgggt tagtgctggc ccttcacata ctgagacatg gaatccttac tactgttctc
 420
 tgaggaaaga ggctgttcc
 439

<210> 944
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 944
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 His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp
 20 25 30
 Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu
 35 40 45
 Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly
 50 55 60
 Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr
 65 70 75 80
 Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val
 85 90 95
 Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly
 100 105 110
 Met Arg Ser Asn Val Pro
 115

<210> 945
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 945

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 120
 tatatatata gcgtgtacaa caaaacatgc actgtttact cagcaccctg tgtttgtctc
 180
 agcaatagct tttctaaaga actgctacta tttgaaatgg agggggaggg gggctcctgga
 240
 cagagtattg tgcaagttga aagtctctgg atggggctat gtatataccta ccagccaatt
 300
 tgggtgcaaa ttggatttga aggcctgcct ctgtccacn
 339

<210> 946

<211> 113

<212> PRT

<213> Homo sapiens

<400> 946

Xaa	Ile	Arg	Glu	Ala	Phe	His	Ile	Phe	Phe	Leu	Leu	Ile	Ile	Ser	Ile
1				5				10						15	
Ala	Leu	Tyr	Val	Glu	Met	Val	Ile	Tyr	Ile	Tyr	Thr	His	Thr	His	Ile
			20					25					30		
Tyr	Val	Cys	Val	Cys	Ile	Tyr	Val	Tyr	Ile	Tyr	Ser	Val	Tyr	Asn	Lys
			35				40					45			
Thr	Cys	Thr	Val	Tyr	Ser	Ala	Pro	Arg	Val	Cys	Leu	Ser	Asn	Ser	Phe
			50			55				60					
Ser	Lys	Glu	Leu	Leu	Leu	Phe	Glu	Met	Glu	Gly	Glu	Gly	Gly	Pro	Gly
65					70					75				80	
Gln	Ser	Ile	Val	Gln	Val	Glu	Ser	Leu	Trp	Met	Gly	Leu	Cys	Ile	Ser
				85					90				95		
Tyr	Gln	Pro	Ile	Trp	Val	Gln	Ile	Gly	Phe	Glu	Gly	Leu	Pro	Leu	Ser
			100					105					110		

Thr

<210> 947

<211> 648

<212> DNA

<213> Homo sapiens

<400> 947

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 ctcgtggcat cacacctgtg cacgggggtg gggaaggagt ggacaggagt ggacaagtca
 120
 agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgcgaa gctttgcaga
 180
 ggagatgatg cttcaaagtt gtccctgttg gggatgagca gccaggcctt tatacactgg
 240
 gacagtcagt catggatacg tggatactct ggaaaccctc atccctggag gtctgagccc
 300

ctggatacca tgcccttctt aggctggagt tgctgccctt gtccatttac cataaaaatt
 360
 ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca
 420
 cgtacatccc caatgtgtac agccctactt ttttctgctg atcaagttca attacttctg
 480
 ctaagatggg gactattctt gcctgctggg ccttggatgc aaggacccca atgttcaggc
 540
 agccttttgg gccttctagc atacgaatca gagcattatc tttaggtgtg gaataagctg
 600
 ccccaaaaacc tgttgaagcc agccaggcac tgtgtctcct tcacgcgt
 648

<210> 948

<211> 154

<212> PRT

<213> Homo sapiens

<400> 948

Met	Glu	Met	Ser	Gly	Gln	Gln	Val	Tyr	Gly	Val	Leu	Val	Ala	Ser	His
1				5					10					15	
Leu	Cys	Thr	Gly	Val	Gly	Lys	Glu	Trp	Thr	Gly	Val	Asp	Lys	Ser	Ser
			20					25					30		
Ser	Ala	Ala	Gly	Ser	Ser	Asp	Ala	Ser	Ala	Phe	Leu	Leu	Cys	Ala	Lys
			35				40					45			
Leu	Cys	Arg	Gly	Asp	Asp	Ala	Ser	Lys	Leu	Ser	Leu	Leu	Gly	Met	Ser
	50					55				60					
Ser	Gln	Ala	Phe	Ile	His	Trp	Asp	Ser	Gln	Ser	Trp	Ile	Arg	Gly	Tyr
65				70						75				80	
Ser	Gly	Asn	Pro	His	Pro	Trp	Arg	Ser	Glu	Pro	Leu	Asp	Thr	Met	Pro
				85					90					95	
Phe	Leu	Gly	Trp	Ser	Cys	Cys	Pro	Cys	Pro	Phe	Thr	Ile	Lys	Ile	Gly
			100					105					110		
Gln	Glu	Asn	Thr	Arg	Thr	His	Leu	Ser	Phe	Ser	Ser	Tyr	Ala	Lys	Pro
			115				120					125			
Val	Leu	Pro	Arg	Thr	Ser	Pro	Met	Cys	Thr	Ala	Leu	Leu	Phe	Ser	Ala
	130					135					140				
Asp	Gln	Val	Gln	Leu	Leu	Leu	Leu	Arg	Trp						
145						150									

<210> 949

<211> 661

<212> DNA

<213> Homo sapiens

<400> 949

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 aagtaatgtg gaattttatc acagtgggtca agaaggcttc agggatagca cagatccaag
 120
 atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatattcg
 180
 aggctgtgct tttcaccatg gcttctctcc agcaattggg gtatttggga cagatggatt
 240

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 661

<210> 950

<211> 210

<212> PRT

<213> Homo sapiens

<400> 950

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		20					25					30			
Val	Thr	Phe	Leu	Asn	Leu	Gly	Gln	Ile	Gln	Glu	His	Gly	Ser	Ser	Tyr
		35				40					45				
Ile	Arg	Gly	Cys	Ala	Phe	His	His	Gly	Phe	Ser	Pro	Ala	Ile	Gly	Val
	50					55				60					
Phe	Gly	Thr	Asp	Gly	Leu	Asp	Ile	Asp	Asp	Asn	Ile	Ile	His	Phe	Thr
65					70					75				80	
Val	Gly	Glu	Gly	Ile	Arg	Ile	Trp	Gly	Asn	Ala	Asn	Arg	Val	Arg	Gly
				85				90					95		
Asn	Leu	Ile	Ala	Leu	Ser	Val	Trp	Pro	Gly	Thr	Tyr	Gln	Asn	Arg	Lys
			100					105				110			
Asp	Leu	Ser	Ser	Thr	Leu	Trp	His	Ala	Ala	Ile	Glu	Ile	Asn	Arg	Gly
	115					120						125			
Thr	Asn	Thr	Val	Leu	Gln	Asn	Val	Val	Ala	Gly	Phe	Gly	Arg	Ala	
	130					135				140					
Gly	Tyr	Arg	Ile	Asp	Gly	Glu	Pro	Cys	Pro	Gly	Gln	Phe	Asn	Pro	Val
145					150					155				160	
Glu	Lys	Trp	Phe	Asp	Asn	Glu	Ala	His	Gly	Gly	Leu	Tyr	Gly	Ile	Tyr
			165					170					175		
Met	Asn	Gln	Asp	Gly	Leu	Pro	Gly	Cys	Ser	Leu	Ile	Gln	Gly	Phe	Thr
			180					185					190		
Ile	Trp	Thr	Cys	Trp	Asp	Tyr	Gly	Ile	Tyr	Phe	Gln	Thr	Thr	Glu	Ser
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<210> 951

<211> 2615

<212> DNA

<213> Homo sapiens

<400> 951

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420
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1320
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 1920
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 1980
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 2460
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 2520
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 2580
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 2615

<210> 952

<211> 357

<212> PRT

<213> Homo sapiens

<400> 952

Xaa	Pro	Ala	Pro	Thr	Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Ala	Val
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Ser	Gly	Ala	Gln	Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys
			20				25					30		Glu
Val	Glu	Thr	Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val
		35				40					45			Asp
Cys	Ser	Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu
		50				55				60				Asp
Thr	Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn
														Glu

65 70 75 80
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu
 85 90 95
 Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu
 100 105 110
 Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Thr Ala Leu
 115 120 125
 Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser
 130 135 140
 His Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser
 145 150 155 160
 Gln Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ser Pro Pro
 165 170 175
 Arg Ala Pro Pro His Glu Gly Arg Pro Ala Cys Ala His His Ser Glu
 180 185 190
 Pro Glu Pro Gly Leu Glu Pro Ala Pro Cys Arg Ala Gln Pro Arg Asp
 195 200 205
 Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile
 210 215 220
 Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu
 225 230 235 240
 Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu
 245 250 255
 Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
 260 265 270
 Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
 275 280 285
 Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
 290 295 300
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
 305 310 315 320
 Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
 325 330 335
 Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
 340 345 350
 Gly Pro Thr Ile Leu
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<210> 953

<211> 347

<212> DNA

<213> Homo sapiens

<400> 953

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 tgttgtacct ggcggctctg cggagtaacc gctgcggaaca cacagtagga cgggagggag
 180
 aagccattgc gtttcaccct ttcattggccc ttcctttccc cttccaagtg agctctttga
 240
 ggtgagtcac ggagggcagt gtcctctctg atcctgtctg ggggtgtcaa atatggccaa
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347

<210> 954
<211> 103
<212> PRT
<213> Homo sapiens

<400> 954
Met Glu Pro Thr Trp Pro Tyr Leu Thr Thr Pro Asp Arg Met Gln Arg
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Asp Thr Ala Leu His Asp Ser Pro Gln Arg Ala His Leu Glu Gly Glu
20 25 30
Arg Lys Gly His Glu Arg Val Lys Arg Asn Gly Phe Ser Leu Pro Ser
35 40 45
Tyr Cys Val Ser Ala Ala Val Thr Pro Gln Ser Arg Gln Val Gln Gln
50 55 60
Ser Arg His Gly Lys Thr Ser Thr Pro Asn Asp Gly Ser Arg Asp Gly
65 70 75 80
Glu Ser Val Val His Thr Leu Arg Gly Asp Pro Arg Glu Thr Gly Leu
85 90 95
Arg Thr Gly Met Ala Ser Arg
100

<210> 955
<211> 634
<212> DNA
<213> Homo sapiens

<400> 955
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120
agggtctctgc aggtgaacgg ttctgcaggt gagcggctct gcaggtgagc ggctctgcat
180
gtgagtgcct ctgtgactgg ctgcgaagca gcatttgtgc acacttgact ggccacaaca
240
gaatgttctt ctctgttgc agcactgagg aggaagctcc tgcctaagcg accacagcca
300
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420
agaggcctcc gttgcacaaa tcacacacct actgtgcctg acgtggctgg gcctccagca
480
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cccacaaacc tctctataca aacacacaaa gctctgggag gctaccctgc atccaagagt
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caccatctca cacctggaac aagggttacg gccg
634

<210> 956

<211> 113

<212> PRT

<213> Homo sapiens

<400> 956

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Gly Arg Leu Gly Arg Ser Phe Leu Leu Ser Ala Asp Asn Arg Glu Glu
      20           25           30
His Ser Val Val Ala Ser Gln Val Cys Thr Asn Ala Ala Cys Glu Pro
      35           40           45
Val Thr Glu Ala Leu Thr Cys Arg Ala Ala His Leu Gln Ser Arg Ser
      50           55           60
Pro Ala Glu Pro Phe Thr Cys Arg Ala Leu His Leu Gln Asn Arg Ser
      65           70           75           80
Pro Ala Glu Pro Phe Thr Cys Arg Thr Ile His Leu Gln Ser Arg Ser
      85           90           95
Pro Ala Glu Pro Phe Thr Cys Arg Ala Ala His Leu Gln Ser Pro Ser
      100           105           110
Arg

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<210> 957

<211> 823

<212> DNA

<213> Homo sapiens

<400> 957

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120
gtacctcctg gccaccacgc actgcgcagc cgtggtgtcc agcctcctgg gcagccccct
180
gcccttggaac aggtaccacg ctcagaactcc aggcttaggg gtccctctgg aatgatgctc
240
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300
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420
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480
ctgcctggct gctctgttgg ccccaggctc cagcacacac tggaggctgc cctcaccct
540
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600
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660
tgtaccatac atcactatgt cttcccaagc tcacacctcc cagctcccag caaagggcag
720
ggcgtgtcta ccaccacca gccactggg gtcccccttc ctgcgcgagg cctccggagc
780

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<210> 958
<211> 105
<212> PRT
<213> Homo sapiens

<400> 958
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Val Ser Gln Val Pro Thr Gly Thr Ser Pro Leu Gln Ala Phe Trp Asp
20 25 30
Pro His Trp Leu Arg Trp Ala Leu His Ser Thr Pro Thr Gly Lys Leu
35 40 45
Leu Phe Leu Pro Ser Ser Lys Val Pro Lys Leu Pro Gly Cys Ser Val
50 55 60
Gly Pro Arg Leu Gln His Thr Leu Glu Ala Ala Pro His Pro Val Ser
65 70 75 80
Trp Phe Arg Leu Leu Gln Ala Leu Ser Ser Ala Gly His Pro Leu Leu
85 90 95
Pro Val Ser Arg Pro Leu Gly Thr Ala
100 105

<210> 959
<211> 586
<212> DNA
<213> Homo sapiens

<400> 959
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120
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300
tccaaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga
360
caaaaaagat ttggaatgga tcctcagacc ctcaaaaagt ttgacatcta caccatcgag
420
agcatcatga ctggttgcac caccgcctgg tatggcaact gctcggcctc cgaccgcaag
480
gcactacaga gggtagtgcg tacggcccag tacatcactg gggctaagct tcctgccatc
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586

<210> 960
<211> 195
<212> PRT

<213> Homo sapiens

<400> 960

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 Ala Asp Asp Thr Thr Val Val Gly Leu Ile Thr Asp Asn Asp Glu Ala
 20 25 30
 Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn
 35 40 45
 Asn Leu Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr
 50 55 60
 Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val
 65 70 75 80
 Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile
 85 90 95
 Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg
 100 105 110
 Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro
 115 120 125
 Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr
 130 135 140
 Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys
 145 150 155 160
 Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys
 165 170 175
 Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr
 180 185 190
 Leu Thr Ile
 195

<210> 961

<211> 502

<212> DNA

<213> Homo sapiens

<400> 961

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 taaactgtat agtaacctgc taaccagtcg gaaagagcta ccaccaatg gagatactaa
 180
 atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc ccactcctga
 240
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 360
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<210> 962
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 962
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 20 25 30
 Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu
 35 40 45
 Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser
 50 55 60
 His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp
 65 70 75 80
 Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys
 85 90 95
 Leu Gln Asn Ile Asp His Pro Phe Thr Arg
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<210> 963
 <211> 1298
 <212> DNA
 <213> Homo sapiens

<400> 963
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 120
 acgccaccca gggccagtcg ggtctgctca cagcccagag aggcgcgtg tccagccgag
 180
 ggcaagagac agagcaggtc cctgtgtatc caagtccttg agcccgtag accggcccca
 240
 ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaaagcca
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 420
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 480
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 780

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 1298

<210> 964

<211> 235

<212> PRT

<213> Homo sapiens

<400> 964

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Gly	His	Ser	Ala	Lys	Arg	Pro	Arg	Pro	Ser	Thr	Gly	Ser	Gln	Lys	Ser
			20					25					30		
Ser	Ser	Ser	Arg	Arg	Pro	Arg	Ser	Arg	Ala	Ala	Asn	Arg	Pro	Gln	Trp
			35					40					45		
Thr	Pro	Gly	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Trp	Ala	Pro	Ala	Asn	Ser
			50					55					60		
Pro	Ser	Arg	Arg	Val	Pro	Arg	Ser	Cys	Gly	Leu	Gly	Ala	Gly	Ser	Gly
65				70					75					80	
Gly	Ser	Pro	Ala	Ala	Ala	Ala	Ser	Thr	Arg	Gln	Ala	Ser	Pro	Trp	Ala
			85						90					95	
Ser	Cys	Pro	Ser	Arg	Thr	Arg	Pro	His	Ser	Ile	Thr	Arg	Ala	Pro	Ala
			100					105					110		
Ser	Arg	Cys	Thr	Gly	Leu	Arg	Ala	Ser	Arg	Thr	Trp	Ala	Ser	Ile	Met
			115					120					125		
Thr	Ile	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Thr	Gly	Ser	His	Ser	Thr
			130					135					140		
Ala	Thr	Arg	Ser	Arg	Asn	Pro	Thr	Trp	Arg	Ala	Ser	Ala	Pro	Thr	Ala
145					150				155					160	
Arg	Pro	Gly	His	Pro	Thr	Ala	Thr	Thr	Thr	Gly	Thr	Arg	Pro	Arg	
			165						170					175	
Ile	Pro	Thr	Thr	Thr	Thr	Thr	Pro	Thr	Ile	Thr	Val	Ala	Pro	Leu	Ile
			180					185					190		
Arg	Gly	Thr	Pro	Thr	Ala	Thr	Ala	Thr	Thr	Ile	Thr	Asn	Pro	His	Met
			195					200					205		
Arg	Pro	Arg	Arg	Gly	Thr	Arg	Leu	Leu	Thr	Ala	Thr	Thr	Met	Gly	Thr
			210					215					220		
Arg	Ala	Arg	Arg	Thr	Leu	Met	Ala	Thr	Thr	Trp					

225

230

235

<210> 965

<211> 336

<212> DNA

<213> Homo sapiens

<400> 965

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nnngtgacca ttatgggtgg tgcccgtacc cgtgaagtgg aaggcggtga ttttgttggc
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120
aataccggcg gtgagagctt tggcattgtc ttggtggaag ccatggcggc aggcgcagcc
180
gttgttgctt cagacttggg ggccttccgc gcagtgtgca acgccgattc cgatgatgtt
240
gccggcgcg tatatcgcaa tgaggatagt aatgaccttg ctcgtgtact caacgaggtg
300
ctcgaggatc ctgagtatcg tgcccgttta gtgcac
336

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<210> 966

<211> 112

<212> PRT

<213> Homo sapiens

<400> 966

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Xaa Val Thr Ile Met Gly Gly Ala Arg Thr Arg Glu Val Glu Gly Val
1      5      10      15
Asp Phe Val Gly Arg Val Ser Asp Ala Glu Lys Ala Glu Ile Leu Gly
20     25     30
Arg Ala Asp Val Tyr Val Ala Pro Asn Thr Gly Gly Glu Ser Phe Gly
35     40     45
Ile Val Leu Val Glu Ala Met Ala Ala Gly Ala Ala Val Val Ala Ser
50     55     60
Asp Leu Glu Ala Phe Arg Ala Val Cys Asn Ala Asp Ser Asp Asp Val
65     70     75     80
Ala Gly Ala Leu Tyr Arg Asn Glu Asp Ser Asn Asp Leu Ala Arg Val
85     90     95
Leu Asn Glu Val Leu Glu Asp Pro Glu Tyr Arg Ala Arg Leu Val His
100    105    110

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<210> 967

<211> 393

<212> DNA

<213> Homo sapiens

<400> 967

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ncaaattggca attcatagcc cgccagatcg gacacggagc tggtaggtatc cacggattcg
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ggcgcgagg cgctgggctc aagctccgct tcggcaccgg tcggcactga ggaatctccg
120
tcggcctccg ctctggccgc agcctgggct gcgccagact ctgcgggagg caccttctcc
180

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cgggttcgcc agccaaatgg cgttgcaggc tccagcatcc agtccggtgc cttcggcacc
 240
 cccgcactgc gcagagaggc cgccagaaac gatggcaccg gcggcgcggg aggtgataca
 300
 ggcgcttcgg ccggagcgct cacggactcc ggcactacag gtgcagcttg cgcttcctgc
 360
 ggcggagcaa cagggtcact tcgaggcggg gat
 393

<210> 968

<211> 125

<212> PRT

<213> Homo sapiens

<400> 968

Pro	Ala	Arg	Ser	Asp	Thr	Glu	Leu	Val	Val	Ser	Thr	Asp	Ser	Gly	Ala
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Glu	Ala	Ser	Gly	Ser	Ser	Ser	Ala	Ser	Ala	Pro	Val	Gly	Thr	Glu	Glu
		20					25					30			
Ser	Pro	Ser	Ala	Ser	Ala	Ser	Ala	Ala	Ala	Trp	Ala	Ala	Pro	Asp	Ser
		35				40					45				
Ala	Gly	Gly	Thr	Phe	Ser	Arg	Val	Arg	Gln	Pro	Asn	Gly	Val	Ala	Gly
	50				55				60						
Ser	Ser	Ile	Gln	Ser	Gly	Ala	Phe	Gly	Thr	Pro	Ala	Leu	Arg	Arg	Glu
65				70				75					80		
Ala	Ala	Arg	Asn	Asp	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Asp	Thr	Gly	Ala
			85				90					95			
Ser	Ala	Gly	Ala	Leu	Thr	Asp	Ser	Gly	Thr	Thr	Gly	Ala	Ala	Cys	Ala
		100					105					110			
Ser	Cys	Gly	Gly	Ala	Thr	Gly	Ser	Leu	Arg	Gly	Gly	Asp			
		115					120					125			

<210> 969

<211> 880

<212> DNA

<213> Homo sapiens

<400> 969

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 120
 atgaattttc gagtaaacctt acatagaatg cctatgagac acaggaagaa ggcagcagac
 180
 aagaatctta ccctgccgtc tttagtatgt gaagtactgg acctgatggt agagtttatt
 240
 gtaacacaca tgatgaagga gtttcctatg gatctctata tacgtgcat ccaggtagta
 300
 cacaaactgc tctgctacca gaagaagtgt cgggtacgcc tgcattacac ctggcgggag
 360
 ctctggtcag ccttgataaa tttgctgaag ttccttatgt caaatgagac tgtacttttg
 420
 gccaaacaca acattttttac attagccctt atgattgtga acctatttaa tatgtttatc
 480

acatatggcg acacatttct gccaaccccc agcagctatg atgaacttta ctatgagatt
 540
 atccgcatgc accagagctt tgacaacctc tactccatgg tcttgaggct ttctaccaat
 600
 gcaggccagt ggaaggaagc agctagcaag gtgacccatg cattgggtaa tatcagagcc
 660
 atcatcaacc actttaaccc caaaattgag tcctacgctg ctgtgaatca catatcccaa
 720
 ctgtcagagg agcaggtgct ggaggtggtg agagccaact atgacacgct cacgctgaag
 780
 ctgcaggatg gcctggacca gtatgagcgc tactcagagc agcacaagga agctgccttc
 840
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 880

<210> 970

<211> 263

<212> PRT

<213> Homo sapiens

<400> 970

Met	Thr	Met	His	Phe	Cys	Met	Met	Ile	Asn	Met	Asn	Phe	Arg	Val	Asn	1	5	10	15
Leu	His	Arg	Met	Pro	Met	Arg	His	Arg	Lys	Lys	Ala	Ala	Asp	Lys	Asn	20	25	30	
Leu	Thr	Leu	Pro	Ser	Leu	Val	Cys	Glu	Val	Leu	Asp	Leu	Met	Val	Glu	35	40	45	
Phe	Ile	Val	Thr	His	Met	Met	Lys	Glu	Phe	Pro	Met	Asp	Leu	Tyr	Ile	50	55	60	
Arg	Cys	Ile	Gln	Val	Val	His	Lys	Leu	Leu	Cys	Tyr	Gln	Lys	Lys	Cys	65	70	75	80
Arg	Val	Arg	Leu	His	Tyr	Thr	Trp	Arg	Glu	Leu	Trp	Ser	Ala	Leu	Ile	85	90	95	
Asn	Leu	Leu	Lys	Phe	Leu	Met	Ser	Asn	Glu	Thr	Val	Leu	Leu	Ala	Lys	100	105	110	
His	Asn	Ile	Phe	Thr	Leu	Ala	Leu	Met	Ile	Val	Asn	Leu	Phe	Asn	Met	115	120	125	
Phe	Ile	Thr	Tyr	Gly	Asp	Thr	Phe	Leu	Pro	Thr	Pro	Ser	Ser	Tyr	Asp	130	135	140	
Glu	Leu	Tyr	Tyr	Glu	Ile	Ile	Arg	Met	His	Gln	Ser	Phe	Asp	Asn	Leu	145	150	155	160
Tyr	Ser	Met	Val	Leu	Arg	Leu	Ser	Thr	Asn	Ala	Gly	Gln	Trp	Lys	Glu	165	170	175	
Ala	Ala	Ser	Lys	Val	Thr	His	Ala	Leu	Val	Asn	Ile	Arg	Ala	Ile	Ile	180	185	190	
Asn	His	Phe	Asn	Pro	Lys	Ile	Glu	Ser	Tyr	Ala	Ala	Val	Asn	His	Ile	195	200	205	
Ser	Gln	Leu	Ser	Glu	Glu	Gln	Val	Leu	Glu	Val	Val	Arg	Ala	Asn	Tyr	210	215	220	
Asp	Thr	Leu	Thr	Leu	Lys	Leu	Gln	Asp	Gly	Leu	Asp	Gln	Tyr	Glu	Arg	225	230	235	240
Tyr	Ser	Glu	Gln	His	Lys	Glu	Ala	Ala	Phe	Phe	Lys	Glu	Leu	Val	Arg	245	250	255	
Ser	Ile	Ser	Thr	Asn	Val	Arg													

260

<210> 971
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 971
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 120
 aatcccaacc ccaaatacct ggttggttaac ggagacgaat ccgaaccgga cacgtgcaag
 180
 gacatgccgc tcattatggc aagcccgac acgcttgctg aagggtgctct tatctccgcg
 240
 tacgctttcg gatccgagca ggctttcatc tacctcgtg gagaagttgt tcaggtagcc
 300
 cggcgccttg aagaaaaaaa aaaaatgcga nnnnnnn
 337

<210> 972
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 972
 Ser Arg Gly Leu Thr Met Glu Pro Ser Glu Val Leu Asn Leu Ile Lys
 1 5 10 15
 Asp Ser Gly Leu Arg Gly Arg Gly Gly Ala Gly Phe Pro Thr Gly Val
 20 25 30
 Lys Trp Ser Phe Val Pro Gln Asn Asn Pro Asn Pro Lys Tyr Leu Val
 35 40 45
 Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu
 50 55 60
 Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg
 65 70 75 80
 Tyr Ala Phe Gly Ser Glu Gln Ala Phe Ile Tyr Leu Arg Gly Glu Val
 85 90 95
 Val Gln Val Ala Arg Arg Leu Glu Glu Lys Lys Lys Met Arg Xaa Xaa
 100 105 110

<210> 973
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 973
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 120
 ccgggacctt ctgtataggc atcacttagg aaccagtcag accatcagat tctcaggacc
 180

cactggatca actgagtcag gaactcaggg ttttcaacac atcctccggg gggattccag
 240
 tggctgtgta actttgagga ccactggcaa agtggctctg gggtcagaga tccgagttca
 300
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 360

<210> 974

<211> 91

<212> PRT

<213> Homo sapiens

<400> 974

Met	Ala	Trp	Ser	Cys	Cys	Met	Val	Leu	Ser	Gly	Val	Arg	Asp	Leu	Leu
1				5					10					15	
Tyr	Arg	His	His	Leu	Gly	Thr	Ser	Gln	Thr	Ile	Arg	Phe	Ser	Gly	Pro
			20					25					30		
Thr	Gly	Ser	Thr	Glu	Ser	Gly	Thr	Gln	Gly	Phe	Gln	His	Ile	Leu	Arg
		35					40					45			
Gly	Asp	Ser	Ser	Gly	Cys	Val	Thr	Leu	Arg	Thr	Thr	Gly	Lys	Val	Ala
	50					55					60				
Leu	Gly	Ser	Glu	Ile	Arg	Val	His	Ile	Leu	Gly	Leu	Pro	Leu	Thr	Asp
65				70					75					80	
Cys	Asn	Gly	Gly	Gln	Val	Thr	Cys	Arg	Ala	Gln					
				85					90						

<210> 975

<211> 2604

<212> DNA

<213> Homo sapiens

<400> 975

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 120
 ccttggataa gtggtttctg attttgagag gacagcagag ggctgtatca cacaagacat
 180
 ttggcattag cctggaagag gtcttggatg acgagtttac ccgccgcaag catcttgaac
 240
 tgaccagcca cgatgcaggt tgaagaagcc accggtcagg ctgcgggccg tcgtcgggga
 300
 aacgtgggtgc gaaggtgtt tggccgcatc cggcgctttt tcagtcgcag gcggaatgag
 360
 cccaccttgc cccgggagtt cactcgcctg gggcgctcag gtgcagtgtc tgtggatagt
 420
 ctggctgagc tggaagacgg agccctgctg ctgcagaccc tgcagctttc aaaaatttcc
 480
 tttccaattg gccaacgact tctgggatcc aaaaggaaga tgagtctcaa tccgattgag
 540
 aaacaaatcc ccaggttgt tgaggcttgc tgccaattca ttgaaaaaca tggcttaagc
 600
 gcagtgggga tttttaccct tgaatactcc gtgcagcgag tgcgtcagct ccgtgaagaa
 660

tttgatcaag gtctggatgt agtgctggat gacaatcaga atgtgcatga tgtggctgca
720
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900
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1020
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1080
aatgtggtcc gtgccatgat tgataactgg gatgtcctct tccaggtgcc tccccatatt
1140
cagaggcagg ttgctaagcg cgtgtggaag tccagcccgg aagcacttga ttttatcaga
1200
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1260
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1320
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1380
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1560
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1740
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1860
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1920
gaaaggccct caagaggcat gctagaacgt taggtcagcc tactgacagc tgacaaacaa
1980
ttaatgcgaa atcatgtcac accaaccat agccgtgtcc acgcagcaac tccaccacct
2040
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2100
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2160
gtttctggga tccaaagtta gagggaaatt tagattttat tgcttgatc tgctttaaag
2220
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2280

ccaagtaggt aaagtcactt gattacaaat gttcttaact atcgtctctg taattccttt
 2340
 atacaggaca gtacaaaatt gtgggacatg ctctggtaac acacagatat gggttgcata
 2400
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 2460
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 2520
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 2580
 gcaaaaaaaaa aaaaaaaaaa aaaa
 2604

<210> 976
 <211> 411
 <212> PRT
 <213> Homo sapiens

<400> 976
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 20 25 30
 Arg Arg Asn Glu Pro Thr Leu Pro Arg Glu Phe Thr Arg Arg Gly Arg
 35 40 45
 Arg Gly Ala Val Ser Val Asp Ser Leu Ala Glu Leu Glu Asp Gly Ala
 50 55 60
 Leu Leu Leu Gln Thr Leu Gln Leu Ser Lys Ile Ser Phe Pro Ile Gly
 65 70 75 80
 Gln Arg Leu Leu Gly Ser Lys Arg Lys Met Ser Leu Asn Pro Ile Ala
 85 90 95
 Lys Gln Ile Pro Gln Val Val Glu Ala Cys Cys Gln Phe Ile Glu Lys
 100 105 110
 His Gly Leu Ser Ala Val Gly Ile Phe Thr Leu Glu Tyr Ser Val Gln
 115 120 125
 Arg Val Arg Gln Leu Arg Glu Glu Phe Asp Gln Gly Leu Asp Val Val
 130 135 140
 Leu Asp Asp Asn Gln Asn Val His Asp Val Ala Ala Leu Leu Lys Glu
 145 150 155 160
 Phe Phe Arg Asp Met Lys Asp Ser Leu Leu Pro Asp Asp Leu Tyr Met
 165 170 175
 Ser Phe Leu Leu Thr Ala Thr Leu Lys Pro Gln Asp Gln Leu Ser Ala
 180 185 190
 Leu Gln Leu Leu Val Tyr Leu Thr Pro Pro Cys His Ser Asp Thr Leu
 195 200 205
 Glu Arg Leu Leu Lys Ala Leu His Lys Ile Thr Glu Asn Cys Glu Asp
 210 215 220
 Ser Ile Gly Ile Asp Gly Gln Leu Val Pro Gly Asn Arg Met Thr Ser
 225 230 235 240
 Thr Asn Leu Ala Leu Val Phe Gly Ser Ala Leu Leu Lys Lys Gly Lys
 245 250 255
 Phe Gly Lys Arg Glu Ser Arg Lys Thr Lys Leu Gly Ile Asp His Tyr
 260 265 270
 Val Ala Ser Val Asn Val Val Arg Ala Met Ile Asp Asn Trp Asp Val

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      275              280              285
Leu Phe Gln Val Pro Pro His Ile Gln Arg Gln Val Ala Lys Arg Val
      290              295              300
Trp Lys Ser Ser Pro Glu Ala Leu Asp Phe Ile Arg Arg Arg Asn Leu
305              310              315              320
Arg Lys Ile Gln Ser Ala Arg Ile Lys Met Glu Glu Asp Ala Leu Leu
      325              330              335
Ser Asp Pro Val Glu Thr Ser Ala Glu Ala Arg Ala Ala Val Leu Ala
      340              345              350
Gln Ser Lys Pro Ser Asp Glu Gly Ser Ser Glu Glu Pro Ala Val Pro
      355              360              365
Ser Gly Thr Ala Arg Ser His Asp Asp Glu Glu Gly Ala Gly Asn Pro
      370              375              380
Pro Ile Pro Glu Gln Asp Arg Pro Leu Leu Arg Val Pro Arg Glu Lys
385              390              395              400
Glu Ala Lys Thr Gly Val Ser Tyr Phe Phe Pro
      405              410

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<210> 977
 <211> 378
 <212> DNA
 <213> Homo sapiens

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<400> 977
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cggacactgc gccaggccag ccacgagtcc attgaggaca gcatgaacag ctatgggtca
120
gagggcaacc ttaactatgg aggagtttgc ctggcgctcg acgcccagtt cagtgacttc
180
ctgggaagca tggggccggc acagtttgtg ggccgccaga ccctggccac cacacccatg
240
ggggatgtgg agatcgggtc gcaggagcgg aacgggtcagt tggaggtgga cattatccag
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360
tacctgctag agatggca
378

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<210> 978
 <211> 126
 <212> PRT
 <213> Homo sapiens

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<400> 978
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Glu Met Pro Ser Arg Thr Leu Arg Gln Ala Ser His Glu Ser Ile Glu
20     25     30
Asp Ser Met Asn Ser Tyr Gly Ser Glu Gly Asn Leu Asn Tyr Gly Gly
35     40     45
Val Cys Leu Ala Ser Asp Ala Gln Phe Ser Asp Phe Leu Gly Ser Met
50     55     60
Gly Pro Ala Gln Phe Val Gly Arg Gln Thr Leu Ala Thr Thr Pro Met

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65		70		75		80									
Gly	Asp	Val	Glu	Ile	Gly	Leu	Gln	Glu	Arg	Asn	Gly	Gln	Leu	Glu	Val
		85		90		95									
Asp	Ile	Ile	Gln	Ala	Arg	Gly	Leu	Thr	Ala	Lys	Pro	Gly	Ser	Lys	Thr
		100		105		110									
Leu	Pro	Ala	Ala	Tyr	Ile	Lys	Ala	Tyr	Leu	Leu	Glu	Met	Ala		
		115		120		125									

<210> 979

<211> 3500

<212> DNA

<213> Homo sapiens

<400> 979

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120
tgacgccctc cccgtacctc gctgagagcc acctgcagac acagcaggcc acagcagaat
180
gcacaggtca ctgttgtagg ggaacaaatc gtaatgccca gagaaaacct cagcctccca
240
aagtgcctggg attacaggcg tgagccacgg cgcttgccct ccttccttca cttttgaaat
300
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360
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420
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480
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600
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660
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720
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780
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900
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1080
acacgtgctc ccagctggag ccctgcgggt agctgggcgt gatcccttgg cgataccaca
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1200

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1260
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1380
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1440
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1500
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1620
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1680
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 Cys Phe Gln Val Leu Thr Ala Ser Gly Trp Ser Leu Glu Ala Thr Glu
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<210> 981
 <211> 404
 <212> DNA
 <213> Homo sapiens

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<210> 982
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<212> PRT
<213> Homo sapiens
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          35          40          45
Asp Asp Glu Asp Val Asp Asp Glu Asn Thr Asp Ile Thr Ala Leu Ala
          50          55          60
Glu Ala Gly Ala Arg Gly Gly Ala Gly Asn His Arg Phe Gly Gly Asp
65          70          75          80
Arg Pro Gly Ser Asp Arg Val Leu Gly Arg Gln Arg Leu Gln Gln Pro
          85          90          95
Arg His Leu Gln Pro Ser Gly Ala Pro Asp Gln Ala Cys Gly Gly Thr
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Gly Ser Glu Pro Gly Arg
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<211> 579
<212> DNA
<213> Homo sapiens
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300
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360
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420
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<210> 984
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 <212> PRT
 <213> Homo sapiens

<400> 984
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 20 25 30
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 35 40 45
 Leu Phe Pro Lys Arg Ala Arg Tyr Pro Ser Phe Ser Gly Pro Leu Tyr
 50 55 60
 Leu Phe Phe Ser Leu Pro Glu Thr Pro Phe Leu Leu Asn Asn Leu Met
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<210> 985
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 <212> DNA
 <213> Homo sapiens

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<210> 986
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 986
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	20	25	30
Ala Asn Phe Lys Ala His Asp Leu Lys Leu Val Thr Glu Ile Asn His			
	35	40	45
Leu Asp Asn Gln Ile Phe Ile Asp Tyr Ala Lys Leu Ile Lys Glu Ser			
	50	55	60
Asp Ala Leu Pro Val Asp Gln Gln Val Ala Phe Phe Leu Asn Asn Met			
65	70	75	80
Gln Ser Ile Ile Asp Gly Lys Pro Glu Leu Asn Ile Thr Glu Leu Ser			
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<210> 987

<211> 4224

<212> DNA

<213> Homo sapiens

<400> 987

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 <211> 873
 <212> PRT
 <213> Homo sapiens

<400> 988

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			20					25					30		
Met	Leu	Leu	Arg	Gly	Leu	Thr	Gln	Ile	Gln	Ser	Arg	Ile	Leu	Gly	Pro
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Gly	Arg	Lys	Cys	Cys	Ala	Leu	Ala	Asn	Leu	Ala	Asp	Met	Leu	Thr	Val
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Phe	Ala	Leu	Thr	Glu	Asp	Asp	Pro	Gln	Glu	Val	Ser	Ala	Thr	Val	Tyr
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Leu	Asp	Lys	Leu	Ala	Thr	Val	Ile	Ser	Val	Trp	Asn	Ser	Asp	Thr	Gln
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Asn	Pro	Tyr	His	Gln	Gln	Ala	Leu	Ala	Glu	Lys	Val	Lys	Glu	Ala	Glu
			100					105					110		
Arg	Asp	Val	Ser	Leu	Thr	Ser	Leu	Ala	Lys	Leu	Pro	Ser	Glu	Thr	Ile
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Phe	Val	Gly	Cys	Glu	Phe	Leu	His	His	Leu	Leu	Arg	Glu	Trp	Gly	Glu
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Glu	Leu	Gln	Ala	Val	Leu	Arg	Ser	Ser	Gln	Gly	Thr	Ser	Tyr	Asp	Ser
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Tyr	Arg	Leu	Cys	Asp	Ser	Leu	Thr	Ser	Phe	Ser	Gln	Asn	Ala	Thr	Leu
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Tyr	Leu	Asn	Arg	Thr	Ser	Leu	Ser	Lys	Glu	Asp	Arg	Gln	Val	Val	Ser
			180					185					190		
Glu	Leu	Ala	Glu	Cys	Val	Arg	Asp	Phe	Leu	Arg	Lys	Thr	Ser	Thr	Val
			195				200						205		
Leu	Lys	Asn	Arg	Ala	Leu	Glu	Asp	Ile	Thr	Ala	Ser	Ile	Ala	Met	Ala
			210			215						220			
Val	Ile	Gln	Gln	Lys	Met	Asp	Arg	His	Met	Glu	Val	Cys	Tyr	Ile	Phe
225				230						235				240	
Ala	Ser	Glu	Lys	Lys	Trp	Ala	Phe	Ser	Asp	Glu	Trp	Val	Ala	Cys	Leu
			245						250					255	
Gly	Ser	Asn	Arg	Ala	Leu	Phe	Arg	Glu	Pro	Asp	Leu	Val	Leu	Arg	Leu
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Leu	Glu	Thr	Val	Ile	Asp	Val	Ser	Thr	Ala	Asp	Arg	Ala	Ile	Pro	Glu
			275				280					285			
Ser	Gln	Ile	Arg	Gln	Val	Ile	His	Leu	Ile	Leu	Glu	Cys	Tyr	Ala	Asp
			290			295					300				
Leu	Ser	Leu	Pro	Gly	Lys	Asn	Lys	Val	Leu	Ala	Gly	Ile	Leu	Arg	Ser
305				310						315				320	
Trp	Gly	Arg	Lys	Gly	Leu	Ser	Glu	Lys	Leu	Leu	Ala	Tyr	Val	Glu	Gly
			325						330					335	
Phe	Gln	Glu	Asp	Leu	Asn	Thr	Thr	Phe	Asn	Gln	Leu	Thr	Gln	Ser	Ala
			340					345					350		
Ser	Glu	Gln	Gly	Leu	Ala	Lys	Ala	Val	Ala	Ser	Val	Ala	Arg	Leu	Val
			355				360					365			
Ile	Val	His	Pro	Glu	Val	Thr	Val	Lys	Lys	Met	Cys	Ser	Leu	Ala	Val

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Val Asn Leu Gly Thr His Lys Phe Leu Ala Gln Ile Leu Thr Ala Phe
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Pro Ala Leu Arg Phe Val Glu Val Gln Gly Pro Asn Ser Ser Ala Thr
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Phe Met Val Ser Cys Leu Lys Glu Thr Val Trp Met Lys Phe Ser Thr
          420          425          430
Pro Lys Glu Glu Lys Gln Phe Leu Glu Leu Leu Asn Cys Leu Met Ser
          435          440          445
Pro Val Lys Pro Gln Gly Ile Pro Val Ala Ala Leu Leu Glu Pro Asp
          450          455          460
Glu Val Leu Lys Glu Phe Val Leu Pro Phe Leu Arg Leu Asp Val Glu
465          470          475          480
Glu Val Asp Leu Ser Leu Arg Ile Phe Ile Gln Thr Leu Glu Ala Asn
          485          490          495
Ala Cys Arg Glu Glu Tyr Trp Leu Gln Thr Cys Ser Pro Phe Pro Leu
          500          505          510
Leu Phe Ser Leu Cys Gln Leu Leu Asp Arg Phe Ser Lys Tyr Trp Gln
          515          520          525
Leu Pro Lys Glu Lys Arg Cys Leu Ser Leu Asp Arg Lys Asp Leu Ala
          530          535          540
Ile His Ile Leu Glu Leu Leu Cys Glu Ile Val Ser Ala Asn Ala Glu
545          550          555          560
Thr Phe Ser Pro Asp Val Trp Ile Lys Ser Leu Ser Trp Leu His Arg
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Cys Lys Leu Ser Glu Asp Glu Trp Thr Ser Gln Ala His Pro Gly Tyr
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Gly Ala Gly Thr Gly Leu Leu Ala Trp Met Glu Cys Cys Cys Val Ser
625          630          635          640
Ser Gly Ile Ser Glu Arg Met Leu Ser Leu Leu Val Val Asp Val Gly
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Val Gln Val Met Pro Trp Cys Ser Pro Gln Glu Trp Gln Arg Leu His
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705          710          715          720
Ala Gln Glu Leu Gln Leu Ser Val Leu Phe Leu Arg Thr Phe Gln Phe
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Leu Cys Ser His Ser Cys Arg Asn Trp Leu Pro Leu Glu Gly Trp Asn
          740          745          750
His Val Val Lys Leu Leu Cys Gly Ser Leu Thr Arg Leu Leu Asp Ser
          755          760          765
Val Arg Ala Ile Gln Ala Ala Gly Pro Trp Val Gln Gly Pro Glu Gln
          770          775          780
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785          790          795          800
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<211> 402
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<213> Homo sapiens
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<210> 990
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<213> Homo sapiens
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965

130

<210> 991
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 359

<210> 992
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 992
 Ser Arg Ile Lys Ala Lys Lys Thr Gln Ala Glu Val Ala Glu Ala Val
 1 5 10 15
 Lys Met Ser Gln Pro Ala Tyr Gln Ala Leu Glu Ser Gly Lys Asn Leu
 20 25 30
 Lys Ser Ala Phe Leu Pro Leu Ile Ala Gln Phe Leu Gly Val Asp Gly
 35 40 45
 Tyr Trp Leu Thr Thr Gly Asn Thr Glu Asp Ser Phe Arg Glu Ser Asp
 50 55 60
 Val Phe Ser Pro Thr Val Val Ser Ala Glu Ser Thr Asp Gln Tyr Val
 65 70 75 80
 Trp Ile Glu Val Val Glu Ala Asn Phe Ser Cys Gly Thr Gly Glu Ser
 85 90 95
 Ile Glu Phe His Phe Asp Ala Ile Asn Gly Lys Ile Pro Phe Pro Ala
 100 105 110
 Ser Phe Phe Lys Glu Lys Arg
 115

<210> 993
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 993
 ngcgcgccgg gcaccacata cgacgacggg acgttattca cctctaactg gtagccgccg
 60
 tcgcggtccg gatccgcgat gatggccgcg tggcctgaag caatggggta ggtgcccggtg
 120

atgcgtcgct ttggcgacag aggtttacgc cgtggggagt tcataaggga aataccagca
 180
 cagggctcgga ccagttgtta cgatcgctgc atgatctact tgcgcagga ttatatcggt
 240
 gagctaccca agcaacatat ctcgctggga aagtttgatc ccgacaatat tcctgcggac
 300
 ccgaacgaac tgtttgccac gtggtttaaa gaagccgttg agaacgaagt cggcgaccct
 360
 actgcggtca ccgtggccac ggtggacgac aacggtcagc ccgatgcgcg agtcgtcgac
 420
 cttctgtacc tcaactccga cggcttccac
 450

<210> 994
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 994
 Met Arg Arg Phe Gly Ala Arg Gly Leu Arg Arg Gly Glu Phe Ile Arg
 1 5 10 15
 Glu Ile Pro Ala Gln Gly Arg Thr Ser Cys Tyr Asp Arg Cys Met Ile
 20 25 30
 Tyr Leu Ser Gln Asp Tyr Ile Gly Glu Leu Pro Lys Gln His Ile Ser
 35 40 45
 Leu Gly Lys Phe Asp Pro Asp Asn Ile Pro Ala Asp Pro Asn Glu Leu
 50 55 60
 Phe Ala Thr Trp Phe Lys Glu Ala Val Glu Asn Glu Val Gly Asp Pro
 65 70 75 80
 Thr Ala Val Thr Val Ala Thr Val Asp Asp Asn Gly Gln Pro Asp Ala
 85 90 95
 Arg Val Val Asp Leu Leu Tyr Leu Asn Ser Asp Gly Phe His
 100 105 110

<210> 995
 <211> 924
 <212> DNA
 <213> Homo sapiens

<400> 995
 cgggagctgg tggaccagga cgtgcagcct gcccgctacc acatcgccct tgggcccgtg
 60
 gtggatggcg acgtgggtccc cgatgaccct gagatcctca tgcagcaggg agaattcctc
 120
 aactacgaca tgctcatcgg cgtcaaccag ggagagggcc tcaagttcgt ggaggactct
 180
 gcagagagcg aggacggtgt gtctgccagc gcctttgact tcaactgtct caactttgtg
 240
 gacaacctgt atggctaccc ggaaggcaag gatgtgcttc gggagaccat caagtttatg
 300
 tacacagact gggccgaccg ggacaatggc gaaatgcgc gcaaaaccct gctggcgctc
 360
 tttactgacc accaatgggt ggcaccagct gtggccactg ccaagctgca cgccgactac
 420

cagtctcccg tctactttta cacctttctac caccactgcc aggcggaggg ccggcctgag
 480
 tgggcagatg cggcgcacgg ggatgaactg ccctatgtct ttggcgtgcc catggtgggt
 540
 gccaccgacc tcttcccttg taactttctcc aagaatgacg tcatgctcag tgccgtggtc
 600
 atgacctact ggaccaactt cgccaagact ggggacccca accagccggt gccgcaggat
 660
 accaagtcca tccacaccaa gcccaatcgc ttcgaggagg tgggtgtggag caaattcaac
 720
 agcaaggaga agcagtatct gcacataggc ctgaagccac gcgtgcgtga caactaccgc
 780
 gccacaagg tggccttctg gctggagctc gtgccccacc tgcacaacct gcacacggag
 840
 ctcttcacca ccaccacgcg cctgcctccc tacgccacgc gctggccgcc tcgtccccc
 900
 gctggcgccc cgggcacacg ccgg
 924

<210> 996
 <211> 308
 <212> PRT
 <213> Homo sapiens

<400> 996
 Arg Glu Leu Val Asp Gln Asp Val Gln Pro Ala Arg Tyr His Ile Ala
 1 5 10 15
 Phe Gly Pro Val Val Asp Gly Asp Val Val Pro Asp Asp Pro Glu Ile
 20 25 30
 Leu Met Gln Gln Gly Glu Phe Leu Asn Tyr Asp Met Leu Ile Gly Val
 35 40 45
 Asn Gln Gly Glu Gly Leu Lys Phe Val Glu Asp Ser Ala Glu Ser Glu
 50 55 60
 Asp Gly Val Ser Ala Ser Ala Phe Asp Phe Thr Val Ser Asn Phe Val
 65 70 75 80
 Asp Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Val Leu Arg Glu Thr
 85 90 95
 Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Arg Asp Asn Gly Glu Met
 100 105 110
 Arg Arg Lys Thr Leu Leu Ala Leu Phe Thr Asp His Gln Trp Val Ala
 115 120 125
 Pro Ala Val Ala Thr Ala Lys Leu His Ala Asp Tyr Gln Ser Pro Val
 130 135 140
 Tyr Phe Tyr Thr Phe Tyr His His Cys Gln Ala Glu Gly Arg Pro Glu
 145 150 155 160
 Trp Ala Asp Ala Ala His Gly Asp Glu Leu Pro Tyr Val Phe Gly Val
 165 170 175
 Pro Met Val Gly Ala Thr Asp Leu Phe Pro Cys Asn Phe Ser Lys Asn
 180 185 190
 Asp Val Met Leu Ser Ala Val Val Met Thr Tyr Trp Thr Asn Phe Ala
 195 200 205
 Lys Thr Gly Asp Pro Asn Gln Pro Val Pro Gln Asp Thr Lys Phe Ile
 210 215 220
 His Thr Lys Pro Asn Arg Phe Glu Glu Val Val Trp Ser Lys Phe Asn

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225          230          235          240
Ser Lys Glu Lys Gln Tyr Leu His Ile Gly Leu Lys Pro Arg Val Arg
          245          250          255
Asp Asn Tyr Arg Ala Asn Lys Val Ala Phe Trp Leu Glu Leu Val Pro
          260          265          270
His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg Leu
          275          280          285
Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro
          290          295          300
Gly Thr Arg Arg
305

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<210> 997
<211> 320
<212> DNA
<213> Homo sapiens

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<400> 997
aaatttaata ccatagcctt ctcttggttg atccttctag gcatgagtta tggcattaaa
60
acgggcatcc atcttggtgt cgatatcgta cttaatgccg tgcctaaacg agtatcaaga
120
gccttgctctt tgttcgggtgc ctttgccgct attatgtacg gtctcattct acttgattct
180
acctggttag ccttactcgg tatcgatgta cgagggtggtg ccatcgaata ttgggcgaag
240
atgttcaaaa taggtattgg tactgaagag cttcgttacc ctatctttat gcaagatatg
300
tttgatttgc gcccacgcgt
320

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<210> 998
<211> 106
<212> PRT
<213> Homo sapiens

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<400> 998
Lys Phe Asn Thr Ile Ala Phe Ser Trp Leu Ile Leu Leu Gly Met Ser
1          5          10          15
Tyr Gly Ile Lys Thr Gly Ile His Leu Gly Val Asp Ile Val Leu Asn
          20          25          30
Ala Val Pro Lys Arg Val Ser Arg Ala Leu Ser Leu Phe Gly Ala Phe
          35          40          45
Ala Ala Ile Met Tyr Gly Leu Ile Leu Leu Asp Ser Thr Trp Leu Ala
          50          55          60
Leu Leu Gly Ile Asp Val Arg Gly Gly Ala Ile Glu Tyr Trp Ala Lys
65          70          75          80
Met Phe Lys Ile Gly Ile Gly Thr Glu Glu Leu Arg Tyr Pro Ile Phe
          85          90          95
Met Gln Asp Met Phe Asp Leu Arg Pro Arg
          100          105

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<210> 999
<211> 401

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<212> DNA

<213> Homo sapiens

<400> 999

acgcgttcag gcggttaaca atcgcgctaa gaagctgacc aaggaaaatg tcggcatggt
 60
 acatctgagc aagagcttca tcggtgttta tctctactca gaaggcaagt ttgtgaccag
 120
 caactatctc aatcgtggct acaaggacat tctgagctat gcagacgatg ctagtctttt
 180
 gcaaaagcct ccagcagtgg cttcagatga tctggataca ggtctcttga agagggcctt
 240
 ggatgagtgg gtggctgatg ctaagaacca cattctcaat actgaaaact tctttagcgg
 300
 gtcaaccggt ctcaacattg acagtttcta cgtcttttgtt gaccaagaca tctgctggca
 360
 gttggcagct attctgaagc agagcatgaa tcgggaattg t
 401

<210> 1000

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1000

Met	Val	His	Leu	Ser	Lys	Ser	Phe	Ile	Gly	Val	Tyr	Leu	Tyr	Ser	Glu
1				5					10					15	
Gly	Lys	Phe	Val	Thr	Ser	Asn	Tyr	Leu	Asn	Arg	Gly	Tyr	Lys	Asp	Ile
			20					25					30		
Leu	Ser	Tyr	Ala	Asp	Asp	Ala	Ser	Leu	Leu	Gln	Lys	Pro	Pro	Ala	Val
		35				40					45				
Ala	Ser	Asp	Asp	Leu	Asp	Thr	Gly	Leu	Leu	Lys	Arg	Ala	Leu	Asp	Glu
	50					55					60				
Trp	Val	Ala	Asp	Ala	Lys	Asn	His	Ile	Leu	Asn	Thr	Glu	Asn	Phe	Phe
65					70				75					80	
Ser	Gly	Ser	Thr	Gly	Leu	Asn	Ile	Asp	Ser	Phe	Tyr	Val	Phe	Gly	Asp
			85					90						95	
Gln	Asp	Ile	Cys	Trp	Gln	Leu	Ala	Ala	Ile	Leu	Lys	Gln	Ser	Met	Asn
			100					105						110	
Arg	Glu	Leu													
															115

<210> 1001

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1001

cgcggtattg caatgcgcct ggtgccgaat gctaaacctg ctcttgattg cccggtactg
 60
 ttcccttatg cccctaattgc ggtgattgtt ggcttcctgg ccactaccgt tggttcaatt
 120
 atcggtatga ttgtcttccc gctgttttgtt ctggcgatga tccttcggg tctgctaact
 180

aaattcttcg ctggtggtgc cgctggagtc tttggcaacg cgatgggagg acgtaaaggg
 240
 gcaattattg gcggcgtagt gcacgggctg tttatcaccc tgttaccagc gatgctaate
 300
 cccttactgg aaaccttcgg cttcaaaggc gtcaccttca gtgattccga t
 351

<210> 1002

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1002

Arg	Gly	Ile	Ala	Met	Arg	Leu	Val	Pro	Asn	Ala	Lys	Pro	Ala	Leu	Asp
1				5					10					15	
Cys	Pro	Val	Leu	Phe	Pro	Tyr	Ala	Pro	Asn	Ala	Val	Ile	Val	Gly	Phe
		20						25					30		
Leu	Ala	Thr	Thr	Val	Gly	Ser	Ile	Ile	Gly	Met	Ile	Val	Phe	Pro	Leu
		35					40					45			
Phe	Gly	Leu	Ala	Met	Ile	Leu	Pro	Gly	Leu	Leu	Thr	Asn	Phe	Phe	Ala
	50					55					60				
Gly	Gly	Ala	Ala	Gly	Val	Phe	Gly	Asn	Ala	Met	Gly	Gly	Arg	Lys	Gly
65					70				75					80	
Ala	Ile	Ile	Gly	Gly	Val	Val	His	Gly	Leu	Phe	Ile	Thr	Leu	Leu	Pro
				85					90					95	
Ala	Met	Leu	Ile	Pro	Leu	Leu	Glu	Thr	Phe	Gly	Phe	Lys	Gly	Val	Thr
			100					105						110	
Phe	Ser	Asp	Ser	Asp											
			115												

<210> 1003

<211> 444

<212> DNA

<213> Homo sapiens

<400> 1003

acgcgtcctc ctttagtcga tcgcgaatat gataggcgaa gcgacgtgat ggtgtgacgc
 60
 acgagcactg ccccatctcc taggcttagg gttatgcaga ctcccatcga cgctacctcc
 120
 acccccgcat ggggcacact ctccggccta aagtcgccgt tcgctgacgg gccacataaa
 180
 ctgcgccgtt tgttcgacgc cgaccctcac cgcgctgagc gctacacctt tgacgtcgcg
 240
 gatttgcacg tcgattttatc gaagaacctc cttaccgacg agattcgtga cgctctcctc
 300
 gaactggctg cgcagatgcg cgtcaccgag cgtcgctgacg cgatgtatgc cggtgagcac
 360
 atcaacgtca ccgaggaccg cgccgtcctc cataccgcgc tgtgtcgtcc ccgcactgac
 420
 gagctgcatg ttgacgggtca ggat
 444

<210> 1004

<211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1004
 Met Gln Thr Pro Ile Asp Ala Thr Ser Thr Pro Ala Trp Gly Thr Leu
 1 5 10 15
 Ser Gly Leu Lys Ser Arg Phe Ala Asp Gly Pro His Lys Leu Arg Arg
 20 25 30
 Leu Phe Asp Ala Asp Pro His Arg Ala Glu Arg Tyr Thr Phe Asp Val
 35 40 45
 Ala Asp Leu His Val Asp Leu Ser Lys Asn Leu Leu Thr Asp Glu Ile
 50 55 60
 Arg Asp Ala Leu Leu Glu Leu Ala Ala Gln Met Arg Val Thr Glu Arg
 65 70 75 80
 Arg Asp Ala Met Tyr Ala Gly Glu His Ile Asn Val Thr Glu Asp Arg
 85 90 95
 Ala Val Leu His Thr Ala Leu Cys Arg Pro Arg Thr Asp Glu Leu His
 100 105 110
 Val Asp Gly Gln Asp
 115

<210> 1005
 <211> 299
 <212> DNA
 <213> Homo sapiens

<400> 1005
 ccatggccat tcctctggtg actgcatcca gtccgatgga tttaaaccacc cccaatgtgc
 60
 tgggtgactcc caagtttaca cctccagcca gggcttctct cctgggtttg catacccacc
 120
 tatctatctg ccttagccac tcgtgtctga cgagcacctc acacctccag aggctcctca
 180
 tttcttccca tgctgtcttc tcccacactc ctccctctca catgagggca acttcatcct
 240
 cccagttgct caggcccca accctccatca gttttgactc ttctctcgca cactactcg
 299

<210> 1006
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 1006
 Met Ala Ile Pro Leu Val Thr Ala Ser Ser Pro Met Asp Leu Asn Thr
 1 5 10 15
 Pro Asn Val Leu Val Thr Pro Lys Phe Thr Pro Pro Ala Arg Ala Ser
 20 25 30
 Leu Leu Gly Leu His Thr His Leu Ser Ile Cys Leu Ser His Ser Cys
 35 40 45
 Leu Thr Ser Thr Ser His Leu Gln Arg Leu Leu Ile Ser Ser His Ala
 50 55 60
 Cys Phe Ser His Thr Pro Pro Ser His Met Arg Ala Thr Ser Ser Ser

Gln Leu Leu Arg Pro Gln Thr Ser Ile Ser Phe Asp Ser Ser Leu Ala
85 90 95

His Tyr Ser

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<210> 1007
<211> 389
<212> DNA
<213> Homo sapiens
```

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<400> 1007
gccggcgcgga agatctaaag agctggaaag gcaaccgcaa gagagcgggg ttcttgctg
60
atgagcgcgcg tttcatggac tccatcttcg gcccggggccc tgggtgtgacg gtctctgaaa
120
tcaacgacgcg caccgaggca cccagaggtg tgacgttgag tgatggccga cgacagggca
180
acgccggagcg aatcggtgac ttcttcgcat cgaaggacta caagccgtcc gcggcgagcc
240
tccgaggtcc ggcgagggat ccgaaatgga tcgacgttca acgctcattc cacgagaacg
300
aagaaggccc gtacagctgg tacacctggc gcgggcaggc ttttgacacg ggcgctggat
360
ggcgtaaata cgtccatgcc gcgacaacg
389

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```
<210> 1008
<211> 105
<212> PRT
<213> Homo sapiens
```

```

<400> 1008
Met Asp Ser Ile Phe Gly Pro Gly Pro Gly Val Thr Val Ser Glu Ile.
  1             5             10             15
Asn Asp Ala Thr Glu Ala Pro Arg Gly Val Thr Leu Ser Asp Gly Arg
      20             25             30
Arg Gln Gly Asn Ala Gly Ala Ile Gly Asp Phe Phe Ala Ser Lys Asp
      35             40             45
Tyr Lys Pro Ser Ala Ala Ser Leu Arg Gly Pro Ala Arg Asp Pro Lys
      50             55             60
Trp Ile Asp Val Gln Arg Ser Phe His Glu Asn Glu Glu Gly Pro Tyr
65             70             75             80
Ser Trp Tyr Thr Trp Arg Gly Gln Ala Phe Asp Thr Gly Ala Gly Trp
      85             90             95
Arg Lys Tyr Val His Ala Ala Thr Thr
      100             105

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```
<210> 1009
<211> 324
<212> DNA
<213> Homo sapiens
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<400> 1009

ngccttcatg gctgntatgc ctggcctcat ccccatccct ggcacccgtg acgatagcca
 60
 cattccactg gtgtttcccc aggaaagcca accctacctg catctcagca gagcttccac
 120
 ggagttggaa ccccgctccg agaggggtgtg ggctcagggg ccaggggtca cacaaactcc
 180
 agaaggagga cgtagtgtgt ttgcaaggct gtcctttgcc ctggttgaat aaccttcggg
 240
 ctgccccgag aggaacgtgg gcattagget gcacccgcag gaagccatgt attttctgag
 300
 aaacttggcc catggtgcag atct
 324

<210> 1010
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 1010
 Met Gly Gln Val Ser Gln Lys Ile His Gly Phe Leu Arg Val Gln Pro
 1 5 10 15
 Asn Ala His Val Pro Leu Gly Ala Asp Arg Arg Leu Phe Asn Gln Gly
 20 25 30
 Lys Gly Gln Pro Cys Lys Pro Thr Thr Ser Ser Phe Trp Ser Leu Cys
 35 40 45
 Asp Pro Trp Pro Leu Ser Pro His Pro Leu Gly Ala Gly Phe Gln Leu
 50 55 60
 Arg Gly Ser Ser Ala Glu Met Gln Val Gly Leu Ala Phe Leu Gly Lys
 65 70 75 80
 His Gln Trp Asn Val Ala Ile Val Thr Gly Ala Arg Asp Gly Asp Glu
 85 90 95
 Ala Arg His Xaa Ser His Glu Gly
 100

<210> 1011
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1011
 ctgcagaaaa ggaggggggt cccatgccaa ggcagaactg tctgggacag acgctgccccg
 60
 gatccctgcg gctgcctgca ctctggacca cgagctctga gagcagcagg ttgagggccg
 120
 gtgggcagca gctcggaggc tccgcgaggt gcaggagacg caggcatggc cggtgagctg
 180
 actcctgagg aggaggccca gtacaaaaag gcttttctccg cggttgacac ggatggaaa
 240
 ggcaccatca atgcccagga gctgggcgcg gcgctgaagg ccacgggcaa gaacctctcg
 300
 gagggcccagc taaagaaact catctccgag
 330

<210> 1012

<211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1012
 Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala
 1 5 10 15
 Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu
 20 25 30
 Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln
 35 40 45
 Leu Lys Lys Leu Ile Ser Glu
 50 55

<210> 1013
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 1013
 nacttgacaca tcgtggtggc gtcgctgcgt gcggcactga caatgtgact ggcgcatctc
 60
 tgggggcgctc tcctcgctgc cgaggagcggc gaggaaggat taacgatgac cagcgacgctc
 120
 cccgggattg gctcgaacgc cgccactttg gcgcggtccc aggctcgag tgacaaggctc
 180
 gaggtgatt tggcgtcca tcccgacaag tggcgcatctc tgggggggga cgtcctact
 240
 ggcagcctgc acatcggtca ctacttcggg tcgctggcga atcggttacg cgtgcagaac
 300
 aagggcattg agtctttcct tgcgctcgt gactaccagg ttatctatga ccgcgggggg
 360
 ggtggtgacc tgcaggccaa tggtatgtcg aatgtcgccg attacctggc aatcggcatt
 420
 gacccaacgc gt
 432

<210> 1014
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1014
 Met Thr Ser Asp Val Pro Gly Ile Gly Ser Asn Ala Ala Thr Leu Ala
 1 5 10 15
 Arg Ser Gln Ala Arg Ser Asp Lys Val Glu Ala Asp Leu Ala Val His
 20 25 30
 Pro Asp Lys Trp Arg Ile Leu Gly Gly Asp Arg Pro Thr Gly Ser Leu
 35 40 45
 His Ile Gly His Tyr Phe Gly Ser Leu Ala Asn Arg Val Arg Val Gln
 50 55 60
 Asn Lys Gly Ile Glu Ser Phe Leu Val Val Ala Asp Tyr Gln Val Ile
 65 70 75 80
 Tyr Asp Arg Gly Gly Gly Gly Asp Leu Gln Ala Asn Val Met Ser Asn

85 90 95
 Val Ala Asp Tyr Leu Ala Ile Gly Ile Asp Pro Thr Arg
 100 105

<210> 1015
 <211> 467
 <212> DNA
 <213> Homo sapiens

<400> 1015
 nngaattcga tggctgtgaa aggtcgagct ctttaagtgtt ttcatatccc ctgtgtgggt
 60
 gaaaacttcc cgatgaaagc ggcacacggtt gaagagctga aagaattgga aagagtttta
 120
 cagcaaaaga agattgaagc agagtgtcctt aaactacgga aggaaattgt agaggctcag
 180
 tctggagtta agttgattaa acagcgtcat gaagaggatg atgaagaaga ggaagaggaa
 240
 gacaagacag taaaatatag caatttgccc aattacctgc ttggtagtct gagtactgat
 300
 tttggggtag atacctcttt attgtcaagc caattggagc ttcattccag agaagagaaa
 360
 atcaacaaaa ttatattatt gaaagatatc atttacaagg taaaaactgt tttcaataat
 420
 gagtttgacg ctgcatataa acaaaaagag tttgaaattg cacgcgt
 467

<210> 1016
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 1016
 Xaa Asn Ser Met Ala Val Lys Gly Arg Ala Leu Lys Cys Phe His Ile
 1 5 10 15
 Pro Cys Val Val Glu Asn Phe Pro Met Lys Ala Arg Thr Val Glu Glu
 20 25 30
 Leu Lys Glu Leu Glu Arg Val Leu Gln Gln Lys Lys Ile Glu Ala Glu
 35 40 45
 Cys Leu Lys Leu Arg Lys Glu Ile Val Glu Ala Gln Ser Gly Val Lys
 50 55 60
 Leu Ile Lys Gln Arg His Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu
 65 70 75 80
 Asp Lys Thr Val Lys Tyr Ser Asn Leu Pro Asn Tyr Leu Leu Gly Ser
 85 90 95
 Leu Ser Thr Asp Phe Gly Val Asp Thr Ser Leu Leu Ser Ser Gln Leu
 100 105 110
 Glu Leu His Ser Arg Glu Glu Lys Ile Asn Gln Ile Ile Leu Leu Lys
 115 120 125
 Asp Ile Ile Tyr Lys Val Lys Thr Val Phe Asn Asn Glu Phe Asp Ala
 130 135 140
 Ala Tyr Lys Gln Lys Glu Phe Glu Ile Ala Arg
 145 150 155

<210> 1017
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 1017
 acgcgtggct ggttgggtat gtggaaccat gtgcgcgcta atgagaagga tgcgaagggg
 60
 aacattaaag tgggtcgccc cggctacttt gcgagggtca tggatttcta tgcgcattat
 120
 ctgaaggggtg cggttaccog tttccgtccg aattttattg tgcaggataa tacgggcccgt
 180
 tggcgtgttc agtcgtcgtg gccgcagccg aatcgcactg ttacttttgc gggaccccgc
 240
 ggcattgtcc gctacggtac gacgttggcg gccgcacgc atgggaatgg tcaggctatt
 300
 ccgcaggcgg atgcacagtc tcttaaccgc gagaa
 335

<210> 1018
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1018
 Met Trp Asn His Val Arg Ala Asn Glu Lys Asp Ala Lys Gly Asn Ile
 1 5 10 15
 Lys Val Gly Arg Pro Gly Tyr Phe Ala Glu Val Met Asp Phe Tyr Ala
 20 25 30
 His Tyr Leu Lys Gly Ala Val Thr Arg Phe Arg Pro Asn Phe Ile Val
 35 40 45
 Gln Asp Asn Thr Gly Arg Trp Arg Val Gln Ser Ser Trp Pro Gln Pro
 50 55 60
 Asn Arg Thr Val Thr Phe Ala Gly Pro Arg Gly Ile Val Arg Tyr Gly
 65 70 75 80
 Thr Thr Leu Ala Ala Arg Thr His Gly Asn Gly Gln Ala Ile Pro Gln
 85 90 95
 Ala Asp Ala Gln Ser Leu Asn Arg Glu
 100 105

<210> 1019
 <211> 454
 <212> DNA
 <213> Homo sapiens

<400> 1019
 acgcgtgaag gggtagtcgt agtagaagtc gtccacaaac acgggccccg gcagggtccag
 60
 ctctggagcc tctctctcaa tggcgttgcc catggtgcct ggcttgggtg atgaggcggg
 120
 tgaagggcgt ggggccaggt ggtgcgggat gaagtcagcc tcgttgaaga gtcgtggct
 180
 ggaggagccg ctgcctgagc cttcagggcc cagtgtgccc aggggccacc gacagagtgg
 240

cagagagcag gtgacttcct ggcaactgcgg agcgaggacc cggagaagta cttcctcaat
 300
 ggtggctgga ccatccagtg gaacggggac taccaggtgg cagggaccac cttcacatac
 360
 gcacgcaggg gcaactggga gaacctcacg tccccgggtc ccaccaagga gcctgtctgg
 420
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 454

<210> 1020

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1020

Met	Ala	Leu	Pro	Met	Val	Pro	Gly	Leu	Gly	Asp	Glu	Ala	Gly	Glu	Gly
1				5				10						15	
Arg	Gly	Ala	Arg	Trp	Cys	Gly	Met	Lys	Ser	Ala	Ser	Leu	Lys	Ser	Ser
			20					25					30		
Trp	Leu	Glu	Pro	Leu	Pro	Glu	Pro	Ser	Gly	Pro	Ser	Val	Pro	Arg	
	35					40					45				
Gly	His	Arg	Gln	Ser	Gly	Arg	Glu	Gln	Val	Thr	Ser	Trp	His	Cys	Gly
	50					55					60				
Ala	Arg	Thr	Arg	Arg	Ser	Thr	Ser	Ser	Met	Val	Ala	Gly	Pro	Ser	Ser
65					70					75				80	
Gly	Thr	Gly	Thr	Thr	Arg	Trp	Gln	Gly	Pro	Pro	Ser	His	Thr	His	Ala
				85					90					95	
Gly	Ala	Thr	Gly	Arg	Thr	Ser	Arg	Pro	Arg	Val	Pro	Pro	Arg	Ser	Leu
			100					105					110		
Ser	Gly	Ser	Ser	Cys	Cys	Ser	Arg	Arg	Ala	Thr	Leu	Gly			
			115				120					125			

<210> 1021

<211> 366

<212> DNA

<213> Homo sapiens

<400> 1021

cagctgtgtc gtgacctcct gtagaccaga gagaggtaga gcatgaaaaa tgctcattga
 60
 gccgagatta tctgacagga ccaaagcata taaagttgac tgaagcagga gcaaacacgc
 120
 tggttgaggg tcaagtgtg gggcagcagc aacaacaaac caaaaaaag ccctttgaac
 180
 tcccttaatg ttgccaaaag gttctggtag agaacaagtc acatgcctaa gaaggtcttt
 240
 taaagggcac tcttgagtt tcagcatttg gtccggggaa ttgcacaagg ctctgcttaa
 300
 atgcagagct ctttctagca tcttcatatt caaggcggaa aaactgagct tggcgaggaa
 360
 ccctgt
 366

<210> 1022

<211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1022
 Met Lys Met Leu Glu Arg Ala Leu His Leu Ser Arg Ala Leu Cys Asn
 1 5 10 15
 Ser Pro Asp Gln Met Leu Lys Leu Gln Glu Cys Pro Leu Lys Asp Leu
 20 25 30
 Leu Arg His Val Thr Cys Ser Leu Pro Glu Pro Leu Gly Asn Ile Lys
 35 40 45
 Gly Val Gln Arg Ala Phe Phe Trp Phe Val Val Ala Ala Pro Ala
 50 55 60
 Leu Asp Pro Gln Pro Ala Cys Leu Leu Leu Leu Gln Ser Thr Leu Tyr
 65 70 75 80
 Ala Leu Val Leu Ser Asp Asn Leu Gly Ser Met Ser Ile Phe His Ala
 85 90 95
 Leu Pro Leu Ser Gly Leu Gln Glu Val Thr Thr Gln Leu
 100 105

<210> 1023
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1023
 gccgggcttc gggctctctga agcgatcaac ctggccgact cggatgcaga tctggacggc
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 ggcatcctga ccatacagca gaccaagttt ggcaagtccc gcatgggtgcc gctacacccc
 120
 agcgtgatcg gtccgatggc agcctaccgg gccttgccgc gccagtacgt gcctgcgaag
 180
 ccgcagatga cattcttcgt gggctcgcgt ggcgtgcacc ggggtgaacc gctgggagat
 240
 aggcaggtgc atcgagtgtt ctgtcagctg cgcgagcaat tgggttgat cgatcgcggc
 300
 ggccatggcc gaccgcgggt gcatgacctg cgccatagct tcgccgtgag acggatgatc
 360
 ctgtggcacc agcagggagc gaaccttgac caacgaatgc tggccctgtc cacgtacatg
 420
 ggccac
 426

<210> 1024
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 1024
 Ala Gly Leu Arg Val Ser Glu Ala Ile Asn Leu Ala Asp Ser Asp Ala
 1 5 10 15
 Asp Leu Asp Gly Gly Ile Leu Thr Ile Gln Gln Thr Lys Phe Gly Lys
 20 25 30
 Ser Arg Met Val Pro Leu His Pro Ser Val Ile Gly Pro Met Ala Ala

```

      35          40          45
Tyr Arg Ala Leu Arg Arg Gln Tyr Val Pro Ala Lys Pro Gln Met Thr
  50          55          60
Phe Phe Val Gly Ser Arg Gly Val His Arg Gly Glu Pro Leu Gly Asp
  65          70          75          80
Arg Gln Val His Arg Val Phe Cys Gln Leu Arg Glu Gln Leu Gly Trp
      85          90          95
Ile Asp Arg Gly Gly His Gly Arg Pro Arg Val His Asp Leu Arg His
      100          105          110
Ser Phe Ala Val Arg Arg Met Ile Leu Trp His Gln Gln Gly Ala Asn
      115          120          125
Leu Asp Gln Arg Met Leu Ala Leu Ser Thr Tyr Met Gly His
      130          135          140

```

<210> 1025

<211> 518

<212> DNA

<213> Homo sapiens

<400> 1025

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naccgctgggt gcgcgcaggt ggccgccggg tccctttgct ccctgcgcaa gccggagggg
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tgcccagaag gctaccacta gcctcagcga aggggtgcgcc ctgagagccg ggtagcctcg
  120
gatagcggcg ctgcgtacgc gatgatggat gagccgtgggt gggaagggcg cgtcgccctcg
  180
gacgtccact gcaccctgcg cgagaaggaa ctgaagctgc ccaccttccg agccactcc
  240
ccactcctga agagccgcgc gttcttcgtg gacatcctga ccctgctgag cagccactgc
  300
cagctctgcc ctgcagcccg gcacctggcc gtctacctgc tggaccactt catggatcgc
  360
tacaacgtca ccacctccaa gcagctctac accgtggccg tctcctgcct cctgcttgca
  420
agtaagtctg aggatcggga agaccacgtc cccaagtggg agcaaataaa cagcacgagg
  480
atcctgagca gccagaactt caccctcacc aagaagga
  518

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<210> 1026

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1026

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Met Met Asp Glu Pro Trp Trp Glu Gly Arg Val Ala Ser Asp Val His
  1          5          10          15
Cys Thr Leu Arg Glu Lys Glu Leu Lys Leu Pro Thr Phe Arg Ala His
      20          25          30
Ser Pro Leu Leu Lys Ser Arg Arg Phe Phe Val Asp Ile Leu Thr Leu
      35          40          45
Leu Ser Ser His Cys Gln Leu Cys Pro Ala Ala Arg His Leu Ala Val
      50          55          60
Tyr Leu Leu Asp His Phe Met Asp Arg Tyr Asn Val Thr Thr Ser Lys

```

65					70					75				80
Gln	Leu	Tyr	Thr	Val	Ala	Val	Ser	Cys	Leu	Leu	Leu	Ala	Ser	Lys Phe
				85					90					95
Glu	Asp	Arg	Glu	Asp	His	Val	Pro	Lys	Leu	Glu	Gln	Ile	Asn	Ser Thr
			100					105					110	
Arg	Ile	Leu	Ser	Ser	Gln	Asn	Phe	Thr	Leu	Thr	Lys	Lys		
		115					120					125		

<210> 1027

<211> 465

<212> DNA

<213> Homo sapiens

<400> 1027

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ggcccaaaag tcatcaaaga aaagctgaca caggagctga aggaccacaa cgccaccagc
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atcctgcagc agctgccgct gctcaaggcc atgcgggaaa agccagccgg aggcattccct
120
gtgctgggca gcctggtgaa caccngtcct gaagcacatc atnnctggct gaaggtcatc
180
acagctaaca tcctccagct gcaggtgaag ccctcggcca atgaccagga gctgctagtc
240
aagatcccc tggacatggt ggctggattc aacacgcccc tggtaagac catcgtggag
300
ttccacatga cgactgaggc ccaagccacc atccgcatgg acaccagtgc aagtggcccc
360
accgcctgg tcctcagtga ctgtgccacc agccatggga gcctgcgcat ccaactgctg
420
cataagctct ccttcaagct gaacgcctca gctaagcagg tcatg
465

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<210> 1028

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1028

Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	Asp	His
1				5				10					15		
Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Lys	Ala	Met	Arg
			20				25					30			
Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	Leu	Val	Asn	Thr
		35				40					45				
Xaa	Pro	Glu	Ala	His	His	Xaa	Trp	Leu	Lys	Val	Ile	Thr	Ala	Asn	Ile
	50				55					60					
Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	Gln	Glu	Leu	Leu	Val
65				70				75						80	
Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	Asn	Thr	Pro	Leu	Val	Lys
			85					90					95		
Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	Glu	Ala	Gln	Ala	Thr	Ile	Arg
		100					105					110			
Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys
		115				120					125				
Ala	Thr	Ser	His	Gly	Ser	Leu	Arg	Ile	Gln	Leu	Leu	His	Lys	Leu	Ser

130 135 140
Phe Lys Leu Asn Ala Ser Ala Lys Gln Val Met
145 150 155

<210> 1029

<211> 479

<212> DNA

<213> Homo sapiens

<400> 1029

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caagcactgg ccacaaatgc ctggcagaac aactgctcat aagtgtgtag ttgttggtat
120
tattactaac caagtgagga aaattatccc tagcaggtcc agatgaccgt gtgcatgaat
180
cacagggaga ccctaaagga tttcctcctg taaagctctt tccccaccta tttgctactg
240
cctgaaattg ctttagcagg aacagaatc tctcatgccca caagtgagca taaagtttaa
300
aatgtaaatg ctctaggaaa aggcaactca tctcttaaata tctctccaag gttcaaatcc
360
tttccaaaga ggaggctttt gtataagtca gaaggcccag tccctgaagg tcatggaaaa
420
ggatcatgaca cacggagggg gtgtcaaagg gagactggga aactgaagat gaagctagc
479

<210> 1030

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1030

Met	Ser	Cys	Leu	Phe	Leu	Glu	His	Leu	His	Phe	Lys	Leu	Tyr	Ala	His
1				5					10					15	
Leu	Trp	His	Glu	Arg	Phe	Cys	Phe	Leu	Leu	Lys	Gln	Phe	Gln	Ala	Val
		20						25					30		
Ala	Asn	Arg	Trp	Gly	Lys	Ser	Phe	Thr	Gly	Gly	Asn	Pro	Leu	Gly	Ser
		35					40					45			
Pro	Cys	Asp	Ser	Cys	Thr	Arg	Ser	Ser	Gly	Pro	Ala	Arg	Asp	Asn	Phe
		50				55					60				
Pro	His	Leu	Val	Ser	Asn	Asn	Asn	Asn	Asn	Tyr	Thr	Leu	Met	Ser	Ser
		65			70					75				80	
Cys	Ser	Ala	Arg	His	Leu	Trp	Pro	Val	Leu	Gly	Arg	Gln	Tyr	Leu	Phe
				85					90					95	
Glu	Pro	Ser	His	Ser	Ser	Val	Arg	Thr	Val	Ser	Leu	His	Ala		
				100					105					110	

<210> 1031

<211> 322

<212> DNA

<213> Homo sapiens

<400> 1031

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 120
 atcgacggcg aaaccgatgt acccgaccgg gcatccaggg cgcaagccaa cgatgtgcat
 180
 ggggtggagcg tcgtcgtcga cccgctcgcc tatcaatggc gacaccctaa ctggcaaggc
 240
 cgcccctggc atgaggcggg gatttacgag ctgcacgttg gcgtactggg cgggtacgcc
 300
 gctgttgaac agcaactgcc gc
 322

<210> 1032

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1032

Xaa	Ala	Phe	Tyr	Val	Ser	Val	Glu	Leu	Glu	Asp	Gly	Lys	Ser	Ile	Ala
1				5					10					15	
Met	Leu	Pro	Gln	Ala	Asp	Gly	Trp	Phe	Glu	Val	Glu	Val	Lys	Cys	Pro
			20					25					30		
Ala	Gly	Thr	His	Tyr	Arg	Tyr	Asn	Ile	Asp	Gly	Glu	Thr	Asp	Val	Pro
		35					40					45			
Asp	Pro	Ala	Ser	Arg	Ala	Gln	Ala	Asn	Asp	Val	His	Gly	Trp	Ser	Val
	50					55					60				
Val	Val	Asp	Pro	Leu	Ala	Tyr	Gln	Trp	Arg	His	Pro	Asn	Trp	Gln	Gly
65					70					75				80	
Arg	Pro	Trp	His	Glu	Ala	Val	Ile	Tyr	Glu	Leu	His	Val	Gly	Val	Leu
			85						90					95	
Gly	Gly	Tyr	Ala	Ala	Val	Glu	Gln	Gln	Leu	Pro					
			100					105							

<210> 1033

<211> 579

<212> DNA

<213> Homo sapiens

<400> 1033

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 60
 acagcgccaa ggggtgtgag gagggccctt cgcggggtcac ggatagggtcc aagggtggcac
 120
 aattcacatt caaatccatc acttttcaca taattgctgt taatatgaac gtcattgagtc
 180
 gttgttgctc gcggttgca gtgggactcc ccatacacgg cagcgagaca tggaggaacc
 240
 atgggactaa ggatcgttgt cgccgctgat ccggcggcag tcgagtacaa ggatgtcgtc
 300
 aaggctgacc tggaagcgga ttcgcgagtc gatgacgtta tcgacgtcgg cggttcaggct
 360
 ggtgacgaca ccctctaccc gcgcacggc atcaaggagg ctcacgtcat caaggacgga
 420

aaagccgatc gaggaatctt tttctgcggc accgggatgg gcatggccat cacggccaac
 480
 aaggtgccag gcattcgcgc ctgcaccgcc cactactcct tctccgtaga gcggctcatc
 540
 atgtccaacg acgcccacgt gctatgcctc ggccaacgc
 579

<210> 1034
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1034
 Met Gly Leu Arg Ile Val Val Ala Ala Asp Pro Ala Ala Val Glu Tyr
 1 5 10 15
 Lys Asp Val Val Lys Ala Asp Leu Glu Ala Asp Ser Arg Val Asp Asp
 20 25 30
 Val Ile Asp Val Gly Val Gln Ala Gly Asp Asp Thr Leu Tyr Pro Arg
 35 40 45
 Ile Gly Ile Lys Gly Ala His Val Ile Lys Asp Gly Lys Ala Asp Arg
 50 55 60
 Gly Ile Phe Phe Cys Gly Thr Gly Met Gly Met Ala Ile Thr Ala Asn
 65 70 75 80
 Lys Val Pro Gly Ile Arg Ala Cys Thr Ala His Asp Ser Phe Ser Val
 85 90 95
 Glu Arg Leu Ile Met Ser Asn Asp Ala His Val Leu Cys Leu Gly Gln
 100 105 110
 Arg

<210> 1035
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 1035
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 gtgtgtatan gaatgtgtgt atgtgtantg gaatgtgtgt gtgtantgga agctgtgtgc
 120
 atatgtnaat gtctgtgtgc atgtacngga atgtgcgcgt gtatggaatg tatctgtgta
 180
 tgtgtatgga ccgtttgtgt gattatgcaa tatgtccgtg tgtgcgtatg gagtgtctca
 240
 gtatggcatg tgtgtgtgta tctactgtgc gtctctgtgt gtgtantgac atgcatatgt
 300
 atagaaagcg tctgcgctgt gtgcatgtgt gtcagtatcg aacgagtcgg agatgtggta
 360
 atn
 363

<210> 1036
 <211> 121
 <212> PRT

<213> Homo sapiens

<400> 1036

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Xaa Ala Cys Asn Val Cys Val Cys Met Xaa Pro Cys Leu Cys Val Cys
 1           5           10           15
Met Xaa Ile Cys Val Cys Ile Xaa Met Cys Val Cys Val Xaa Glu Cys
      20           25           30
Val Cys Val Xaa Glu Ala Val Cys Ile Cys Xaa Cys Leu Cys Ala Cys
      35           40           45
Thr Xaa Met Cys Ala Cys Met Glu Cys Ile Cys Val Cys Val Trp Thr
      50           55           60
Val Cys Val Ile Met Gln Tyr Val Arg Val Cys Val Trp Ser Val Ser
65           70           75           80
Val Trp His Val Cys Val Tyr Leu Leu Cys Val Ser Val Cys Val Xaa
      85           90           95
Thr Cys Ile Cys Ile Glu Ser Val Cys Ala Val Cys Met Cys Val Ser
      100          105          110
Ile Glu Arg Val Gly Asp Val Val Xaa
      115          120

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<210> 1037

<211> 5832

<212> DNA

<213> Homo sapiens

<400> 1037

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gggacttacg gtccacagat gagccagtat ggaccacaag gtaactactc cagacccccca
120
gcgtatagtg ggggtgcccag tgcaagctac agcgggccag ggcccgggtat gggatatcagt
180
gccaacaacc agatgcatgg acaagggcca agccagccat gtgggtgctgt gcccctggga
240
cgaatgccat cagctgggat gcagaacaga ccatttcctg gaaatatgag cagcatgacc
300
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360
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420
caaagcaggc aaggcagttt ccccgcatg aaccagagtg gacttatggc ttccagctct
480
ccctacagcc agcccatgaa caacagctct agcctgatga acacgcaggc gccgcctac
540
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600
tctcttggtg aatccaaaact gcccctgcct ctcaaagcag acggcaaaga agaaggcact
660
ccacagcccg agagcaagtc aaaggatagc tacagctctc agggatatttc tcagccccc
720
acccagggca acctgccagt cccttcccca atgtccccc gctctgctag catctctca
780
tttcatggag atgaaagtga tagcattagc agcccaggct ggccaaagac tccatcaagc
840

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cctaagtcca gctcctccac cactactggg gagaagatca cgaaggtgta cgagctgggg
 900
 aatgagccag agagaaagct ctgggtcgac cgatacctca ccttcatgga agagagaggc
 960
 tctcctgtct caagtctgcc tgccgtgggc aagaagcccc tggacctgtt ccgactctac
 1020
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 1080
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 1140
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 1200
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 1260
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 2460

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2520
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2580
aagattacct ccaaagatat cggtactcct gaggcgtggc gtgtgatgat gtcccttaaa
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2880
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3180
gacaccaccg agcacattca gactcacttt gagagcaaga tggaaattcc tcctcgcagg
3240
cgccacctc ccccttaag ctccgcaggc aagaagaaag agctggcagg caaaggcgac
3300
tctgaagagc agcaagagaa aagcatcata gcaaccattg atgacgtcct gtctgctcgg
3360
ccaggggcat tgccggaaga cgcaaacctt gggcccccaga ccgaaagcag taagtttccc
3420
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3480
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3540
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3660
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3720
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<211> 1485

<212> PRT

<213> Homo sapiens

<400> 1038

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Gln	Gly	Asn	Tyr	Ser	Arg	Pro	Pro	Ala	Tyr	Ser	Gly	Val	Pro	Ser	Ala
		35					40					45			
Ser	Tyr	Ser	Gly	Pro	Gly	Pro	Gly	Met	Gly	Ile	Ser	Ala	Asn	Asn	Gln
50						55					60				
Met	His	Gly	Gln	Gly	Pro	Ser	Gln	Pro	Cys	Gly	Ala	Val	Pro	Leu	Gly
65					70					75					80
Arg	Met	Pro	Ser	Ala	Gly	Met	Gln	Asn	Arg	Pro	Phe	Pro	Gly	Asn	Met
				85					90					95	
Ser	Ser	Met	Thr	Pro	Ser	Ser	Pro	Gly	Met	Ser	Gln	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Met	Gly	Pro	Pro	Met	Pro	Thr	Val	Asn	Arg	Lys	Ala	Gln	Glu	Ala
			115					120					125		
Ala	Ala	Ala	Val	Met	Gln	Ala	Ala	Ala	Asn	Ser	Ala	Gln	Ser	Arg	Gln
			130				135					140			
Gly	Ser	Phe	Pro	Gly	Met	Asn	Gln	Ser	Gly	Leu	Met	Ala	Ser	Ser	Ser
145					150					155					160
Pro	Tyr	Ser	Gln	Pro	Met	Asn	Asn	Ser	Ser	Ser	Leu	Met	Asn	Thr	Gln
				165					170					175	
Ala	Pro	Pro	Tyr	Ser	Met	Ala	Pro	Ala	Met	Val	Asn	Ser	Ser	Ala	Ala
			180					185					190		
Ser	Val	Gly	Leu	Ala	Asp	Met	Met	Ser	Pro	Gly	Glu	Ser	Lys	Leu	Pro
			195				200					205			
Leu	Pro	Leu	Lys	Ala	Asp	Gly	Lys	Glu	Glu	Gly	Thr	Pro	Gln	Pro	Glu
			210			215					220				
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225					230					235					240
Thr	Pro	Gly	Asn	Leu	Pro	Val	Pro	Ser	Pro	Met	Ser	Pro	Ser	Ser	Ala
				245					250					255	
Ser	Ile	Ser	Ser	Phe	His	Gly	Asp	Glu	Ser	Asp	Ser	Ile	Ser	Ser	Pro
				260				265					270		
Gly	Trp	Pro	Lys	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Ser	Ser	Ser	Thr	Thr
			275				280						285		
Thr	Gly	Glu	Lys	Ile	Thr	Lys	Val	Tyr	Glu	Leu	Gly	Asn	Glu	Pro	Glu
			290				295					300			
Arg	Lys	Leu	Trp	Val	Asp	Arg	Tyr	Leu	Thr	Phe	Met	Glu	Glu	Arg	Gly
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Thr Ser Ser Ser Ala Ala Ser Ser Leu Lys Lys Gln Tyr Ile Gln Tyr
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Leu Phe Ala Phe Glu Cys Lys Ile Glu Arg Gly Glu Glu Pro Pro Pro
385          390          395          400
Glu Val Phe Ser Thr Gly Asp Thr Lys Lys Gln Pro Lys Leu Gln Pro
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Pro Ser Pro Ala Asn Ser Gly Ser Leu Gln Gly Pro Gln Thr Pro Gln
          420          425          430
Ser Thr Gly Ser Asn Ser Met Ala Glu Val Pro Gly Asp Leu Lys Pro
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Pro Thr Pro Ala Ser Thr Pro His Gly Gln Met Thr Pro Met Gln Gly
          450          455          460
Gly Arg Ser Ser Thr Ile Ser Val His Asp Pro Phe Ser Asp Val Ser
465          470          475          480
Asp Ser Ser Phe Pro Lys Arg Asn Ser Met Thr Pro Asn Ala Pro Tyr
          485          490          495
Gln Gln Gly Met Ser Met Pro Asp Val Met Gly Arg Met Pro Tyr Glu
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Pro Asn Lys Asp Pro Phe Gly Gly Met Arg Lys Val Pro Gly Ser Ser
          515          520          525
Glu Pro Phe Met Thr Gln Gly Gln Met Pro Asn Ser Ser Met Gln Asp
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Met Tyr Asn Gln Ser Pro Ser Gly Ala Met Ser Asn Leu Gly Met Gly
545          550          555          560
Gln Arg Gln Gln Phe Pro Tyr Gly Ala Ser Tyr Asp Arg Arg His Glu
          565          570          575
Pro Tyr Gly Gln Gln Tyr Pro Gly Gln Gly Pro Pro Ser Gly Gln Pro
          580          585          590
Pro Tyr Gly Gly His Gln Pro Gly Leu Tyr Pro Gln Gln Pro Asn Tyr
          595          600          605
Lys Arg His Met Asp Gly Met Tyr Gly Pro Pro Ala Lys Arg His Glu
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Gly Asp Met Tyr Asn Met Gln Tyr Ser Ser Gln Gln Gln Glu Met Tyr
625          630          635          640
Asn Gln Tyr Gly Gly Ser Tyr Ser Gly Pro Asp Arg Arg Pro Ile Gln
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Gly Gln Tyr Pro Tyr Pro Tyr Ser Arg Glu Arg Met Gln Gly Pro Gly
          660          665          670
Gln Ile Gln Thr His Gly Ile Pro Leu Gln Met Met Gly Gly Pro Leu
          675          680          685
Gln Ser Ser Ser Ser Glu Gly Pro Gln Gln Asn Met Trp Ala Ala Arg
          690          695          700
Asn Asp Met Pro Tyr Pro Tyr Gln Asn Arg Gln Gly Pro Gly Gly Pro
705          710          715          720
Thr Gln Ala Pro Pro Tyr Pro Gly Met Asn Arg Thr Asp Asp Met Met
          725          730          735
Val Pro Asp Gln Arg Ile Asn His Glu Ser Gln Trp Pro Ser His Val
          740          745          750
Ser Gln Arg Gln Pro Tyr Met Ser Ser Ser Ala Ser Met Gln Pro Ile

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770	775	780
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785	790	795
Asn Arg Met Ser Pro Ser Lys Ser Pro Phe Leu Pro Ser Met Lys Met		800
	805	810
Gln Lys Val Met Pro Thr Val Pro Thr Ser Gln Val Thr Gly Pro Pro		815
	820	825
Pro Gln Pro Pro Pro Ile Arg Arg Glu Ile Thr Phe Pro Pro Gly Ser		830
	835	840
Val Glu Ala Ser Gln Pro Val Leu Lys Gln Arg Arg Lys Ile Thr Ser		845
	850	855
Lys Asp Ile Val Thr Pro Glu Ala Trp Arg Val Met Met Ser Leu Lys		860
865	870	875
Ser Gly Leu Leu Ala Glu Ser Thr Trp Ala Leu Asp Thr Ile Asn Ile		880
	885	890
Leu Leu Tyr Asp Asp Ser Thr Val Ala Thr Phe Asn Leu Ser Gln Leu		895
	900	905
Ser Gly Phe Leu Glu Leu Leu Val Glu Tyr Phe Arg Lys Cys Leu Ile		910
	915	920
Asp Ile Phe Gly Ile Leu Met Glu Tyr Glu Val Gly Asp Pro Ser Gln		925
	930	935
Lys Ala Leu Asp His Asn Ala Ala Arg Lys Asp Asp Ser Gln Ser Leu		940
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Ala Asp Asp Ser Gly Lys Glu Glu Glu Asp Ala Glu Cys Ile Asp Asp		960
	965	970
Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu Asp Ser Glu Lys Thr Glu		975
	980	985
Ser Asp Glu Lys Ser Ser Ile Ala Leu Thr Ala Pro Asp Ala Ala Ala		990
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Asp Pro Lys Glu Lys Pro Lys Gln Ala Ser Lys Phe Asp Lys Leu Pro		1005
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Ile Lys Ile Val Lys Lys Asn Asn Leu Phe Val Val Asp Arg Ser Asp		1020
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Leu Gly Gly Gly Asp Thr Thr Glu His Ile Gln Thr His Phe Glu Ser		1055
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	1090	1095
Gln Glu Lys Ser Ile Ile Ala Thr Ile Asp Asp Val Leu Ser Ala Arg		1100
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Pro Gly Ala Leu Pro Glu Asp Ala Asn Pro Gly Pro Gln Thr Glu Ser		1120
	1125	1130
Ser Lys Phe Pro Phe Gly Ile Gln Gln Ala Lys Ser His Arg Asn Ile		1135
	1140	1145
Lys Leu Leu Glu Asp Glu Pro Arg Ser Arg Asp Glu Thr Pro Leu Cys		1150
	1155	1160
Thr Ile Ala His Trp Gln Asp Ser Leu Ala Lys Arg Cys Ile Cys Val		1165
	1170	1175
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 Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro Gln Thr Tyr Glu
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 Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser Lys Asp Glu Trp
 1235 1240 1245
 Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr Leu Val Thr Leu
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 1285 1290 1295
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 Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly Asp Arg Lys Asn
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 Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser Asn Leu Ala Gln
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 Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile
 1380 1385 1390
 Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr Met Ala Gln Tyr
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<211> 379

<212> DNA

<213> Homo sapiens

<400> 1039

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